

178157

STIC-Biotech/ChemLib

From: Whiteman, Brian  
Sent: Tuesday, January 31, 2006 1:19 PM  
To: STIC-Biotech/ChemLib  
Subject: seq search

10/800,256

SEQ ID NO: 1  
us patents and published us patent applications

Thank you,

Brian Whiteman  
Remsen, 2D14  
mail box 2C18  
Patent Examiner - Art Unit 1635  
United States Patent and Trademark Office  
(571) 272-0764

RECEIVED  
JAN 31 2006  
STIC

\*\*\*\*\*  
Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

***This Page Blank (uspio)***



FT intron (3075) . (3289)  
FT CDS (3290) . (4384)  
FT intron (4385) . (4543)  
FT CDS (4544) . (6205)  
FT intron (6206) . (6411)  
FT CDS (6412) . (8145)  
FT intron (8146) . (8380)  
FT CDS (8381) . (14955)  
FT intron (14956) . (15186) .

FEATURES  
source 1. 15186  
/organism="Newcastle disease virus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:11176"

ORIGIN

Query Match 99.9%; Score 3353.2; DB 6; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3353; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACCGGTGAAGATTCTGGATCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60  
Db 4498 ACCGGTGAAGATTCTGGATCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 4557  
QY 61 TTCTACCAAGAACCCAGCACCTATGATGCTGATCTATCCGGGTTGGCTGGCACTGAGTTG 120  
Db 4558 TTCTACCAAGAACCCAGCACCTATGATGCTGATCTATCCGGGTTGGCTGGCACTGAGTTG 4617  
QY 121 CATCTGTCGGGCAAACTCCATTTGATGGCAGCCCTTGCAGCTGCGAGAAATTGGTTAC 180  
Db 4618 CATCTGTCGGGCAAACTCCATTTGATGGCAGCCCTTGCAGCTGCGAGAAATTGGTTAC 4677  
QY 181 AGGAGCAAAAGCCGTCACATATACCTCATCCAGACAGATCAATAGTTAAAGCT 240  
Db 4678 AGGAGCAAAAGCCGTCACATATACCTCATCCAGACAGATCAATAGTTAAAGCT 4737  
QY 241 CTTCCGGAATCTGCGCAAGATTAAGAGGCATGTGCGAAAGCCCTTGGATGCAATCAA 300  
Db 4738 CTTCCGGAATCTGCGCAAGATTAAGAGGCATGTGCGAAAGCCCTTGGATGCAATCAA 4797  
QY 301 CAGGACATTGACCACTTTTGTCTCACCCCTTGTGATCTTATCCGTAGATACAAAGATC 360  
Db 4798 CAGGACATTGACCACTTTTGTCTCACCCCTTGTGATCTTATCCGTAGATACAAAGATC 4857  
QY 361 TGTGACATCACTTGAGAGGGGAGAGACAGGGGCGCCTTATAGGCGCCATTATTTGGCGTGT 420  
Db 4858 TGTGACATCACTTGAGAGGGGAGAGACAGGGGCGCCTTATAGGCGCCATTATTTGGCGTGT 4917  
QY 421 GGCCTTTGGGGTTGCAACTGCGCGCAAAATTAACGCGCGCGAGCTTGATACAAGCCAA 480  
Db 4918 GGCCTTTGGGGTTGCAACTGCGCGCAAAATTAACGCGCGCGAGCTTGATACAAGCCAA 4977  
QY 481 ACAAATATGCTGCGCAACATCTCTCCGACTTTAAAGAGCATTTGCCGCAACCATAGGGTGT 540  
Db 4978 ACAAATATGCTGCGCAACATCTCTCCGACTTTAAAGAGCATTTGCCGCAACCATAGGGTGT 5037  
QY 541 GCATGAGGTCACTGACGGATTATGCAACTAGCAGTGGCAGTTGGGAAATGACAGATT 600  
Db 5038 GCATGAGGTCACTGACGGATTATGCAACTAGCAGTGGCAGTTGGGAAATGACAGATT 5097  
QY 601 TGTAAATGACCAATTTAATAAAGAGCTCAGAAATTAAGACTGATCAAAATTTGCACACA 660  
Db 5098 TGTAAATGACCAATTTAATAAAGAGCTCAGAAATTAAGACTGATCAAAATTTGCACACA 5157  
QY 661 AGTTGGTGTAGAGCTCAACCTGTACTTAACCGAATTGACTACATATTTGGACCAAAAT 720  
Db 5158 AGTTGGTGTAGAGCTCAACCTGTACTTAACCGAATTGACTACATATTTGGACCAAAAT 5217  
QY 721 CACTTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGGAAA 780  
Db 5218 CACTTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGGAAA 5277  
QY 781 TATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840

Db 5278 TATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATCGG 5337  
QY 841 TACCGGCTTAATGACCGGTAAACCTATTTCTATACGACTCAACAGACTCAACTTGGGTAT 900  
Db 5338 TACCGGCTTAATGACCGGTAAACCTATTTCTATACGACTCAACAGACTCAACTTGGGTAT 5397  
QY 901 ACAAGTAACTCTACCTTCACTCGGGAACCTAAATTAATGCGTGGCCACTTACTTGGAAAC 960  
Db 5398 ACAAGTAACTCTACCTTCACTCGGGAACCTAAATTAATGCGTGGCCACTTACTTGGAAAC 5457  
QY 961 CTTATCCGTAAAGACAAACGAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGGTGACACA 1020  
Db 5458 CTTATCCGTAAAGACAAACGAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGGTGACACA 5517  
QY 1021 GGTGCGTTCTGTATGAGAAAGCTTGACACCTGATCTGTATAGAACTGACTTGAATTT 1080  
Db 5518 GGTGCGTTCTGTATGAGAAAGCTTGACACCTGATCTGTATAGAACTGACTTGAATTT 5577  
QY 1081 ATAATTGACAAAGATTAAGTAAAGTTCCCTATGTCCTCGGTATTTATTCCTGCTTGAACGG 1140  
Db 5578 ATAATTGACAAAGATTAAGTAAAGTTCCCTATGTCCTCGGTATTTATTCCTGCTTGAACGG 5637  
QY 1141 CAATAGCTCGGCTGTATGTAATCAAAAGACGAGGCGCACTTAACACATACATGAC 1200  
Db 5638 CAATAGCTCGGCTGTATGTAATCAAAAGACGAGGCGCACTTAACACATACATGAC 5697  
QY 1201 TATCAAAAGTTCACTCATCCGCAACTGCAAGATGACAAACATGTAGATGTGTAAACCCCC 1260  
Db 5698 TATCAAAAGTTCACTCATCCGCAACTGCAAGATGACAAACATGTAGATGTGTAAACCCCC 5757  
QY 1261 GGGTATCATATGCGAAACATATGAGAGCCGTGTCTTAATAGATTAACATATGAGCA 1320  
Db 5758 GGGTATCATATGCGAAACATATGAGAGCCGTGTCTTAATAGATTAACATATGAGCA 5817  
QY 1321 TGTTTATCCTTATGGGGGGAATACTTAAGGCTCAGTGGGGAATTCGATGTAACCTATCA 1380  
Db 5818 TGTTTATCCTTATGGGGGGAATACTTAAGGCTCAGTGGGGAATTCGATGTAACCTATCA 5877  
QY 1381 GAAGAAATATCTCAATACAAAGATTCTCAAGTAAATTAACAGGCAATCTTGATATCTCAAC 1440  
Db 5878 GAAGAAATATCTCAATACAAAGATTCTCAAGTAAATTAACAGGCAATCTTGATATCTCAAC 5937  
QY 1441 TGAAGTTGGGAATGTCACAACTCGATCACTGAATGCTTGAATATGTTAGAGAAAGCAA 1500  
Db 5938 TGAAGTTGGGAATGTCACAACTCGATCACTGAATGCTTGAATATGTTAGAGAAAGCAA 5997  
QY 1501 CAGAAAATAGCAAAAGTCAATGTCAAACGACTAGACATCTGCTCTCATATCTATAT 1560  
Db 5998 CAGAAAATAGCAAAAGTCAATGTCAAACGACTAGACATCTGCTCTCATATCTATAT 6057  
QY 1561 CGTTTGACTATCATATCTCTTGTGTTTGGTATACCTTATGCTGATCTACATGCTACT 1620  
Db 6058 CGTTTGACTATCATATCTCTTGTGTTTGGTATACCTTATGCTGATCTACATGCTACT 6117  
QY 1621 AATGTACAAAGCAAAAGCGCGCAACAAAACCTTATTAATGCTTGGGATATATCTAGGA 6177  
Db 6118 AATGTACAAAGCAAAAGCGCGCAACAAAACCTTATTAATGCTTGGGATATATCTAGGA 6237  
QY 1681 TCGATGAGAGCCACTACAAATAATGGAACAAGTGAAGGAAGGAAGGTTCCCTAATAG 1740  
Db 6178 TCGATGAGAGCCACTACAAATAATGGAACAAGTGAAGGAAGGAAGGTTCCCTAATAG 6297  
QY 1741 TAATTTGTGAAAGATTCTGGTGTCTGTCACTTACAGAGATTAAAGAAAACTACCGGT 1800  
Db 6298 TAATTTGTGAAAGATTCTGGTGTCTGTCACTTACAGAGATTAAAGAAAACTACCGGT 6357  
QY 1801 TGTAGATGACCAAGAGCGATATACGGGTAGAAACGTTAAGAGAGCGCCCTCTCAATTGC 1860  
Db 6357 TGTAGATGACCAAGAGCGATATACGGGTAGAAACGTTAAGAGAGCGCCCTCTCAATTGC 6417  
QY 1861 GAGCGAGGCTTCAACACTCCGTTCTACCGCTTACCGGACAAAGCTCTCAATCAATGAGAC 1920



D 6358 GAGCAGGCTTCAACCTCCGTTCTACCGCTTACCGCAACAGTCTCATATGAGAC 6417  
Q 1921 CGCGCCGTTAGCCCAAGTTGCTTAGAGATGAGAAAGAGGCAAAAAATACAATGGCC 1980  
D 6418 CGCGCCGTTAGCCCAAGTTGCTTAGAGATGAGAAAGAGGCAAAAAATACAATGGCC 6477  
Q 1981 TTGATATTCGGGATTGCAATCTTATTTTAAAGTAGAGACCTTGGCTATATCTGTAGCC 2040  
D 6478 TTGATATTCGGGATTGCAATCTTATTTTAAAGTAGAGACCTTGGCTATATCTGTAGCC 6537  
Q 2041 TCCCTTTTATATACAGGGGGCTAGGACACCTAGCGATCTTTAGAGCATCCGACTAGG 2100  
D 6538 TCCCTTTTATATACAGGGGGCTAGGACACCTAGCGATCTTTAGAGCATCCGACTAGG 6597  
Q 2101 ATTTCCAGGCGAGAAAGAAAGATTACATCTACCTGGTTCATCAAGATAGTAGAT 2160  
D 6598 ATTTCCAGGCGAGAAAGAAAGATTACATCTACCTGGTTCATCAAGATAGTAGAT 6657  
Q 2161 AGGATATATAGCAAGTGGCCCTTGAAGTCTCCGTTGGCATTTTAAATATGAGACCA 2220  
D 6658 AGGATATATAGCAAGTGGCCCTTGAAGTCTCCGTTGGCATTTTAAATATGAGACCA 6717  
Q 2221 ATATGAAACGAAATACATCTCTCTTATGAGATTAAGAGCTGCAACAGAGTGG 2280  
D 6718 ATATGAAACGAAATACATCTCTCTTATGAGATTAAGAGCTGCAACAGAGTGG 6777  
Q 2281 TGGGGGCACTATTCATGACCCAGATTAATATAGGGGGATAGCAAAATCATTTGTA 2340  
D 6778 TGGGGGCACTATTCATGACCCAGATTAATATAGGGGGATAGCAAAATCATTTGTA 6837  
Q 2341 GATGATGCTAGTGAATGTCATCATATTCATCTCTGATTTCAAGAACATCTGAATTTT 2400  
D 6838 GATGATGCTAGTGAATGTCATCATATTCATCTCTGATTTCAAGAACATCTGAATTTT 6897  
Q 2401 ATCCCGGCGCTATACAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 2460  
D 6898 ATCCCGGCGCTATACAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 6957  
Q 2461 ACCCATTAAGTCTACCCATTAATGTAATTTGTCTGATGACAGATCATCTCATTTCA 2520  
D 6958 ACCCATTAAGTCTACCCATTAATGTAATTTGTCTGATGACAGATCATCTCATTTCA 7017  
Q 2521 TATCAGATTTAGGACCTTGTGTGCTCCGACATCTGCAACAGGAGGATTTCTTTTCT 2580  
D 7018 TATCAGATTTAGGACCTTGTGTGCTCCGACATCTGCAACAGGAGGATTTCTTTTCT 7077  
Q 2581 ACTTGTGCTTCACTCAACCTGAGACAGACCCAAATGCGAAGTCTTGTGATGTAGTGA 2640  
D 7078 ACTTGTGCTTCACTCAACCTGAGACAGACCCAAATGCGAAGTCTTGTGATGTAGTGA 7137  
Q 2641 ACTTGTGCTTCACTCAACCTGAGTGTGCTGAAAGTCAACGAGACAGAGAAAGATTAT 2700  
D 7138 ACTTGTGCTTCACTCAACCTGAGTGTGCTGAAAGTCAACGAGACAGAGAAAGATTAT 7197  
Q 2701 AACTCAGCTGTCTTACGCGGATGTACATGAGAGTTAGGGTTGACGCGCAGATACAC 2760  
D 7198 AACTCAGCTGTCTTACGCGGATGTACATGAGAGTTAGGGTTGACGCGCAGATACAC 7257  
Q 2761 GAAAGAGACCTAGTGTCAACATTTATTCGGGAGCTGGGTGCGCACTACCCAGAGTA 2820  
D 7258 GAAAGAGACCTAGTGTCAACATTTATTCGGGAGCTGGGTGCGCACTACCCAGAGTA 7317  
Q 2821 GGGGGTGGATCTTTATTTGAGCGGCGGTATGTTCTCAGTCTACGAGGGTTAAACCC 2880  
D 7318 GGGGGTGGATCTTTATTTGAGCGGCGGTATGTTCTCAGTCTACGAGGGTTAAACCC 7377  
Q 2881 AATTCAACCACTGACCTGTACAGAAAGGAAATATGTATATCAAGCATACATGAC 2940  
D 7378 AATTCAACCACTGACCTGTACAGAAAGGAAATATGTATATCAAGCATACATGAC 7437  
Q 2941 ACATGCCAGATGAGCAAGATCACTCAAGTTGAAATGGCCAAAGTCTTGTATAGCTTGA 3000  
D 7438 ACATGCCAGATGAGCAAGATCACTCAAGTTGAAATGGCCAAAGTCTTGTATAGCTTGA 7497

Q 3001 CGGTTGGTGGGAAACGCTACAGAGGCTATCTTATCTATCAAGGTCTCAATCTTA 3060  
D 7498 CGGTTGGTGGGAAACGCTACAGAGGCTATCTTATCTATCAAGGTCTCAATCTTA 7557  
Q 3061 GCGGAAAGCCCGGATCTGACCTGATCCGCCCAACAGTCAACATCATGGGGCGAAAGC 3120  
D 7558 GCGGAAAGCCCGGATCTGACCTGATCCGCCCAACAGTCAACATCATGGGGCGAAAGC 7617  
Q 3121 AGAATCTCAGAGGAGACATCTCATTTCTTGTATCAACAGAGGCTCATACTTCTCT 3180  
D 7618 AGAATCTCAGAGGAGACATCTCATTTCTTGTATCAACAGAGGCTCATACTTCTCT 7677  
Q 3181 CCGCGTTATATATCTTATGACAGTCAAGCAACAAACAGCACTTTCAATGCTTAT 3240  
D 7678 CCGCGTTATATATCTTATGACAGTCAAGCAACAAACAGCACTTTCAATGCTTAT 7737  
Q 3241 ACATTCAGATGCTTACCTGCGCCAGATAGTATCCCTTCCAGGGCTTACAGAAAGTCCC 3300  
D 7738 ACATTCAGATGCTTACCTGCGCCAGATAGTATCCCTTCCAGGGCTTACAGAAAGTCCC 7797  
Q 3301 AACTGCTGTACTGAGTCTATACAGATTCATATCCCTAATCTTATAGAAAC 3358  
D 7798 AACTGCTGTACTGAGTCTATACAGATTCATATCCCTAATCTTATAGAAAC 7855

RESULT 2  
AR492934  
LOCUS AR492934 15186 bp DNA linear PAT 15-MAY-2004  
DEFINITION Sequence 134 from patent US 6719979.  
ACCESSION AR492934  
VERSION AR492934.1 GI:47264085  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15186)  
AUTHORS Peeters,B.P.H., de Leeuw,O.S. and Gielkens,A.L.J.  
TITLE Newcastle disease virus infectious clones, vaccines and diagnostic assays  
JOURNAL Patent: US 6719979-A 134 13-APR-2004;  
ID=Leijstcad, Instituut voor Dieronderij en Diergezondheid B.V.;  
Leijstcad;  
EPX;

FEATURES  
source location/Qualifiers  
1..15186  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 99.9%; Score 3353.2; DB 6; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Q 1 ACGGGTGAAGATTCTGATCCCGTTGCGCCCTTCAGAGTGAAGATGGGCTTCAGACC 60  
D 4498 ACGGGTGAAGATTCTGATCCCGTTGCGCCCTTCAGAGTGAAGATGGGCTTCAGACC 4557  
Q 61 TTCTACCAAGAACCCAGACCTATGATGCTGACTATATCCGGGTTGCGTGCATGAGTTG 120  
D 4558 TTCTACCAAGAACCCAGACCTATGATGCTGACTATATCCGGGTTGCGTGCATGAGTTG 4617  
Q 121 CATCTGCCGCAAACTCCATGTAGGAGAGCCCTTTCAGAGCTGAGAAATTTGTGTAC 180  
D 4618 CATCTGCCGCAAACTCCATGTAGGAGAGCCCTTTCAGAGCTGAGAAATTTGTGTAC 4677  
Q 181 AGAGACAAGCCGCTCAACATATACCTCATCCAGACAGATCAATAGTTAAAGT 240  
D 4678 AGAGACAAGCCGCTCAACATATACCTCATCCAGACAGATCAATAGTTAAAGT 4737  
Q 241 CTTCCCAATCTGCGCAAGATAGAGGCAATGTGCGAAAGCCCTTTGATGATACAA 300  
D 4738 CTTCCCAATCTGCGCAAGATAGAGGCAATGTGCGAAAGCCCTTTGATGATACAA 4797

QY 301 CAGACATTGACACTTGTCTCACCCCCTGTGATCTATCCGTAGATACAGAGTCTC 360  
DB 4798 CAGAGACTTGACCACTTTGTCTCACCCCCTGTGATCTATCCGTAGATACAGAGTCTC 4857  
QY 361 TGTGACTTACACTCTGAGAGGGGAGACAGGGGCGCTTATAGGGCCCTTATTTGGCGGTGT 420  
DB 4858 TGTGACTTACACTCTGAGAGGGGAGACAGGGGCGCTTATAGGGCCCTTATTTGGCGGTGT 4917  
QY 421 GGCTCTTGGGGTTGGCACTGCGGCACAAATACAGGGCGCGAGCTGTGATACAGGCCAA 480  
DB 4918 GGCTCTTGGGGTTGGCACTGCGGCACAAATACAGGGCGCGAGCTGTGATACAGGCCAA 4977  
QY 481 ACAAATGCTGCCCAACATCTCCGACTTAAAGAGAGATTGGCCGCAACCAATGAGCGTGT 540  
DB 4978 ACAAATGCTGCCCAACATCTCCGACTTAAAGAGAGATTGGCCGCAACCAATGAGCGTGT 5037  
QY 541 GCATGAGGTCACTGACGGATTATTCGCAACTAGCAGTGGCAGTTGGGAAGATGCAGCGTT 600  
DB 5038 GCATGAGGTCACTGACGGATTATTCGCAACTAGCAGTGGCAGTTGGGAAGATGCAGCGTT 5097  
QY 601 TGTAAAGAACCAANTTAATAAAGCTCAGGAAATTAGACTGCAATTAATGACAGCA 660  
DB 5098 TGTAAAGAACCAANTTAATAAAGCTCAGGAAATTAGACTGCAATTAATGACAGCA 5157  
QY 661 AGTTGGTGAAGCTCAACCTGTACTTAACCGAATTGACTACAGTATTGGGACCACAAT 720  
DB 5158 AGTTGGTGAAGCTCAACCTGTACTTAACCGAATTGACTACAGTATTGGGACCACAAT 5217  
QY 721 CACTTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACAACTTACGTGTGGAAA 780  
DB 5218 CACTTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACAACTTACGTGTGGAAA 5277  
QY 781 TATGATTAATCTTATGCTAAGTTAGGTAGGGAACAATCAACTCAGCTCAATTAATCGG 840  
DB 5278 TATGATTAATCTTATGCTAAGTTAGGTAGGGAACAATCAACTCAGCTCAATTAATCGG 5337  
QY 841 TAGCGGCTTATCAACCGGTAAACCTTATCTATACGACTCAAGACTCACTTGGGTAT 900  
DB 5338 TAGCGGCTTATCAACCGGTAAACCTTATCTATACGACTCAAGACTCACTTGGGTAT 5397  
QY 901 ACAAGTAACCTCTACCTTCAGTCGGGAACCTTAATATATGCGTCCACTCTTGGAAAC 960  
DB 5398 ACAAGTAACCTCTACCTTCAGTCGGGAACCTTAATATATGCGTCCACTCTTGGAAAC 5457  
QY 961 CTTATCCGTAGACAACCGGGGATTTGCTCGGCACTTGTCCCAAAAGGTGAGACA 1020  
DB 5458 CTTATCCGTAGACAACCGGGGATTTGCTCGGCACTTGTCCCAAAAGGTGAGACA 5517  
QY 1021 GGTGCGTTCTGTGATAGAAACTTGCACCTCATCTGATAGAAACTGACTTGAATTT 1080  
DB 5518 GGTGCGTTCTGTGATAGAAACTTGCACCTCATCTGATAGAAACTGACTTGAATTT 5577  
QY 1081 ATATGTGACAAGAAATAGTAACGTTCCCTATGTCCCTGGTATTTTATCTGTGACGG 1140  
DB 5578 ATATGTGACAAGAAATAGTAACGTTCCCTATGTCCCTGGTATTTTATCTGTGACGG 5637  
QY 1141 CAATACGTGGGCTGTATGTATCTCAAGACCGAAGGGGCACTTACACATGACATGAC 1200  
DB 5638 CAATACGTGGGCTGTATGTATCTCAAGACCGAAGGGGCACTTACACATGACATGAC 5697  
QY 1201 TATCAAGTTCACTGACATCGCAACTGCAAGATGACAAACATGTAGATGTGTTAAACCCCC 1260  
DB 5698 TATCAAGTTCACTGACATCGCAACTGCAAGATGACAAACATGTAGATGTGTTAAACCCCC 5757  
QY 1261 GGGTATCATATCGCAAAACTATGAGAAGCGGTGTCTTAATAGTAAACAATCATGCAA 1320  
DB 5758 GGGTATCATATCGCAAAACTATGAGAAGCGGTGTCTTAATAGTAAACAATCATGCAA 5817  
QY 1321 TGTTTTATCTTGAAGGGGATTAATTTAAGGCTCAAGTGGGGAATTCATGTAACTTATCA 1380  
DB 5818 TGTTTTATCTTGAAGGGGATTAATTTAAGGCTCAAGTGGGGAATTCATGTAACTTATCA 5877

QY 1381 GAGAAATATCTCAATACAGATTTCTCAAGTAAATTAACAGGGCAATCTTGATATCTCAAC 1440  
DB 5878 GAGAAATATCTCAATACAGATTTCTCAAGTAAATTAACAGGGCAATCTTGATATCTCAAC 5937  
QY 1441 TGAAGTTGGGAATGTCAACAACCTCGATCAGTATGTCTTGAATTAAGTAGAGAAAGCAA 1500  
DB 5938 TGAAGTTGGGAATGTCAACAACCTCGATCAGTATGTCTTGAATTAAGTAGAGAAAGCAA 5997  
QY 1501 CAGAAAATAGACAAAGTCAATGTCAACCTGATAGACACATCTGTCTCATTAATCTATAT 1560  
DB 5998 CAGAAAATAGACAAAGTCAATGTCAACCTGATAGACACATCTGTCTCATTAATCTATAT 6057  
QY 1561 CGTTTGAATCATATATCTTGTGTTTGGTATTAATGCTTGAATTTAGCATGCTACT 1620  
DB 6058 CGTTTGAATCATATATCTTGTGTTTGGTATTAATGCTTGAATTTAGCATGCTACT 6117  
QY 1621 AATGTACAGCAAAAGGCGCAAAAACCTTATATGGCTGGGGAATTAATCTCTAGA 1680  
DB 6118 AATGTACAGCAAAAGGCGCAAAAACCTTATATGGCTGGGGAATTAATCTCTAGA 6177  
QY 1681 TCAGATGAGAGCCACTACAAAATGTGAACACAGATGAGGAAGAAAGTTCCCTAATAG 1740  
DB 6178 TCAGATGAGAGCCACTACAAAATGTGAACACAGATGAGGAAGAAAGTTCCCTAATAG 6237  
QY 1741 TAAATTTGTGAAGTTCTGTGATGCTGTCAAGTTCAAGAGTTAAGAAAACCTACCGGT 1800  
DB 6238 TAAATTTGTGAAGTTCTGTGATGCTGTCAAGTTCAAGAGTTAAGAAAACCTACCGGT 6297  
QY 1801 TGTAGATGACCAAGGACGATACCGGGTGAACGGTGAAGAGAGGCGCCCTCAATTCG 1860  
DB 6298 TGTAGATGACCAAGGACGATACCGGGTGAACGGTGAAGAGAGGCGCCCTCAATTCG 6357  
QY 1861 GAGCCAGGCTTCAACAACCTCCGTTCTACCGCTTCAACGACCAACAGTCTCAATCATGAC 1920  
DB 6358 GAGCCAGGCTTCAACAACCTCCGTTCTACCGCTTCAACGACCAACAGTCTCAATCATGAC 6417  
QY 1921 CGCGCGTTAAGCCAAAGTTGCTGTAGAGATGATGAAAAGAGGCAAAAATACATGGCC 1980  
DB 6418 CGCGCGTTAAGCCAAAGTTGCTGTAGAGATGATGAAAAGAGGCAAAAATACATGGCC 6477  
QY 1981 TTGATATTCGGGATTCGAATCTTATCTTAACAGTATGACCTTGGCTATATCTGTAGCC 2040  
DB 6478 TTGATATTCGGGATTCGAATCTTATCTTAACAGTATGACCTTGGCTATATCTGTAGCC 6537  
QY 2041 TCCCTTTATATAGCATGAGGGGCTAGACACACTAGCGATCTTGTAGCATACGACTAGG 2100  
DB 6538 TCCCTTTATATAGCATGAGGGGCTAGACACACTAGCGATCTTGTAGCATACGACTAGG 6597  
QY 2101 ATTTCCAGGGCAGAGAAAAGATTACATCTACCTGTTCATCAATCAAGTGTATGAT 2160  
DB 6598 ATTTCCAGGGCAGAGAAAAGATTACATCTACCTGTTCATCAATCAAGTGTATGAT 6657  
QY 2161 AGGATATATTAAGAAAGTGGCGCTTGAAGTCCCGTGGCAATGTTAATATCTAGACCA 2220  
DB 6658 AGGATATATTAAGAAAGTGGCGCTTGAAGTCCCGTGGCAATGTTAATATCTAGACCA 6717  
QY 2221 ATTATGAAGCAATTAATCATCTCTCTTATCAGATTAATGAGCTGCAACCAAGTGGG 2280  
DB 6718 ATTATGAAGCAATTAATCATCTCTCTTATCAGATTAATGAGCTGCAACCAAGTGGG 6777  
QY 2281 TGGGGGGCACATATCATGACCAAGTATATAGGGGGGATAGGCAAAAGATCATTTGTA 2340  
DB 6778 TGGGGGGCACATATCATGACCAAGTATATAGGGGGGATAGGCAAAAGATCATTTGTA 6837  
QY 2341 GATGATCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400  
DB 6838 GATGATCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6897  
QY 2401 ATCCCGGCGCTACTACAGGATCAGGTGCACTGCAATACCTCAATTTGACATGAGTGT 2460  
DB 6898 ATCCCGGCGCTACTACAGGATCAGGTGCACTGCAATACCTCAATTTGACATGAGTGT 6957  
QY 2461 ACCCATTAATGCTACACCCATTAATGTATGTCTGTGATGACAGAGATCACTCAATTC 2520

Db 6958 ACCATTACTGCTACACCCCAATATATATTTGTCGATGCAAGATCACTTCACATTCA 7017  
Qy 2521 TATCAGATTATTAAGCACTTGTGTGCTCCGACATCTGCAACAGAGGATTTCTTTTCT 2580  
Db 7018 TATCAGATTATTAAGCACTTGTGTGCTCCGACATCTGCAACAGAGGATTTCTTTTCT 7077  
Qy 2581 ACTGTGCGTTCCATCAACCTTGACGACACCCCAAAATCGAAAGTCTTGACGTGATGCA 2640  
Db 7078 ACTGTGCGTTCCATCAACCTTGACGACACCCCAAAATCGAAAGTCTTGACGTGATGCA 7137  
Qy 2641 ACTTCCCTGGGTTGTGATGATGCTGTCTCCGAAGTCAACGAGACAGAGAAAGATAT 2700  
Db 7138 ACTTCCCTGGGTTGTGATGATGCTGTCTCCGAAGTCAACGAGACAGAGAAAGATAT 7197  
Qy 2701 AACTCAGCTGCTCTTACGCGGATGATGATGAGAGGTTAGGGTTGACGCGCAGTACAC 2760  
Db 7198 AACTCAGCTGCTCTTACGCGGATGATGATGAGAGGTTAGGGTTGACGCGCAGTACAC 7257  
Qy 2761 GAAAAGACCTAGATGTCACAACTTATTCGCGGACTGCGGCACTACCCAGAGATA 2820  
Db 7258 GAAAAGACCTAGATGTCACAACTTATTCGCGGACTGCGGCACTACCCAGAGATA 7317  
Qy 2821 GGGGGTGAATCTTTTATTTAGACGCGCGTATGTTCTCAGTCTACGAGGGTTAAAA 2880  
Db 7318 GGGGGTGAATCTTTTATTTAGACGCGCGTATGTTCTCAGTCTACGAGGGTTAAAA 7377  
Qy 2881 AATTCAACCCAGTGCACCTGTACAGAGAGGAAATATGATGATATCAAGCGATACAA 2940  
Db 7378 AATTCAACCCAGTGCACCTGTACAGAGAGGAAATATGATGATATCAAGCGATACAA 7437  
Qy 2941 ACATGCCAGATGAGCAAGACTTACCAATTCGAATGCGCAAGTCTTCGTATTAAGCTGGA 3000  
Db 7438 ACATGCCAGATGAGCAAGACTTACCAATTCGAATGCGCAAGTCTTCGTATTAAGCTGGA 7497  
Qy 3001 CGGTTTGTGGGAAACGATACAGCAGGCTATCTTATCTATCAAGGTCTCAACATCCTTA 3060  
Db 7498 CGGTTTGTGGGAAACGATACAGCAGGCTATCTTATCTATCAAGGTCTCAACATCCTTA 7557  
Qy 3061 GGGGAAACCCGGATCTGATCTGTACCGGCCAAACAGTCACTCAATGGGGCCGAAAGC 3120  
Db 7558 GGGGAAACCCGGATCTGATCTGTACCGGCCAAACAGTCACTCAATGGGGCCGAAAGC 7617  
Qy 3121 AGAATTCTCAGTAGGAGACATCTCATTCTTGTATCAACAGAGGATCATCATCTCTCT 3180  
Db 7618 AGAATTCTCAGTAGGAGACATCTCATTCTTGTATCAACAGAGGATCATCATCTCTCT 7677  
Qy 3181 CCGCGCTTATATATCTTATGACAGTCAAGCAAAAAAGCCACTTTCATATGCTTAT 3240  
Db 7678 CCGCGCTTATATATCTTATGACAGTCAAGCAAAAAAGCCACTTTCATATGCTTAT 7737  
Qy 3241 ACATTCAATGCTTCACTCGGCGCAGTATGATCCCTTCCAGGCTTCAGCAAGATGCC 3300  
Db 7738 ACATTCAATGCTTCACTCGGCGCAGTATGATCCCTTCCAGGCTTCAGCAAGATGCC 7797  
Qy 3301 AACTCGGTGTATCTGAGTCTATACAGATCATATCCCTAATCTTCTATAGAAAC 3358  
Db 7798 AACTCGGTGTATCTGAGTCTATACAGATCATATCCCTAATCTTCTATAGAAAC 7855

RESULT 3  
AX008510  
LOCUS AX008510 15186 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 162 from Patent WO9966045.  
ACCESSION AX008510  
VERSION AX008510.1 GI:9996061  
KEYWORDS  
SOURCE Newcastle disease virus  
ORGANISM Newcastle disease virus  
Virus; ssRNA negative-strand viruses; Mononegavirales;  
Paramyxoviridae; Paramyxovirinae; Avulavirinae.  
REFERENCE  
1 Gielkens, A.L., Koch, G., De Leeuw, O. and Peeters, B.P.

TITLE Newcastle disease virus infectious clones, vaccines and diagnostic assays  
JOURNAL Patent: WO 9966045-A 162 23-DEC-1999;  
GIELEKENS ARNOUD LEONARD JOSEF (NL); KOCH GUS (NL); LEEUW OLAV SVEN DE (NL); PEETERS BERNARDUS PETRUS HUBER (NL); STICHTING DIENST LANDBOUWKUNDI (NL)  
FEATURES  
SOURCE  
location/Qualifiers  
1..15186  
/organism="Newcastle disease virus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:11176"  
1..121  
/note="Nucleotide sequence of NDV strain Ia Sota"  
122..1591  
/note="unassigned protein product; 'Nucleotide sequence of NDV strain Ia Sota'"  
/db\_xref="GI:9996062"  
/protein\_id="CAC07407.1"  
/translation="MSSVPEDEYEQLLAQTRENGAHGCGEGKSTLKVDVPEVTLNSDD  
PEDRWSPVFCRLIAVSEDANKPLRQALISLCSHQVNRNHYALAKONKATLAVL  
EIDGFANGTPOFNRRSGVSEERAPRQFAMIGSLPRACNSGTPPTAGAEADPDITD  
TLERILSLIOAWWTYAKMTAYETLAESETRINKYMOOGRVOKXILVPCRSSTIO  
LTRRSLAATRIPLVSELKRNTRAGSTYTNLVGDVSYIRNTGLAFETLKYGIN  
TKTSALSLSGDIQRMKQMLRYRKGNAPMTLILGSDMSFAPAEYQILYRA  
MGMAVSLDKGTGYFARDFMSTSPMLGVEYQALQCGSNRSQCPAEGEYFMDL  
AAARVSDTSSLYMPTQOVGLTGLSEGGQALQCGSNRSQCPAEGEYFMDL  
MRVANSRMAPNSAQTPSGPPEPTPGSDNDTDMGY"  
1592..1886  
/note="Nucleotide sequence of NDV strain Ia Sota"  
1887..3074  
/note="unassigned protein product; 'Nucleotide sequence of NDV strain Ia Sota'"  
/db\_xref="GI:9996063"  
/translation="MATFTDAEIDELFETSGTVIDNITRQKPAETVGSATPQGT  
KVLSAWEKHGSLQPPASQDNPDROSDSKQPSPEQTTPHDSPAPASQPPQIARD  
EAVDQRTGASLILMDLKLINRKSNAKGPSPQEGHQPTQCGSOPSRGNS  
OERPDONVRAKPNQGDVNTAAYHGGESLSGATPHLRSEIQDLTYSADHYO  
PPDFVQANMSMHEALISQVSKYDQDLYLKQTSIPMMRSEIQDLTYSADHYO  
GMMKILDPGCANTSSLDLRAVASHVLYSGRDPSPYTYGGSEMLNKISQVPHP  
SELIKPATACGPDIQVAKDTVRALIMSRPMHSSAKLKLDAAGSIEETRKLRLA  
LNG"  
3075..3289  
/note="Nucleotide sequence of NDV strain Ia Sota"  
3290..4384  
/note="unassigned protein product; 'Nucleotide sequence of NDV strain Ia Sota'"  
/db\_xref="GI:9996064"  
/translation="WDSRTITGLYFDSAHSSNULAPPLYLQGTGDKQIAPRYR  
RLDLWDSKEDSVFTTYGFI FQVGEBAVVMGIMDDPKRELISAAALCLGSVNTGD  
LIELARCLTMIVTCKKSNTERBEMVAPQVLOSQVNRNHYALAKONKATLAVL  
EKIPSGGTELYKNEFVSLVVPKQDVYKIPAAVLKVGSSLYNALVTVINVEDPSS  
PLVKSLSKSDSYVANI.FLHIGMTYDTRGKQVTPKLRKIRSLSLGSLVGLGP  
SVLVKARGARTKLAPFPSSSGTACRYIANASPOVALIIMSQTRACLSRVKIIIDAGTQ  
RAVAVDADHEVTSTKLEKHTLAKTNEFKK"  
4385..4543  
/note="Nucleotide sequence of NDV strain Ia Sota"  
4544..6205  
/note="unassigned protein product; 'Nucleotide sequence of NDV strain Ia Sota'"  
/db\_xref="GI:9996065"  
/translation="MGSRPSTKNPAPMMLTIRVALVLSICIPANSIDGRPLAAGIYV  
TGBKAVVITSSQSGTIVYLLRNLPDCKACAKAPADAYNRITLTLTLPGSIRRI  
QESVTVSSGGRQGLIGALIGYALGALTAQTAAALIOAKONANNTLRKXSIAA  
TNEAVHEVTGLOLAVAGKQOPVNDQNKTAQELDCKIAQOVVEALNLYTELT  
TVSGPQITSPALNKLTIOALYNLAGGMDYLTKLGVGNQLSLISGSLITNPILY  
DSQTLGLIGVTLPSVGNLNMRAETLETLSVSTRGFASALVPKVTQVGSVIEILD

Intron  
CDS

TSYCIETDLDLCTRIIVTPMSPGITSCLSGNTSACMYSTEGALLTPYVITIGSVYA  
NCHMTTCRCVNPBPIISQNGEAVSLIDKOSCNVLSGGITLHSGEFDVYKXNISI  
ODSVOITTGNDLIDSTELGNNNSINSLNLEESNRCLDYNVLSTSLIYIYVLT  
IISLVFGIILSLIACIYMYKQAKQKTLMLGNNTLDQMBATTYK"  
6206..6411  
6412..8145  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAC07411.1"  
/db\_xref="GI:9996066"  
/translation="MDRAVSQVLALENDERAKXNWRILPRLAILFLVTLATLSVSLT  
LYMGASTPSDLVGIPIRISRAEKITSTLGSNDVDRIYKOVALLESPLALANTET  
IMAGTSLSYQINGANNNGMGAIPHDPYIGIGKELIVDDSDVTSFSPASAOEHL  
NFIAPPTGGGCTRIPEFMSATHCYTHNVILSGCDHSHSYOYLAIVLRTSATGR  
VFPSLRSINLDTDNKSCSVSATPLGCMILCSKYETEEDNYSNAPTRMVGARLG  
FDQVHEKLDLDTLLFGDWVANYRGVGGSFIDRSVWVSFVYGLKPSPADYQEGY  
VIYKRYDTCPEDDVDQIRAKSKYKRGGRIGQALISIKYTSIGEDPULVYRP  
NITVLMGEBRILTVGSHFLYQKSSYFSPALLYPNTVSKRTIHTSPPTNATRP  
GS1PCQASARCPNSCVTVYTDYPIPLFYNNHILRGVFTMLDGVQRLNPAVAEFS  
TSRSRLTRVSSSTKAAYTSTCFKVKIKNTYCLSLAEISNTLFGHFRIVPLLEIL  
KDDGVREARSG"  
8146..8380  
8381..14995  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAC07412.1"  
/db\_xref="GI:9996067"  
/translation="MASSGPRBAEHQIILPEPHLSPLVYKHLIYWKLRGLPLPDEC  
DPRHLISROWKILLESASPDEMTLIGUAVHQTLMHNRIGVLAHPRCLBOIANE  
VDSNTKFKRIEKKIQHNTRYGELFRLCTHLEKLSGWSNNRSEBSIRTD  
PAFMFKSWSTAKFAMLHIKQIOLHMLVAATKRSANAKLWMLRHQGVQVPELVVLT  
THNENKFTCLQELVLMYADMMEGRDVNIISTVAHLISLSEKLDIDLRLDALAK  
DLGNQYDVVSLMEGFAYGAVQLEPSTGAGDFAFNLQELKILGLPNDIAESV  
THA1ATVSGLEONQAAEMLCILRMGHPLLESILAKAVRSQWCAKRVDPMDILQV  
LSFPGKITINGYRKAGAGWPRYKVDITKVGICQLHADSLSHDIMLEEVYSLSL  
EFPECIAYDVNTLMFPLKDKALHPNDNMLSPRRLISEDQKYEATSTRRLI  
EFLSNDPDKYKEMEYLTLEYLDDNVAVSLSKEEVANGKIFAKLTKKLCNCOY  
MAEGILADQAPFPOGNGVIODSISLTKSMAMQSLEPNENKRIITDCRKSVRNRRH  
DQSKNRRAVATFTTDLQKCLMWRQYTKLFAMHNLGPHFEFEMHLRMDTT  
MFGDPPNPSPDSDCDLSRPNDIYIVASRGIGELCKQMLMTISIAIIOAAAS  
HCRYACVQGDNOVIATNTRVRSDDSBEWLTQHOASDPFELIHNHILIGNHLD  
RETRSDTFPIYSKRIFKDGLISQVLKNSKLVAGSDSENTVMSKALIVAVRL  
CENGLPDKCYLYNIMSVCQYTFDESFTTNSHPLSPIMNLIILRPGNGWABL  
LGLSLNQSLRYLNRNIGDGTAFABEIKLEAVGLSPIMNLIILRPGNGWABL  
CNDPSENFETVASPNIVLKHTQORVLETCNSPLSGVTEDEABEKLAEILNO  
EVIHPRVAAHIMASVGRKOGLVDNTNVIKIALTRPGLGIKXLMIVYSSSH  
AMLPDRVSSSSNRNPLVSSNCSLTLAYARRSRSPITGKKIIGVSNPDTIELY  
EGEILSVGGCTRCDSGDEQFTWHLPSNIELTDDISKNPPMRPVIGSKTQERRAS  
LAKIAMSHPVKALRASVLIWAVGNEVMVTAALTIASRCNVNLEYRLISPLT  
AGNLOHRLDDGITQMTFTPALYKCHLTFYPMILKGSCKESKRMQWFTNRVMLG  
LSLIESIFPMITTTRYDEITLHSHKSCCIREAPVAVPELIGVPELRTVSNKEM  
YDPSVSEGGPARLDLAFKSYELNLESYPIELMNLISISGKLIGQSVISYEDS  
IKODAILVYDNTRWISERQNSDVRLFEJALAEVLJDCSQLYLAEVRGLDNIVDN  
GDYKMPGILNSNIATISHPVHSLRLAVGLNHGSHQALDTEIEMSAKLVASC  
TRRIVISGLVGNKXDILPSCVLDNLEMKOOLISRLCCYTVLFATTRIEPKIRGLT  
ABEKSILTEYLSADAVKPLSPDOVSSPNIIITPPANLYVSRSLMILIERBDR  
DTIALLFPOBPLEFSPVODIGARVDPFROPAAFLQELDISAPRAFTLSOIH  
PELTSPPREDDIYVRIYFRIGTRASSWYASHSLIAPVPERCAHMSIYLAESGAL  
MSLELHVPHETIYNTLFSNEMNPPORHGPPTQOLNVYVRNLOAEYTCDDGPIQ  
EFPPLEMENTEESDLTSDKAVGYTSAVPASVSLHCDIEIPGSSQSDLECIYAL  
SLIAMSREGGVVIILVLYAMGYFHLMLNLPACSTKGIISNGACQIMDECIYAL  
FVNGYLGPTFVEHVMATKILVORHSLTSLKSDIEITLRTFSQORVNDLSSPAP  
RLIKYLAKNIDTALIEAGQVPRFCASLTSSTANTITOLTOIASHIDIVINSVPI  
BAEGDLADIVFLTPYNLSTDGKKRISLIQCTROIIEVTLIGLREVENLAKIGDISLY  
LKNATIMEDILIPRTYLNKSHSTCPKYLAVAGITKLKEMFTDTSVLVLTQAKQFYMKT  
IGNAVKGYVNSCDS"  
14996..15186

Intron  
CDS

Query Match 99.9%; Score 3353.2; DB 6; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ORIGIN  
Intron

Query Match 99.9%; Score 3353.2; DB 6; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ACGGGTAGAAAGATTCTGGAATCCCGGTTGGCCCTCCAGGTGCAAGATGGGGCTCCAGACC	60
Db	4498	ACGGGTAGAAAGATTCTGGAATCCCGGTTGGCCCTCCAGGTGCAAGATGGGGCTCCAGACC	4557
Qy	61	TTCTACCAAGAACCCAGACACCTATGATGCTATGATCCGGGTTGCGGTGCACTGAGTTG	120
Db	4558	TTCTACCAAGAACCCAGACACCTATGATGCTATGATCCGGGTTGCGGTGCTAGAGTTG	4617
Qy	121	CATCTGTCCGGCAAACTCCATTGATGGCAGGCGCTTTGCAAGCTGCAGGAATTGTGTTAC	180
Db	4618	CATCTGTCCGGCAAACTCCATTGATGGCAGGCGCTTTGCAAGCTGCAGGAATTGTGTTAC	4677
Qy	181	AGGAGACAAACCGGTCAACATATACCTATATCCGACAGATCAATCATATGTTAAGCT	240
Db	4678	AGGAGACAAACCGGTCAACATATACCTATATCCGACAGATCAATCATATGTTAAGCT	4737
Qy	241	CTCTCCGAACTCTGCGCAAGGATTAAGAGGAGCATGCGCAAGCCCTTGGATGCAATCA	300
Db	4738	CTCTCCGAACTCTGCGCAAGGATTAAGAGGAGCATGCGCAAGCCCTTGGATGCAATCA	4797
Qy	301	CAGGACATTGACCACTTTGCTCAACCCCTTGGTGACTCTATCCGTAGATACAGAGTC	360
Db	4798	CAGGACATTGACCACTTTGCTCAACCCCTTGGTGACTCTATCCGTAGATACAGAGTC	4857
Qy	361	TGTGACTACATCTGAGAGGGGGAGACAGGGGGCGCTTATAGGCGCTTATTTGGCGGTG	420
Db	4858	TGTGACTACATCTGAGAGGGGGAGACAGGGGGCGCTTATAGGCGCTTATTTGGCGGTG	4917
Qy	421	GGCTCTTGGGGTTCGCACTGCGCGCACAATATACAGGGCGCGAGCTCTGATACAGGCA	480
Db	4918	GGCTCTTGGGGTTCGCACTGCGCGCACAATATACAGGGCGCGAGCTCTGATACAGGCA	4977
Qy	481	ACAAAATGCTGCCAATCCTCTCGACTTAAGAAGAGATTGCGGCAACAATGAGCTGT	540
Db	4978	ACAAAATGCTGCCAATCCTCTCGACTTAAGAAGAGATTGCGGCAACAATGAGCTGT	5037
Qy	541	GCAATGAGTACATGACGATTAATCCGACATGACAGTGGCAGTGGGAAGATGACAGAGTT	600
Db	5038	GCAATGAGTACATGACGATTAATCCGACATGACAGTGGCAGTGGGAAGATGACAGAGTT	5097
Qy	601	TGTTAATGACCAATTTAATATAAAGCTCAGAAATAGACTGCATCAAAATTGACACAGA	660
Db	5098	TGTTAATGACCAATTTAATATAAAGCTCAGAAATAGACTGCATCAAAATTGACACAGA	5157
Qy	661	AGTTGTGTAGAGCTCAACCTGTACCTTAACCGAATTGACTACAGTATTCGACCAACAAT	720
Db	5158	AGTTGTGTAGAGCTCAACCTGTACCTTAACCGAATTGACTACAGTATTCGACCAACAAT	5217
Qy	721	CACCTACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCTGTGAAA	780
Db	5218	CACCTACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCTGTGAAA	5277
Qy	781	TATGATATTCTTATGACTAAGTTAGTGAAGGAACAATCACTGACCTAATTCGG	840
Db	5278	TATGATATTCTTATGACTAAGTTAGTGAAGGAACAATCACTGACCTAATTCGG	5337
Qy	841	TAGGGGCTTATGACCGGTAACTTATACGACTCAAGACTCAAGCTCACTTTGGGTAT	900
Db	5338	TAGGGGCTTATGACCGGTAACTTATACGACTCAAGACTCAAGCTCACTTTGGGTAT	5397
Qy	901	ACAGGTAACTCTACCTTCACTCGGAAACCTTAATATATGCGTGGCCACTACTTGGAAAC	960
Db	5398	ACAGGTAACTCTACCTTCACTCGGAAACCTTAATATATGCGTGGCCACTACTTGGAAAC	5457
Qy	961	CTTATCCGTAAAGCAACACGAGGGATTGGCTCGGCACTTGCCCAAAAGTGGGACACA	1020
Db	5458	CTTATCCGTAAAGCAACACGAGGGATTGGCTCGGCACTTGCCCAAAAGTGGGACACA	5517
Qy	1021	GGTCGGTTCTGTATAGAAAGAACTTGACACCTCATACTGTATAGAACTGACTTGAATTT	1080
Db	5518	GGTCGGTTCTGTATAGAAAGAACTTGACACCTCATACTGTATAGAACTGACTTGAATTT	5577
Qy	1081	ATAATGTACAAAGATAGTAAAGTTCCCTATGTCCTGATTTATTTCTTGAGCGG	1140

Db 5578 ATATTGTAAGAAATAGTAAGCTTCCCTATGTCCTGTAATTTATTCCTGCTTGAAGCGG 5637  
Qy 1141 CAATACGTCGGCTGTATGTACTCAAAAGACGAAAGCGCACTTACTACCAATCATGATAC 1200  
Db 5638 CAATACGTCGGCTGTATGTACTCAAAAGACGAAAGCGCACTTACTACCAATCATGATAC 5697  
Qy 1201 TATCAAAAGTTCAAGTCATCGCCAACTGCAAGATGCAACATGTAGATGTGTAACCCCCC 1260  
Db 5698 TATCAAAAGTTCAAGTCATCGCCAACTGCAAGATGCAACATGTAGATGTGTAACCCCCC 5757  
Qy 1261 GGGTATCATATCGGAAAACTATGAGAAAGCCGTGCTCTAATAGATAAACAATGCAATGCAA 1320  
Db 5758 GGGTATCATATCGGAAAACTATGAGAAAGCCGTGCTCTAATAGATAAACAATGCAATGCAA 5817  
Qy 1321 TGTTTTATCCTTAGCGGGATTAATCTTAAAGGCTCAGTGGGAAATTCAGTGTATCTTATCA 1380  
Db 5818 TGTTTTATCCTTAGCGGGATTAATCTTAAAGGCTCAGTGGGAAATTCAGTGTATCTTATCA 5877  
Qy 1381 GAAGAAATATCTCAATACAGAAATTCAGATATAATAACAGGCAATCTTGATATCTCAAC 1440  
Db 5878 GAAGAAATATCTCAATACAGAAATTCAGATATAATAACAGGCAATCTTGATATCTCAAC 5937  
Qy 1441 TGAGCTTGGGAATGTCAACAACTCGATCAGTAATGCTTTGAATAAGTTAGAGAAAGCAA 1500  
Db 5938 TGAGCTTGGGAATGTCAACAACTCGATCAGTAATGCTTTGAATAAGTTAGAGAAAGCAA 5997  
Qy 1501 CAGAAACTAGCAAAAGTCATGTCAAACCTGACTAGCAATCTGCTCATTAACCTATAT 1560  
Db 5998 CAGAAACTAGCAAAAGTCATGTCAAACCTGACTAGCAATCTGCTCATTAACCTATAT 6057  
Qy 1561 CGTTTGAATCATATCTCTTGTGTTTGTGTAATCTTAAGCCTGANTCTAGCATGTACTCT 1620  
Db 6058 CGTTTGAATCATATCTCTTGTGTTTGTGTAATCTTAAGCCTGANTCTAGCATGTACTCT 6117  
Qy 1621 AATGTACAGCAAAAGCGCAACAAAACTTATATGCTTGGGAATATACTCTTGA 1680  
Db 6118 AATGTACAGCAAAAGCGCAACAAAACTTATATGCTTGGGAATATACTCTTGA 6177  
Qy 1681 TCAGATGAGGCCCTCAAAAATGTGAACAAGTGAAGAAAGGTTTCCCTAAATAG 1740  
Db 6178 TCAGATGAGGCCCTCAAAAATGTGAACAAGTGAAGAAAGGTTTCCCTAAATAG 6237  
Qy 1741 TAAATTTGTGAAGATTCCTGTAGTGTCTGTCAGTTCAGAGATTAAGAAAACTACCGGT 1800  
Db 6238 TAAATTTGTGAAGATTCCTGTAGTGTCTGTCAGTTCAGAGATTAAGAAAACTACCGGT 6297  
Qy 1801 TGTAGATGACCAAAAGACGATATACGGGTAGAACGGTAAGAGAGCGCCCTCAATTGC 1860  
Db 6298 TGTAGATGACCAAAAGACGATATACGGGTAGAACGGTAAGAGAGCGCCCTCAATTGC 6357  
Qy 1861 GAGCGAGGCTTCAACACTCCGTTCTACCGCTTACCGCAACAAGTCTCTCATATGTGAC 1920  
Db 6358 GAGCGAGGCTTCAACACTCCGTTCTACCGCTTACCGCAACAAGTCTCTCATATGTGAC 6417  
Qy 1921 CGGCGCGTTAGCAAGTTGGCTTGAAGATGAGAAAGAGGCAAAAAATATCATGTGGCG 1980  
Db 6418 CGGCGCGTTAGCAAGTTGGCTTGAAGATGAGAAAGAGGCAAAAAATATCATGTGGCG 6477  
Qy 1981 TTTGATATTCGCGATTTGCAATCTTATCTTAAACAGTATGACCTTGGCTATATCTGTAGCC 2040  
Db 6478 TTTGATATTCGCGATTTGCAATCTTATCTTAAACAGTATGACCTTGGCTATATCTGTAGCC 6537  
Qy 2041 TCCCTTTATATAGATGGGGCTAGCACACCTAGCCGATCTTTAGGCAATCCGACTAGG 2100  
Db 6538 TCCCTTTATATAGATGGGGCTAGCACACCTAGCCGATCTTTAGGCAATCCGACTAGG 6597  
Qy 2101 ATTTCAGGGGAGAAAGAAATTAACATCTACCTGTTCATCAATCAAGATGTAGAT 2160  
Db 6598 ATTTCAGGGGAGAAAGAAATTAACATCTACCTGTTCATCAAGATGTAGAT 6657  
Qy 2161 AGATATATTAAGCAAGTGGCCCTTGAAGTCTCCGTTGGCATTTAAATATGAGACACA 2220  
|||||

Db 6658 AGATATATTAAGCAAGTGGCCCTTGAAGTCTCCGTTGGCATTTAAATACTGAGACACA 6717  
Qy 2221 ATTATGAACGCATTAACATCTCTCTCTTATCAGATTAATGAGCTGCAAAACAAGTGGG 2280  
Db 6718 ATTATGAACGCATTAACATCTCTCTCTTATCAGATTAATGAGCTGCAAAACAAGTGGG 6777  
Qy 2281 TGGGGGCACTATCCATGACCCAGATTAATATAGGGGGGATTAAGCAAAAGAACTCATGTA 2340  
Db 6778 TGGGGGCACTATCCATGACCCAGATTAATATAGGGGGGATTAAGCAAAAGAACTCATGTA 6837  
Qy 2341 GATGATGCTAGTATGTCACATCATCTATCCCTCTGCAATTCGAAGAAATCTGAATTTT 2400  
Db 6838 GATGATGCTAGTATGTCACATCATCTATCCCTCTGCAATTCGAAGAAATCTGAATTTT 6897  
Qy 2401 ATCCGGGCGCTTACTACAGATCAGGTTGCACTCGAATACCTCATTTGACATGAGTCT 2460  
Db 6898 ATCCGGGCGCTTACTACAGATCAGGTTGCACTCGAATACCTCATTTGACATGAGTCT 6957  
Qy 2461 ACCCATTAAGCTTACACCCATTAATGTAAATATGTCTGGAATGCAAGATCACTCATTTCA 2520  
Db 6958 ACCCATTAAGCTTACACCCATTAATGTAAATATGTCTGGAATGCAAGATCACTCATTTCA 7017  
Qy 2521 TATCAGATTTTGAACCTTGTGTGCTCCGACATCTGCAACAGGAGGGATTTCTTTTCT 2580  
Db 7018 TATCAGATTTTGAACCTTGTGTGCTCCGACATCTGCAACAGGAGGGATTTCTTTTCT 7077  
Qy 2581 ACTCTGGCTTCATCAACCTTGAACGACACCCAAATCGAAAGTCTTGCAAGTGTAGTCA 2640  
Db 7078 ACTCTGGCTTCATCAACCTTGAACGACACCCAAATCGAAAGTCTTGCAAGTGTAGTCA 7137  
Qy 2641 ACTCCCTGGGTTGTATGTCTGTCTCGAAAGTCAAGGAGACAGAGGAAAGATTAAT 2700  
Db 7138 ACTCCCTGGGTTGTATGTCTGTCTCGAAAGTCAAGGAGACAGAGGAAAGATTAAT 7197  
Qy 2701 AACTCAGCTGTCCTGAACGCGGATGCTACATGAGAGGTTAGGGTTGACGCGCAAGTACCAC 2760  
Db 7198 AACTCAGCTGTCCTGAACGCGGATGCTACATGAGAGGTTAGGGTTGACGCGCAAGTACCAC 7257  
Qy 2761 GAAAGGACCTAGATGTCAACAACATTATTCGGGACCTGGTGCGCAACTACCCAGAGATA 2820  
Db 7258 GAAAGGACCTAGATGTCAACAACATTATTCGGGACCTGGTGCGCAACTACCCAGAGATA 7317  
Qy 2821 GGGGGTGGATCTTTTATTTGACAGCGCGGATAGTTCCTCAGTCTACGAGGGTTAAACC 2880  
Db 7318 GGGGGTGGATCTTTTATTTGACAGCGCGGATAGTTCCTCAGTCTACGAGGGTTAAACC 7377  
Qy 2881 AATTCAACCAAGTACCTGTACAGAAAGGAAATATGTGATATCAAGCCGATTAACATGAC 2940  
Db 7378 AATTCAACCAAGTACCTGTACAGAAAGGAAATATGTGATATCAAGCCGATTAACATGAC 7437  
Qy 2941 ACATGCCAGATGACAAAGATCTACAGATTGGAATGGCCAAAGTCTTGATTAAGCCTTGA 3000  
Db 7438 ACATGCCAGATGACAAAGATCTACAGATTGGAATGGCCAAAGTCTTGATTAAGCCTTGA 7497  
Qy 3001 CGGTTTGGTGGAAACGATACAGACAGGCTATCTTATCTATCAAGGTGTCAACATCTTTA 3060  
Db 7498 CGGTTTGGTGGAAACGATACAGACAGGCTATCTTATCTATCAAGGTGTCAACATCTTTA 7557  
Qy 3061 GCGCAAGACCCGGTATCTGACTGTACCGCCCAACACAGTCACTCATATGCGGGCGAAGGC 3120  
Db 7558 GCGCAAGACCCGGTATCTGACTGTACCGCCCAACACAGTCACTCATATGCGGGCGAAGGC 7617  
Qy 3121 AGAATTCACAGTAAGGAGACATCATTTCTGTATCAACAGAGGGTCACTACTTCTCT 3180  
Db 7618 AGAATTCACAGTAAGGAGACATCATTTCTGTATCAACAGAGGGTCACTACTTCTCT 7677  
Qy 3181 CCCCGTTATATATTCCTATGACAGTCAAGCAAAACAGCACCTCTTCATATGTCCTTAT 3240  
Db 7678 CCCCGTTATATATTCCTATGACAGTCAAGCAAAACAGCACCTCTTCATATGTCCTTAT 7737  
Qy 3241 ACATTCATATGCTTCACTCGGCGAGTATATCCCTTGGCATTTGAGCAAGATGCCCC 3300  
Db 7738 ACATTCATATGCTTCACTCGGCGAGTATATCCCTTGGCATTTGAGCAAGATGCCCC 7797  
|||||



Qy 3301 AACTCGTGTGTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358  
Db 7798 AACCTGCTGTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 7855

RESULT 4  
AF077761 15186 bp RNA linear VRL 23-MAR-1999  
LOCUS Newcastle disease virus strain Lasota, complete genome.  
DEFINITION AF077761  
ACCESSION AF077761  
VERSION AF077761.1 GI:3386504  
KEYWORDS  
SOURCE  
ORGANISM  
Newcastle disease virus  
Newcastle disease virus  
Viruses; ssRNA negative-strand viruses; Mononegavirales;  
Paramyxoviridae; Paramyxovirinae; Avulavirus.  
REFERENCE  
1 (bases 1 to 15186)  
de Leeuw, O. and Peeters, B.  
Complete nucleotide sequence of Newcastle disease virus: evidence  
for the existence of a new genus within the subfamily  
Paramyxovirinae  
J. Gen. Virol. 80 (Pt 1), 131-136 (1999)  
JOURNAL  
PUBMED 9934695  
REFERENCE 2 (bases 1 to 15186)  
de Leeuw, O.S. and Peeters, B.P.H.  
Direct Submission  
TITLE Submitted (14-JUL-1998) Avian Virology, Institute for Animal  
Science and Health (ID-DLO), Edelhertweg 15, Lelystad, Flevoland  
8219 PA, The Netherlands  
JOURNAL  
PUBMED 122.1591  
REFERENCE 1.15186  
Location/Qualifiers  
FEATURES  
source  
/organism="Newcastle disease virus"  
/mol\_type="genomic RNA"  
/strain="Lasota"  
/db\_xref="taxon:11176"  
56.1792  
/gene="NP"  
56.1792  
/gene="NP"  
/product="nucleocapsid protein"  
122.1591  
/product="NP"  
/codon\_start=1  
/product="nucleocapsid protein"  
/protein\_id="AAC28371.1"  
/db\_xref="GI:3386505"  
/translation="MSSVFPDEYEQLLAQTRPENGAGGEGEKSTLKVDVPEFTLNSD  
PEIDMSFVVFCLRIAVSEBANKPLRQALISLCSHQQVMKNHYAIAKQNEATLAVL  
EIDGFANGTPOFNRSQVSEERAQRFAMISLPRACSGNGRPFVTAGADPADPDITD  
LTREILSLIOQVWTVAKAMTAYETADESETRRLINKMOGRVQKTYILPVCSTIO  
LTRQSLAVRILPVSSELKRGNTAGSTYNNIVGDVDSYRNTGLTAPELTLKYGIN  
TKTSALALSSISGDIQKMKQLRIYRKGDNAFYMTILGSDQMSFPAEAYQIXSRA  
MGVASVLDKGTGKQFARDEWSTFWRLGVEYVQAQGSINEDAAELKLTLPAMKCL  
AAAQRVSDTSSILYMPITQGVLTGLSEGSQALQGSNRSQGPBAAGDETQFDLL  
MRAVANSMRAEPNAQCTPQSGPPPTGSPQDNDTDMGY"  
1804.3244  
/gene="NP"  
1804.3244  
/gene="NP"  
/product="phosphoprotein"  
1887.3074  
/gene="NP"  
/codon\_start=1  
/product="phosphoprotein"  
/protein\_id="AAC28372.1"  
/db\_xref="GI:3386506"  
/translation="MATFTDAEIDELPETSQTVINDITTAQKPAETVGSAPFOGKT  
KVLAAEKSGSTOPASQNDPBDSDQVNPQETTPHSDPATSPADOPKAGS  
EAYDTORTGASNSLLMLDKLSRKSNAKKGPMSSFOEGNHQRPTOOQSGOPRQAS  
QERQONVKAAPNGQTDVNTAYHGQWEESSLSGATPHALRSQSDNTLVSADHQ  
PPVDFOAMMSMEAIQSQRVSKVDYLDLVTKQTSIIPMKRSEIQDLKTSVAVNEANI  
GMKILDPGCAINSSLSDLRAVASHPLVSGPDPSPRYVTQGGEMALNKLSQVPPHP

gene 3256.4487  
/gene="M"  
3256.4487  
/gene="M"  
/product="matrix protein"  
3290.4384  
/gene="M"  
/codon\_start=1  
/product="matrix protein"  
/protein\_id="AAC28373.1"  
/db\_xref="GI:3386507"  
/translation="MDSRTIGLYPDSANSSNLLAFPIVLYQGTGQKQIADQYRIQ  
RLDLMTDSKEDSVFITYGPIFQVNEEAVNGMIDDKPKRELISAMLCLGSVPTGD  
LILAAACLETMIWYCKKSATNTERMVSVVOAFQVQSCHVANRKSVAVAHVXKAP  
EKI PGSGTLEYKVPVSLIVVPRKDVKIPLAALVYQSSSLYNLALNTINVEVDPS  
PIYKSKSDSPGYANLPLHIGMTVTPRNGKVTDTDEKTRISLDISGLDVGDP  
SVLVKAGARTKLALPFFSSGACTPIYANASQVAKILMSQTAICLRSVKILTIQAGIQ  
RAVAVYADHEVTSTKLEKHTLAKNPFKK"  
4498.6279  
/gene="F"  
4498.6279  
/gene="F"  
/product="fusion protein"  
4544.6205  
/gene="F"  
/codon\_start=1  
/product="fusion protein"  
/protein\_id="AAC28374.1"  
/db\_xref="GI:3386508"  
/translation="MGSRPSTKNPAPMMLTIRVALVLSCTCPANSDIGREPLAAGIV  
TCGRKAVNIYSSQGTGSIIVLPLNLPDKXCAKAPADAYNRPLTTLPLGSIIRI  
QESVTSVGGROGLIGALIGVALGATTAQITAAALIOAQONANILPESISA  
TNEAVHVTGDSOLAVAGKMOQFVNDQNTAOBLDCIKIAQVGEINLIVTELT  
TVGFPQITSPLAKLTIQALYNLAGSNMIDLTKLVGNNOISLIGSGILITNPILY  
DSQTLQIGIVLTPSVGNLNNRATYLETLSVSTKGFASALVPKYVTQVGYIIBED  
TSYCIETDLDLYCTRIVTFPMSPGIYSCLSGNTSACWYSTEGALTTPWYTIQSVIA  
NCKMTTCRCVNPFGIISQNYGEASLIDKSCNVLISGITLRLSGFVTYQKNISI  
QDSOVLIITGNLIDISTELGNVNSISNALNLTRESNRKLDKVNKLTSTSLATYIVLT  
IISLVFGIISLILACYLMYKQKQKQTLMLGNNTIDQMAATTIKM"  
6321.8312  
/gene="HN"  
6321.8312  
/gene="HN"  
/product="hemagglutinin-neuraminidase"  
6412.8145  
/gene="HN"  
/codon\_start=1  
/product="hemagglutinin-neuraminidase"  
/protein\_id="AAC28376.1"  
/db\_xref="GI:3386510"  
/translation="MDRAVSOVALENDERAKNTWRLIPRIAILPLTVVTLAISVSL  
LYSMGASTPBDLVGIFTRISRAEKITSTIGSNQDVYDRIRYKVALESPLALNTEET  
IMNALTSLSQOINGAANNSSWGAPIHDPDTIGIGELIVDDSDVTSFYSPAFQEBL  
NFIIPATPGGCTRIIPSPDMSATHYCTHNVILSGCRDHSYQYALGVLRYSATGR  
VFPSLRSILNLDTONRKSQSVATPLGCDMLCSKYETEEDBYNSAVPRMVGRLG  
FDQGYHEKLDVTLTFGDWVANYBGVGGGFIISRYWFSYVGLKPPSPEDTVOEGKY  
VITYKRYNDPCPDQDQIIPMAKSYSGRGRGRIQOALISITVSTIGEDPVLIVP  
NITYLWAGSRKILIVGSHFLYORGSSYSPALLIYPTVSNKRTATLHSPPTPAFRP  
GSILPQASARCSPNSCVTVYTDYPLIPKNNHLRQFGIMLDGVQARLNPASAVFDS  
TSRSRITRVSSSTKAAYTSTCFKVKVKNKYCLSIABISNTLIFGFRIVPLVELL  
KDDGVEARSG"  
8370.15073  
/gene="L"  
8370.15073  
/gene="L"  
/product="large polymerase protein"  
8381.14995  
/gene="L"  
/codon\_start=1  
/product="large polymerase protein"  
/protein\_id="AAC28375.1"

/db xref="GI:3386509"  
/translation="MASSGPERAEHQIILPEPHISSPLVXKLIYWKLTGLPIPDEBC  
D/PHILSRQMKILBESPTERMIKIGRAVHQTLMHNSITITVLPRCELOJLANIE  
VPDSNFKRLEKIKIQLHNTYGEI.FRLCTHIEKLIKSSMSNVNRSFSSIRPD  
PAWPHSKMAKFAHMIKOIOLHLMVAATRAAKKLWLTHKVOFVPTPLVVV  
THHNENKFTCLTOELVUMYADMBGRDUNNISTPAHILBSLCKIDDIILDALAK  
DLGNQVDFVSLMEGFAYGAVOLBEPGTFAPFANLOBLKOITLGLPELASEV  
THAIATVFSLEQOQAEMLCILRLMGPBLESRIIAKAVSQCAKRMADPMDILOY  
LSPEKGTIINGVRKNAGVWRVAVDITYGVIQOLHADSMEIHDIMLEKYSLSL  
EFPECIYDPTVNTSMFLKDKALHPNDNMASPRNNLPGKIKIIGVSNPDIETLY  
EPLESNDPDKEMEYLTLELYLBDNVAVSYLKEKVENGRIPAKITKLMCOV  
MABEILADQIAPFQNGVLODSILTKMSLAMSQSLFNSKRIITOCKERSVSNRHH  
DPSKNRKRVATFIITDLOKYCLNWRVQITLFPALAINOLMGLKPFHEVHLRLMDIT  
MPVADPNPQSDPDCDLSRVPNDIIVYSRGGIIEGLCOGLWMIISAIIOQLAAS  
HCRVACWQGNQVIAVTRVRSDDSEPMVTOHQASDFEKLHVNHLIOLHADS  
RETRSDTFEYSKRIFKDGAISQVKNSSKLTVAGSDSENMVAVSIVAVL  
CENGLPRDFCYLYNIMSVOYVETSPSITNNSHPLDNOIEMIDISFMSVYLTVAL  
LGLSINQYERLYTRNIGDQETTRPAIKLEAVGLSPINMTNIIIRPRENGMAL  
CNDSYFNFEVASPNIVLKKHQIVLFECSNPLLSGVTAEAEKMADEFLNLO  
EVHPRVAAHIMEASVGRKQIOGLVDTNTVIKIALTRPDIKILMRIVNSMH  
AMLPRDVPSSSRNHPVSSNMCSLTADYARNRWSPLTGGKIKIGVSNPDIETLY  
EGELISVSGCTRCDSGDEOPTMHLPSNIELDTSKNPMRPVLYSGKTOERBAVS  
LAKIAMSPHYKALBASVLIAYGDNVNMWTAALIAKRCVNLLEYLRLSPLEP  
AGNDQRLDGIOTMFTPASLRCHLFTYPMILKCSLKESKRMFTNRVMLIG  
LSLBSIFPMPTTTRTYDEITLHLSKSCCIREAPVAVPELGLVBEIRVSNKEM  
YDPSVEEDGFARLDLAIPKSYELNLESYPTIELMNLISISGLIQSVSVYDEDS  
IKNDALIVYONTRMISEAONSQVRLFEVAALEVLNDCSGLIYLRGNDVLNM  
GDLYKMPGILISNIAATISHPVHSLHAGVYNHGSQHLADPTDEMSAGLIVSC  
TRVYSGISGNKIDLPSPVLDNDLNBKMLQILSRICLITVLPATREIPKRGIT  
AEKCSILTEYLSDAVPLSPDVSSIMSPNITTEPANLYNRSRLNIRREBR  
DITIALFPOEPLPEPSVODIGARVDPTRQPAOLFEDLSAPARAYATFOH  
PELTPSPBEDYLVRLEFRGIGTASSMYKASHLSPEVCAAGNSLYAIESGAI  
MSLELHVPHETIYNTLFSNEMNPPORHRRPPTOLNIVVYNIABVCKOGFPO  
EPRPEMTEBESDTSKAVGYTTSAPVRPSVLIKCDIEIPGNSOILDOALAT  
SLIAMSVRREGVITIKVLYAMGYTHLMLNLPACSTKGYILNSGYACGDECTIV  
PVNGYLGKPTFVHEVVMARTLVGRHGTILSKSDEITLRLTFSQORVADILSSPL  
RLIKYLNKIDITLIEAGQVPRPCEASLSTLANITOLTOIILASHIDIVRSVTP  
BAEGLDADYVLFRTYPLNLTGDKRSTLICTROILLEVTLIGLEVMINKGDIISIV  
LKMISMEDILPLRTYLKHSICPKYKAVIGITLXEMFIDTSLVLYTRAQOKRYMT  
IGNAVKGYNSNCS"

## ORIGIN

Query Match 99.9%; Score 3353.2; DB 13; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3353; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ACCGGTGAAGATTCTGATCCGGTGGCGCCTCCAGGTGCAAGATGGGCTCCAGACC 60  
DB 4498 ACCGGTGAAGATTCTGATCCCGGTTGGCGCCTCCAGGTGCAAGATGGGCTCCAGACC 4557  
QY 61 TTCTACCAAGAACCCAGACCTTATGATGCTGACATATCCGGGTTGCCGTGGCACTGAGTTG 120  
DB 4558 TTCTACCAAGAACCCAGACCTTATGATGCTGACATATCCGGGTTGCCGTGGCACTGAGTTG 4617  
QY 121 CATCTGCCGCAAACTCCATTTGATGCAAGGCTCTTGACAGCTCAGAGAAATTTGGTTAC 180  
DB 4618 CATCTGCCGCAAACTCCATTTGATGCAAGGCTCTTGACAGCTCAGAGAAATTTGGTTAC 4677  
QY 181 AGGAGCAAAAGCCGCTCAACATATACCTCATCTCCAGACAGAGATCAATCATATTAAAGCT 240  
DB 4678 AGGAGCAAAAGCCGCTCAACATATACCTCATCTCCAGACAGAGATCAATCATATTAAAGCT 4737  
QY 241 CTTCCCGAATCTGCCCAAGATTAAGAGGCAATGCGCAAGCCCCCTTGGATGCAATACAA 300  
DB 4738 CTTCCCGAATCTGCCCAAGATTAAGAGGCAATGCGCAAGCCCCCTTGGATGCAATACAA 4797  
QY 301 CAGGACATGACCACTTTGCTCACCCCCCTTGATGACTCTATCCGTAAGATCAAGAGATC 360  
DB 4798 CAGGACATGACCACTTTGCTCACCCCCCTTGATGACTCTATCCGTAAGATCAAGAGATC 4857  
QY 361 TGTGACTTACATCTTGAGAGGGGAGACAGGGCGCTTATAGCCCATTAATTTGGCGGTGT 420  
DB 4858 TGTGACTTACATCTTGAGAGGGGAGACAGGGCGCTTATAGCCCATTAATTTGGCGGTGT 4917

QY 421 GGCTCTGGGGTTGCAACTGCGCGACAAATPACAGCGCGCGAGCTCTGATACAAAGCCA 480  
DB 4918 GGCTCTGGGGTTGCAACTGCGCGACAAATPACAGCGCGCGAGCTCTGATACAAAGCCA 4977  
QY 481 ACAAATGCTGCGCAACATCCCTCGACCTTAAGAGAGAGATTCGCGCAACCAATGAGGCTGT 540  
DB 4978 ACAAATGCTGCGCAACATCCCTCGACCTTAAGAGAGAGATTCGCGCAACCAATGAGGCTGT 5037  
QY 541 GCATGAGGTCACTGACGGAATTAATGCAACTAGCAGTGGCAGTTGGGAAGATGACAGATT 600  
DB 5038 GCATGAGGTCACTGACGGAATTAATGCAACTAGCAGTGGCAGTTGGGAAGATGACAGATT 5097  
QY 601 TGTTAATGACCAATTATTAATAAAGAGTCAAGAAATTAAGCTGCATCAAAATTTGACACGCA 660  
DB 5098 TGTTAATGACCAATTATTAATAAAGAGTCAAGAAATTAAGCTGCATCAAAATTTGACACGCA 5157  
QY 661 AGTTGGTGTAGAGTCAACCTGTATCTTACCGGAATTAAGTCAAGATTAATGCGACCAAAAT 720  
DB 5158 AGTTGGTGTAGAGTCAACCTGTATCTTACCGGAATTAAGTCAAGATTAATGCGACCAAAAT 5217  
QY 721 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTTACATCTAGCTGGTGGAAA 780  
DB 5218 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTTACATCTAGCTGGTGGAAA 5277  
QY 781 TATGATTAATCTTATTTGACTAAGTTAGGTGTAGGGAAACAATCAACTCAGCTTAAATCGG 840  
DB 5278 TATGATTAATCTTATTTGACTAAGTTAGGTGTAGGGAAACAATCAACTCAGCTTAAATCGG 5337  
QY 841 TAGCGGCTTAATCAACCGGTAACTTATTCATNACACTCACAGACTCAACTCTTGGGTAT 900  
DB 5338 TAGCGGCTTAATCAACCGGTAACTTATTCATNACACTCACAGACTCAACTCTTGGGTAT 5397  
QY 901 ACGGTATCTCTACCTTCACTGCGGGAACCTTAATTAATGCGGCACTTACTTGGAAAC 960  
DB 5398 ACGGTATCTCTACCTTCACTGCGGGAACCTTAATTAATGCGGCACTTACTTGGAAAC 5457  
QY 961 CTTATCCGTGAAGCAACAACGAGGATTTGGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
DB 5458 CTTATCCGTGAAGCAACAACGAGGATTTGGCTCGGCACTTGTCCCAAAAGTGTGACACA 5517  
QY 1021 GGTCGGTCTGTGATAGAAAGACTTGCACCTCATCTGATATAGAACTGACTTAATTT 1080  
DB 5518 GGTCGGTCTGTGATAGAAAGACTTGCACCTCATCTGATATAGAACTGACTTAATTT 5577  
QY 1081 ATATTGTACAAGAAATATTAAGTTCCTATGTCCTCGATATTAATCTCGCTGAGCGG 1140  
DB 5578 ATATTGTACAAGAAATATTAAGTTCCTATGTCCTCGATATTAATCTCGCTGAGCGG 5637  
QY 1141 CAATACGTGGGCTGTATGTACTCAAGAAGCGGCACTTACTACACCATATGATGAC 1200  
DB 5638 CAATACGTGGGCTGTATGTACTCAAGAAGCGGCACTTACTACACCATATGATGAC 5697  
QY 1201 TATCAAGGTTCAGTCACTGCGCAACTGCAAGATGACAAACATGTAGATGTGTAAACCCGCC 1260  
DB 5698 TATCAAGGTTCAGTCACTGCGCAACTGCAAGATGACAAACATGTAGATGTGTAAACCCGCC 5757  
QY 1261 GGGTATCATATCGCAAAACTATGAGAGAGCCGTGTCTCTAATAGATTAACAATCATATGCA 1320  
DB 5758 GGGTATCATATCGCAAAACTATGAGAGAGCCGTGTCTCTAATAGATTAACAATCATATGCA 5817  
QY 1321 TGTTTTATCTTATGGGCGGAGTAACTTTAAGGCTCAGTGGGGAATTTGATGTAACTTATCA 1380  
DB 5818 TGTTTTATCTTATGGGCGGAGTAACTTTAAGGCTCAGTGGGGAATTTGATGTAACTTATCA 5877  
QY 1381 GAAGATATCTCAATACAGAGATTCCTCAAGTAAATTAATAAGGCAATCTTATATCTCAAC 1440  
DB 5878 GAAGATATCTCAATACAGAGATTCCTCAAGTAAATTAATAAGGCAATCTTATATCTCAAC 5937  
QY 1441 TGAGCTTGGAAATGTCAACAATCTGATCAGTAATGCTTTGAATTAAGTTAAGGAAAGCAA 1500  
DB 5938 TGAGCTTGGAAATGTCAACAATCTGATCAGTAATGCTTTGAATTAAGTTAAGGAAAGCAA 5997

OY	1501	TAGAAAATACAAAGCAAGCATGTCACAACTGACATGCACTGCTCATCTATCTATAT	1560
Db	5998	CAGAAAATACAAAGCAAGCATGTCACAACTGACATGCACTGCTCATCTATCTATAT	6057
OY	1561	CGTTTGGACTATCATATCTCTTGTTTTTGGTATACCTTAGCTGATTCAGCATCTACT	1620
Db	6058	CGTTTGGACTATCATATCTCTTGTTTTTGGTATACCTTAGCTGATTCAGCATCTACT	6117
OY	1621	AATGTACAGCAAAAAGCGGCACAAAACCCTTATATATGCTTGGGAATATATCTTAGA	1680
Db	6118	AATGTACAGCAAAAAGCGGCACAAAACCCTTATATATGCTTGGGAATATATCTTAGA	6177
OY	1681	TCAGATGAGACCCACTACAAAATGTGAACACAGATGAGAACAGAGGTTCCCTAATAG	1740
Db	6178	TCAGATGAGACCCACTACAAAATGTGAACACAGATGAGAACAGAGGTTCCCTAATAG	6237
OY	1741	TAAATTGTGTAAAGTTCTTGATAGTCTGTCAAGTTACAGAGATTAAAGAAAACACCGGT	1800
Db	6238	TAAATTGTGTAAAGTTCTTGATAGTCTGTCAAGTTACAGAGATTAAAGAAAACACCGGT	6297
OY	1801	TGTAGATGACCAAAAGGACGATATACGGGTAGAACGGTAAAGAGAGCGCCCTCAATTGC	1860
Db	6298	TGTAGATGACCAAAAGGACGATATACGGGTAGAACGGTAAAGAGAGCGCCCTCAATTGC	6357
OY	1861	GAGCCAGGCTTCACAACTCCGTTCTACCGCTTCACCGACAAACAGTCTCTCAATATAGAC	1920
Db	6358	GAGCCAGGCTTCACAACTCCGTTCTACCGCTTCACCGACAAACAGTCTCTCAATATAGAC	6417
OY	1921	CGCGCCGTTAGCAAGTTGCGGTAGAGATGATGAAGAAAGAGGCAAAAATATACATGGCGC	1980
Db	6418	CGCGCCGTTAGCAAGTTGCGGTAGAGATGATGAAGAAAGAGGCAAAAATATACATGGCGC	6477
OY	1981	TTGATATTCCGGATTGCAATCTTATTCTTAAACAGTAGTACCTTGCTATATCTGTAGCC	2040
Db	6478	TTGATATTCCGGATTGCAATCTTATTCTTAAACAGTAGTACCTTGCTATATCTGTAGCC	6537
OY	2041	TCCCTTTATATAGCATGGGGGCTTAGCACACTTAGCCATCTTGTAAGCATCCGACATAGG	2100
Db	6538	TCCCTTTATATAGCATGGGGGCTTAGCACACTTAGCCATCTTGTAAGCATCCGACATAGG	6597
OY	2101	ATTTCACAGGAGAAAGAAAGTTACATCTACACTGTTGCCATCAAGATGTAGTAGAT	2160
Db	6598	ATTTCACAGGAGAAAGAAAGTTACATCTACACTGTTGCCATCAAGATGTAGTAGAT	6657
OY	2161	AGGATATATTAAGCAAGTGCGCCCTTGAGTCTCCGTTGGCATTTGTAATATCTAGACACA	2220
Db	6658	AGGATATATTAAGCAAGTGCGCCCTTGAGTCTCCGTTGGCATTTGTAATATCTAGACACA	6717
OY	2221	ATTATGAACGCATPAACATCTCTCTCTTATCAGATTAAATGAGCTGCACAAACAGTGGG	2280
Db	6718	ATTATGAACGCATPAACATCTCTCTCTTATCAGATTAAATGAGCTGCACAAACAGTGGG	6777
OY	2281	TGGGGGGGCACTATCCATGAGCCAGATTATATAGGGGGGATAGGCAAAAGACTAATGTA	2340
Db	6778	TGGGGGGGCACTATCCATGAGCCAGATTATATAGGGGGGATAGGCAAAAGACTAATGTA	6837
OY	2341	GATGATGCTAATGATGTCACATCAATCTATCCCTCTGCAATTTCAAGACATCTGAATTTT	2400
Db	6838	GATGATGCTAATGATGTCACATCAATCTATCCCTCTGCAATTTCAAGACATCTGAATTTT	6897
OY	2401	ATCCGGGCGCTTACTACAGATTCAGAGTTGCACTCGAATACCTCTATTTGACATGAGTCT	2460
Db	6898	ATCCGGGCGCTTACTACAGATTCAGAGTTGCACTCGAATACCTCTATTTGACATGAGTCT	6957
OY	2461	ACCCATTATCTGTACACCCATTAATGTATATTTGCTGTGATGACAGATCACTCAATTTCA	2520
Db	6958	ACCCATTATCTGTACACCCATTAATGTATATTTGCTGTGATGACAGATCACTCAATTTCA	7017
OY	2521	TATCAGATTATAGCACTTGTTGTGCTCGGACATCTGCACAGGAGGGGTATTTCTTTCT	2580
Db	7018	TATCAGATTATAGCACTTGTTGTGCTCGGACATCTGCACAGGAGGGGTATTTCTTTCT	7077
OY	2581	ACTCTGCGCTTCATCACTCGACACACCAAAATCGAAAGTCTTGCAAGTGTAGTGCA	2640

Db	7078	ACTCTGGTTCCATCAACCTGGACGACACCCAAAATCCGAAGTCTTGCAGTGTAGTGCA	7137
QY	2641	ACTCCCTGGGTGTGATATGCTGTGCTGAAAGTCACGAGACAGAGAAAGATTAT	2700
Db	7138	ACTCCCTGGGTGTGATATGCTGTGCTGAAAGTCACGAGACAGAGAAAGATTAT	7197
QY	2701	AACACAGCTGTCCCTACGGGAGATGGACATAGGGAAGTTAAGGTTGACGGGCAGTACAC	2760
Db	7198	AACACAGCTGTCCCTACGGGAGATGGACATAGGGAAGTTAAGGTTGACGGGCAGTACAC	7257
QY	2761	GAAGAAGACCTAGATGTCAACAATTATCGGGGACTGGGTGGCCACTACCCAGAGTA	2820
Db	7258	GAAGAAGACCTAGATGTCAACAATTATCGGGGACTGGGTGGCCACTACCCAGAGTA	7317
QY	2821	GGGGGTGATCTTTTATATGACAGCGCGGTATGTTCTCAGTCTACGAGGTTAAACCC	2880
Db	7318	GGGGGTGATCTTTTATATGACAGCGCGGTATGTTCTCAGTCTACGAGGTTAAACCC	7377
QY	2881	AATTACACCCAGTACACTGTACAGAGAAAGAAATATGTATATACAAACGATACATGAC	2940
Db	7378	AATTACACCCAGTACACTGTACAGAGAAAGAAATATGTATATACAAACGATACATGAC	7437
QY	2941	ACATGCCAGATAGACAAAGCTACCCAGATTCGAATGGCCCAAGTCTTCATTAAGCTTGA	3000
Db	7438	ACATGCCAGATAGACAAAGCTACCCAGATTCGAATGGCCCAAGTCTTCATTAAGCTTGA	7497
QY	3001	CGGTTTGTTGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTCTCAACATCTTA	3060
Db	7498	CGGTTTGTTGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTCTCAACATCTTA	7557
QY	3061	GGCGAAGACCCGGTACTGACTGTACCCGCCAACAAGTACACATATGGGGGGCGAAGGC	3120
Db	7558	GGCGAAGACCCGGTACTGACTGTACCCGCCAACAAGTACACATATGGGGGGCGAAGGC	7617
QY	3121	AGAATTCTCAGACTAGGAGCATCTCATTTCTTGTATCAACGAGGCTCATCTACTTCT	3180
Db	7618	AGAATTCTCAGACTAGGAGCATCTCATTTCTTGTATCAACGAGGCTCATCTACTTCT	7677
QY	3181	CCCGCGTTATATATCTTATGACAGTACAGCAAAACAGCCACTCTTCATATGCTCTTAT	3240
Db	7678	CCCGCGTTATATATCTTATGACAGTACAGCAAAACAGCCACTCTTCATATGCTCTTAT	7737
QY	3241	ACATTCAATGCTTCACTGGCGCAGGTAGTATCCCTTGCAGAGCTTCAGCAAGATGCCCC	3300
Db	7738	ACATTCAATGCTTCACTGGCGCAGGTAGTATCCCTTGCAGAGCTTCAGCAAGATGCCCC	7797
QY	3301	AACCTGGTGTACTGAGGCTCTATACAGATCCATATCCCTATCTTCATAGAAACC	3358
Db	7798	AACCTGGTGTACTGAGGCTCTATACAGATCCATATCCCTATCTTCATAGAAACC	7855
RESULT 5			
NDVY18898			
LOCUS	NDVY18898	15186 bp	RNA linear VRL 18-APR-2005
DEFINITION	Newcastle disease virus cDNA to complete genomic RNA, clone 30.		
ACCESSION	Y18898		
VERSION	Y18898.1	GI:5578883	
KEYWORDS	F gene; fusion protein; hemagglutinin-neuraminidase; HN gene; L gene; large protein; M gene; matrix protein; NP gene; nucleocapsid protein; P gene; phosphoprotein.		
SOURCE	Newcastle disease virus		
ORGANISM	Newcastle disease virus		
REFERENCE	Viruses; asRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirinae.		
AUTHORS	1 Romer-Oberdorfer, A., Mundt, E., Mebatsion, T., Buchholz, U. J. and Mettenleiter, T. C.		
TITLE	Generation of recombinant lentogenic Newcastle disease virus from cDNA		
JOURNAL	J. Gen. Virol. 80 (PT 11), 2987-2995 (1999)		
PUBMED	10580061		
REFERENCE	2 (bases 1 to 15186)		



AUTHORS Romer-Oberdorfer, A.  
TITLE Direct Submission  
JOURNAL Submitted (31-MAR-1999) A. Romer-Oberdorfer, Federal Research  
Centre for, Virus Diseases of Animals, Insel Riem, D-17498, FRG

FEATURES  
source Location/Qualifiers  
1.15186

gene /organism="Newcastle disease virus"  
/mol\_type="genomic RNA"  
/db\_xref="taxon:11176"  
/clone="30"  
56.11792  
/gene="NP"  
56.11792  
/gene="NP"  
/product="nucleocapsid protein"  
122.1591  
/gene="NP"  
/codon\_start=1  
/product="nucleocapsid protein"  
/protein\_id="CAB51322.1"  
/db\_xref="GI:5578884"  
/db\_xref="GOA:Q9MMH9"  
/db\_xref="InterPro:IPR002021"  
/db\_xref="UniProt/TREMBL:Q9MMH9"  
/translation="MSSVPDEYEQLLAQTTPNGAHGSGEGKSTLKVDVPVFTLNSDD  
PEDRWFVFCRLAVSEDAKPLQCALISLCSHSQVMNHVALAGKQVETLAVL  
EIDGFAGTPOFNRRSGVSEBAQRFAMIGSLPRASNGTPTTAGADPADITD  
TLERILSLQAOVWTAKAMTAYETADESERRRINRYMOGGRVOKKTLIVPCSTIO  
LITRQSLAVRIFLVSELKRGANTRGSTYTNLVGDVSTIRNTGLTAFITLKGIN  
TKTSALSLSLSDI IQMKQIMRLYRKMGDAPYMTLLGSDQMSFAPAEYAOUSFA  
MGAAVLDKGTGKYQFARDPMWSTFMRIGVEYAOQSSINEDMAAEIKLTPARRGL  
AAAQRVSEETSSIDMPTQOVGLTGLSEGSQALQCGSNRSQCPPEAGCGETQFLDL  
MRVANSMEAPNSAQGTPOSGPPPTPGPSQDNDTNGY"

CDS  
/gene="P"  
1804.3244  
/gene="P"  
1804.3244  
/gene="P"  
/product="phosphoprotein"  
1887.3074  
/gene="P"  
/codon\_start=1  
/product="phosphoprotein"  
/protein\_id="CAB51323.1"  
/db\_xref="GI:5578885"  
/db\_xref="GOA:Q9MMH8"  
/db\_xref="InterPro:IPR004897"  
/db\_xref="UniProt/TREMBL:Q9MMH8"  
/translation="MATFDAEIDELFETSGTIGNITTAQGEPAETVSGSAIPQGT  
KVLAAAEKHGSIQPPASQNPDRQDSKQSTPEQOTPHDSPPATSAQPPQATD  
EAYDQTRTGASNSLIMDLKLSNKSNAKGPWSSPOEGNHORPTQOQSGSPRGS  
LBPQNVKAAFGNQTGTDVNTAHGQNEBSQLSAGATPHALRSQSDNTLVADHYQ  
PVDFVQAMMSWEAISIQRVSKVDYQDLVTKQTSIIPMMSEIQQLKTSVAWEANL  
GMKKILDPGCANISLSDRLAVASHPLVLSGPPSPYVYOGGEMALINKLSQVPHF  
SELIKPATACGPDIGVEKDTVRALIMSRPMHPSSAKLSKLDAAGSIEERIKRLA  
LNG"

gene /gene="M"  
3256.4487  
/gene="M"  
3256.4487  
/gene="M"  
/product="matrix protein"  
3290.4384  
/gene="M"  
/codon\_start=1  
/product="matrix protein"  
/protein\_id="CAB51324.1"  
/db\_xref="GI:5578886"  
/db\_xref="GOA:Q9W7T8"  
/db\_xref="InterPro:IPR000982"  
/db\_xref="UniProt/TREMBL:Q9W7T8"  
/translation="MDSSTRTIGLVFDSAHSSNLIAPPIVLQDTGDKKOIAPQYRIQ  
RLDIWDISKEDSVFITTYGPIFGVNGEATVGMIDDKPKELLAAAMLCGVSNTD  
LIELARCLTMIVTCKKSAINTERVFSVQAPOVLQSCRVAANKYSSVNAVKKVAP  
EKIPGSGTLFKVNFVSLTVVKKDYKIPAAVLKVGSSLYNLALNVTINVEVDRS

gene /gene="P"  
1804.3244  
/gene="P"  
1804.3244  
/gene="P"  
/product="phosphoprotein"  
1887.3074  
/gene="P"  
/codon\_start=1  
/product="phosphoprotein"  
/protein\_id="CAB51323.1"  
/db\_xref="GI:5578885"  
/db\_xref="GOA:Q9MMH8"  
/db\_xref="InterPro:IPR004897"  
/db\_xref="UniProt/TREMBL:Q9MMH8"  
/translation="MATFDAEIDELFETSGTIGNITTAQGEPAETVSGSAIPQGT  
KVLAAAEKHGSIQPPASQNPDRQDSKQSTPEQOTPHDSPPATSAQPPQATD  
EAYDQTRTGASNSLIMDLKLSNKSNAKGPWSSPOEGNHORPTQOQSGSPRGS  
LBPQNVKAAFGNQTGTDVNTAHGQNEBSQLSAGATPHALRSQSDNTLVADHYQ  
PVDFVQAMMSWEAISIQRVSKVDYQDLVTKQTSIIPMMSEIQQLKTSVAWEANL  
GMKKILDPGCANISLSDRLAVASHPLVLSGPPSPYVYOGGEMALINKLSQVPHF  
SELIKPATACGPDIGVEKDTVRALIMSRPMHPSSAKLSKLDAAGSIEERIKRLA  
LNG"

gene  
mRNA  
CDS

gene /gene="F"  
4498.6279  
/gene="F"  
4498.6279  
/gene="F"  
/product="fusion protein"  
4544.6205  
/gene="F"  
/codon\_start=1  
/product="fusion protein"  
/protein\_id="CAB51325.1"  
/db\_xref="GI:5578887"  
/db\_xref="GOA:Q9MMH7"  
/db\_xref="InterPro:IPR000776"  
/db\_xref="UniProt/TREMBL:Q9MMH7"  
/translation="MSSRPSTKPPAPMLITIRVALVYSCICPANSIDGRPLAAGIV  
TGDAVNIYYSRQGSITIVKLLPMLPROKACAPADATYRITLTLPLGDSIRKI  
QESVTVTSGGRQRLIGAILGVVALGATAQITPAALIOAKNANVILRLKESILA  
TNEAVHEVTGLSQLAVAVGMOQFVNDQENKIQEIDCIKIAQVGEVLVYLELT  
TVRPOITSPALNKLTIOALYNLAGAMDYLLTQLGNNOLSLISGLITGNPILY  
DSQQLGIGIYVTLPSVGNLNMATYVETLSYTKGPASALVPKVVTVQVSVEILD  
TSCLETDLVICTRIYVTPMSRGITISCLGNTSACMYSTEGALLTPYMTKSVIA  
NCKMTTCRCVNPPIISQNYGEAVSLIDKSCVNLISGGLTRLSGDFVYQKNISI  
QDSQVLIITGMULDISTELGANNYSINLNLKLEENRKLDRKNVLTLSALITIVLT  
IISLVFGLITLILACYIMYKQAKQKTLMLGNNTLDMRATTGN"

gene /gene="HN"  
6321.8312  
/gene="HN"  
6321.8312  
/gene="HN"  
/product="hemagglutinin-neuraminidase"  
6412.8145  
/gene="HN"  
/codon\_start=1  
/product="hemagglutinin-neuraminidase"  
/protein\_id="CAB51326.1"  
/db\_xref="GI:5578888"  
/db\_xref="GOA:O90340"  
/db\_xref="InterPro:IPR000665"  
/db\_xref="UniProt/TREMBL:O90340"  
/translation="MDRAVSQVALLNDRERKNTWRLIRIALIFLVVTLAISVSL  
LYSWGASTPDLVIGIPTRISRAEKITSTLGSNDVDVRIYKQVALSSPLALNTEET  
NLVMAITSLYOINAAANSQGAIPHDPVIGIKGLIYDDADVTSFYSAPAEHL  
NFIAPPTTSGGCTRIIPSEDMATHYCYTHNHTLISGGDHSYOLILGVYRTSATG  
VPSTLASINLUDTQNRKSGSVATPLPGCMILCSKATETEEDVNSAVPRMGARIG  
FDQGYHKKDLDVTTLFQGDWVANYPGVGGSFIDSRVFSYVGGIKPNSPSTVDEGKY  
VLYKRVNDDPBDQYDIRAKSXYKRGEGKRIQQAIIISIKVTSIGEDPVATVP  
NTVYLMGAEBRILTVGTSHEFLYORGSSYFEPALLYPMTVSNKATLHSPTYFNAFTP  
GSIIPCOASARCPMSCVGVTDPPPLIFYRNHTLGVETMLDGOARLNDASAVPS  
TSRSRITRVSSSSTKAAVYTSCTCKVKYKTKYCLSLAELISNTLFGFRIVPLVEIL  
KDDGVEARSG"  
8370.115073  
/gene="L"  
8370.115073  
/gene="L"  
/product="large protein"  
8381.14995  
/gene="L"  
/codon\_start=1  
/product="large protein"  
/protein\_id="CAB51327.1"  
/db\_xref="GI:5578889"  
/db\_xref="GOA:Q9MMH6"  
/db\_xref="InterPro:IPR001016"  
/db\_xref="UniProt/TREMBL:Q9MMH6"  
/translation="MASSGPERAEHOIILPESHSSPLVYKHLLYYKILGLPLPDEC  
DPHLLISRWKKTILBSASPDTERMTLGAAYHOTQNLNHSRGNVYRSEFSIRTD  
VPSTNFKRTEIEKKIQHNTRYGSLFRLLTTHLEKLLGSWSNNTVRSSEFSIRTD  
PAWPSHFKSTAFAMLIHQIQRHLWVARTSAANLVLWTHKQVQVTPPLVAV  
THNENKFTCLQVLELVYADMEGRGMVNIISTAVAHLSLSEKDIIDILRLDALAK  
DLGNQYDVVSLMEGFAYGAVQLLEPSTGTFAGDFAFNLIQELKIIDILGLLPNDIAESV

gene  
mRNA  
CDS

gene /gene="HN"  
6321.8312  
/gene="HN"  
6321.8312  
/gene="HN"  
/product="hemagglutinin-neuraminidase"  
6412.8145  
/gene="HN"  
/codon\_start=1  
/product="hemagglutinin-neuraminidase"  
/protein\_id="CAB51326.1"  
/db\_xref="GI:5578888"  
/db\_xref="GOA:O90340"  
/db\_xref="InterPro:IPR000665"  
/db\_xref="UniProt/TREMBL:O90340"  
/translation="MDRAVSQVALLNDRERKNTWRLIRIALIFLVVTLAISVSL  
LYSWGASTPDLVIGIPTRISRAEKITSTLGSNDVDVRIYKQVALSSPLALNTEET  
NLVMAITSLYOINAAANSQGAIPHDPVIGIKGLIYDDADVTSFYSAPAEHL  
NFIAPPTTSGGCTRIIPSEDMATHYCYTHNHTLISGGDHSYOLILGVYRTSATG  
VPSTLASINLUDTQNRKSGSVATPLPGCMILCSKATETEEDVNSAVPRMGARIG  
FDQGYHKKDLDVTTLFQGDWVANYPGVGGSFIDSRVFSYVGGIKPNSPSTVDEGKY  
VLYKRVNDDPBDQYDIRAKSXYKRGEGKRIQQAIIISIKVTSIGEDPVATVP  
NTVYLMGAEBRILTVGTSHEFLYORGSSYFEPALLYPMTVSNKATLHSPTYFNAFTP  
GSIIPCOASARCPMSCVGVTDPPPLIFYRNHTLGVETMLDGOARLNDASAVPS  
TSRSRITRVSSSSTKAAVYTSCTCKVKYKTKYCLSLAELISNTLFGFRIVPLVEIL  
KDDGVEARSG"  
8370.115073  
/gene="L"  
8370.115073  
/gene="L"  
/product="large protein"  
8381.14995  
/gene="L"  
/codon\_start=1  
/product="large protein"  
/protein\_id="CAB51327.1"  
/db\_xref="GI:5578889"  
/db\_xref="GOA:Q9MMH6"  
/db\_xref="InterPro:IPR001016"  
/db\_xref="UniProt/TREMBL:Q9MMH6"  
/translation="MASSGPERAEHOIILPESHSSPLVYKHLLYYKILGLPLPDEC  
DPHLLISRWKKTILBSASPDTERMTLGAAYHOTQNLNHSRGNVYRSEFSIRTD  
VPSTNFKRTEIEKKIQHNTRYGSLFRLLTTHLEKLLGSWSNNTVRSSEFSIRTD  
PAWPSHFKSTAFAMLIHQIQRHLWVARTSAANLVLWTHKQVQVTPPLVAV  
THNENKFTCLQVLELVYADMEGRGMVNIISTAVAHLSLSEKDIIDILRLDALAK  
DLGNQYDVVSLMEGFAYGAVQLLEPSTGTFAGDFAFNLIQELKIIDILGLLPNDIAESV

gene  
mRNA  
CDS

gene /gene="L"  
8370.115073  
/gene="L"  
8370.115073  
/gene="L"  
/product="large protein"  
8381.14995  
/gene="L"  
/codon\_start=1  
/product="large protein"  
/protein\_id="CAB51327.1"  
/db\_xref="GI:5578889"  
/db\_xref="GOA:Q9MMH6"  
/db\_xref="InterPro:IPR001016"  
/db\_xref="UniProt/TREMBL:Q9MMH6"  
/translation="MASSGPERAEHOIILPESHSSPLVYKHLLYYKILGLPLPDEC  
DPHLLISRWKKTILBSASPDTERMTLGAAYHOTQNLNHSRGNVYRSEFSIRTD  
VPSTNFKRTEIEKKIQHNTRYGSLFRLLTTHLEKLLGSWSNNTVRSSEFSIRTD  
PAWPSHFKSTAFAMLIHQIQRHLWVARTSAANLVLWTHKQVQVTPPLVAV  
THNENKFTCLQVLELVYADMEGRGMVNIISTAVAHLSLSEKDIIDILRLDALAK  
DLGNQYDVVSLMEGFAYGAVQLLEPSTGTFAGDFAFNLIQELKIIDILGLLPNDIAESV

THAIAIVSGLEONQAEMLCILRLNGHPLLESRIAKAVRSQMCAPXNDPFIIMLOY  
LSFPGKTIINGYRKNAGVMPRVKVDITKRVIGQLADDAEASHDITMLEYKSLSL  
EFPFCEIYDVTNLSMFLKDKAIAPNDMLASPRNLSEDDQHXKETSRLSLI  
EPLSNODFPIKEMEYLTLETRDNDVAYSLSKEVKNNGEIPAKLTKLRNCOV  
MARGCILADOPAPROGNGVODSILTKSLAMSOSFVNSFKRIIDCKERSNRRH  
DPSKRRRVATFITTDLOKTCIANRQVITKUPAHAINOLMGPHPEBHTILMDOT  
MEVADPNPSPDPTDCLSRVPNDIIVSARGGIBGLCQKLMETISAIIOQLAABS  
HCVACMVQDNOVIATVREVRSDSEPMVLTOLQSDMFKEILHVNAILGHNLDS  
RETRSDPTFPIYKRIIFKDGAILSOVLKNSKLVIVSGDSENYVMSFASVATPAL  
CENGLPDPCYLANIYMSVOYTFPDSFSTNNSHPLDNOSEDISFVSYVATPQ  
LGLSINVOELRYTRNIDPDTTAPAFIKLEANGILSPIMNITLIRPQNGMAL  
CNDPYNSFETVASPNIVLKHORVLPFCNSPILSGVHTENDEAEKALAEILNO  
EVHPRVAHAIMEASVGRKKQIOGLVDITNTVTKILTRPGLIKRUKRIVYSSKH  
AMLEGDVFSSRNHPLVSSNMSCSLIAAYARNRSPLTGKSLIGVSNPTIELV  
EGEILSVGGCTCRSDSEOPFWFHLPSNLEITDTSKNPMRPVYSGSTOERBAS  
LAKIAHMSPHVKALRASVLIYAVSGENVMWTAALIAKRCNVNLESLDPLPT  
AGLQHRIDGDIOTMPTTASLIYAVSPYIHISNDOSLPFEBEGKEENVYOOIMLG  
LSLIESIFPMTTTRTDEITLHLSKFSGCCIRBPAPVPELLIGVBEILATYSNKM  
YDPSVSEGDPRDLATFPKSYELNLSYPIELMNILSTISGKILGOSVYSDEBTS  
IKDIAIIVYDNTNMISEAOISDVRLFEVALLEVLLDCSYOLVYLRGLDNLVLM  
GDLYKNMFGILLNSIAATISHPIVHSRLHVGVLNHDGSHQLDVDFIERMSAKLVSC  
TRBVISGLYSGNKYDLPSPVLNDNLNEKMLQILSRCLCYLTVLFAITREIPIKRGIT  
AEEKSILTEYLLSDAKPLSPROVSIMSPPNITPAMLYMSRSKSLIHERREH  
DTILALPFOBPLEPPSVODIGARVODPTROPAPLIGELDISAPARYATLSQIH  
PELTPSPBEDYLVRVLPFRLGTASSWYASHLSVPEVCASHGNSLVABSGFAL  
MSLELHVPHEITTYNTLFSNEMNPQRHGPPTQIOLNVRNLOAEVTKDGFQ  
EFPRLMENTEESDLTKVYVITSAPRVSILHCDIEIPGNSQVSLDLQALIA  
SLIAMSVEREGVITIKVYAMGYFHLMLNLPACSTGKILFISONGAGDMECYLV  
FWNGYLGPTFVHEVVRMAKTUORHGTILSKDEITLFTLSORORVDDILSSPLP  
RLIKYLNKIDTALIBAGQVPRFPCSELSVSTIANITOTTOIASHIDIVYISVITM  
EAGSDIADVFLFTPYNLSTDGKRRTSLKCTROILEVTLIGLKEVLENKIGDITSLV  
LKMISWEDILPLRTYLNKSHSTCPKCYLKAVALIGITLKKEMFTDTSVLTLRAQOKRMKT  
IGNAVKGYNSNCDS"

## ORIGIN

Query Match 99.9%; Score 3353.2; DB 13; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3353; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACGGGTGAAGATTCTGGATCCGGTTGGGGCCCTCCAGGTGAAGANTGGGCTCCAGACC 60  
DB 4498 ACGGGTGAAGATTCTGGATCCGGTTGGGGCCCTCCAGGTGAAGANTGGGCTCCAGACC 4557  
QY 61 TTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTTGCGCTGCACCTGAGTTG 120  
DB 4558 TTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTTGCGCTGCACCTGAGTTG 4617  
QY 121 CATCTGTCGGGCAAACTTCATTGATGCGAGGCTCTTGGACGCTCGAGAAATTGGTTTAC 180  
DB 4618 CATCTGTCGGGCAAACTTCATTGATGCGAGGCTCTTGGACGCTCGAGAAATTGGTTTAC 4677  
QY 181 AGGAGCAAAAGCCGTCAACATATACCTCATCCCAAGCAGAGATCAATCATAGTTAAAGT 240  
DB 4678 AGGAGCAAAAGCCGTCAACATATACCTCATCCCAAGCAGAGATCAATCATAGTTAAAGT 4737  
QY 241 CCTCCCAATCTGCGCAAGATAAGAGGCAATGTGCCAAAGCCCTCTTGATGATCAACAA 300  
DB 4738 CCTCCCAATCTGCGCAAGATAAGAGGCAATGTGCCAAAGCCCTCTTGATGATCAACAA 4797  
QY 301 CAGGACATTGACCACTTTGCTACCCCCCTTGGTACTCTATCCGTAGAGATACAAAGATC 360  
DB 4798 CAGGACATTGACCACTTTGCTACCCCCCTTGGTACTCTATCCGTAGAGATACAAAGATC 4857  
QY 361 TGTGACATCACTCTGAGGGGGGAGACAGGGGGCGCTTATAGCCCAATTATTTGGCGGTT 420  
DB 4858 TGTGACATCACTCTGAGGGGGGAGACAGGGGGCGCTTATATAGCCCAATTATTTGGCGGTT 4917  
QY 421 GGCTCTTGGGGTTGCAACTGCGGCAAAATAACAGCGGCGCAGACTCTGATACAGCCAA 480  
DB 4918 GGCTCTTGGGGTTGCAACTGCGGCAAAATAACAGCGGCGCAGACTCTGATACAGCCAA 4977  
QY 481 ACAAAATGCTGCAACATCTCTCGACTTAAAGAGACATTGCGCAACCAATGAGGCTGT 540

DB 4978 ACAAAATGCTGCAACATCTCTCGACTTAAAGAGACATTGCGCAACCAATGAGGCTGT 5037  
QY 541 GCATGAGAGTCACTGACGGAATTATCGCACTAGACATGGCCAGTTGGAGAATGACAGCATT 600  
DB 5038 GCATGAGAGTCACTGACGGAATTATCGCACTAGACATGGCCAGTTGGAGAATGACAGCATT 5097  
QY 601 TGTGTAATGACCAATTTAATTAACACAGTCCAGGAATTAAGATGCAAAATTTGACAGCA 660  
DB 5098 TGTGTAATGACCAATTTAATTAACACAGTCCAGGAATTTAGACTGCAAAATTTGACAGCA 5157  
QY 661 AGTTGGTGTAGAGCTCAACCTGTACCTTAACCGAATTGACTCAAGTATTCGAGCCACAAT 720  
DB 5158 AGTTGGTGTAGAGCTCAACCTGTACCTTAACCGAATTGACTCAAGTATTCGAGCCACAAT 5217  
QY 721 CACTTCACTGCTTTTAAACAGCTGACTATTCAGGCACTTTACATTTAGCTGTGGAAA 780  
DB 5218 CACTTCACTGCTTTTAAACAGCTGACTATTCAGGCACTTTACATTTAGCTGTGGAAA 5277  
QY 781 TATGATTAATCTTATTTAGCTAAGTTAGTGGGAAACAATCAACTCAGCTCATTAATCGG 840  
DB 5278 TATGATTAATCTTATTTAGCTAAGTTAGTGGGAAACAATCAACTCAGCTCATTAATCGG 5337  
QY 841 TAGCGGCTTATATCAACGGTAACTTATCTATACGACTCAAGACTCAACTCTTGGGTTAT 900  
DB 5338 TAGCGGCTTATATCAACGGTAACTTATCTATACGACTCAAGACTCAACTCTTGGGTTAT 5397  
QY 901 ACAAGTAACTCTACCTTCACTGAGGAACTTAATATATATGCTGGCCACTTATTTGAAAC 960  
DB 5398 ACAAGTAACTCTACCTTCACTGAGGAACTTAATATATATGCTGGCCACTTATTTGAAAC 5457  
QY 961 CTTATCCGTAAAGCAACCAAGGGGATTTGGCTGGGCACTTGTCCCAAAAGTGGTGAACA 1020  
DB 5458 CTTATCCGTAAAGCAACCAAGGGGATTTGGCTGGGCACTTGTCCCAAAAGTGGTGAACA 5517  
QY 1021 GGTCCGTTCTGTGATAGAGAACTTGACACCTCATATCTGATAGAACTGACTAGATT 1080  
DB 5518 GGTCCGTTCTGTGATAGAGAACTTGACACCTCATATCTGATAGAACTGACTAGATT 5577  
QY 5578 ATATTTGACAAGAAATAGTAAGTTAGTCCCTATGTCCCTGATATTATCTGCTTGAACGG 5637  
DB 1141 CAATACGTGGGCTGTATGTATCTCAAAAGACCGGAAGGGCACTTATCAACATGACATGAC 1280  
QY 5638 CAATACGTGGGCTGTATGTATCTCAAAAGACCGGAAGGGCACTTATCAACATGACATGAC 5697  
DB 1201 TATCAAAAGTTCACTGATCGGCAACTGCAAGATGACAAACATGTAGATGTGTAAACCCCC 1260  
QY 5698 TATCAAAAGTTCACTGATCGGCAACTGCAAGATGACAAACATGTAGATGTGTAAACCCCC 5757  
DB 1261 GGGTATCATATCGCAAAACTATGAGAAAGCCGTGTCTCTAATAGATTAACAATCATGCA 1320  
QY 5758 GGGTATCATATCGCAAAACTATGAGAAAGCCGTGTCTCTAATAGATTAACAATCATGCA 5817  
DB 1321 TGTGTTATCTTAGGCGGGATTAATTTAAGGCTCAGTGGGGAAATTCATGTAACTTATCA 1380  
QY 5818 TGTGTTATCTTAGGCGGGATTAATTTAAGGCTCAGTGGGGAAATTCATGTAACTTATCA 5877  
DB 1381 GAAGAATATCAATATACAAAGATCTCAAGTAAATTAACAAGGCAATCTTGATATCTCAAC 1440  
QY 5878 GAAGAATATCAATATACAAAGATCTCAAGTAAATTAACAAGGCAATCTTGATATCTCAAC 5937  
DB 1441 TGAGCTTGGGAATGTCAACAACTCGATCAGTAATGCTTTGAATAAGTTAGAGAAACAA 1500  
QY 5938 TGAGCTTGGGAATGTCAACAACTCGATCAGTAATGCTTTGAATAAGTTAGAGAAACAA 5997  
DB 1501 CAGAAAATAGACAAAGTCAATGTCAATCTGATAGACATCTGCTCTCATTTACTTAT 1560  
QY 5998 CAGAAAATAGACAAAGTCAATGTCAATCTGATAGACATCTGCTCTCATTTACTTAT 6057  
DB 1561 CGTTTATGACTATCAATCTGCTTGTGTTTGGATATCTTAAAGCTGATTTAGAGTCACT 1620  
QY 6058 CGTTTATGACTATCAATCTGCTTGTGTTTGGATATCTTAAAGCTGATTTAGAGTCACT 6117

QY	1621	AATGTACAGCAAAAGGCGCAACAAAACCTTATATATGCGTTGGAAATATATCTACGA	1680
Db	6118	AATGTACAGCAAAAGGCGCAACAAAACCTTATATATGCGTTGGAAATATATCTACGA	6177
QY	1681	TCAGATGAGACCCCTACAAAATAGTGAACACAGATAGAGAAAGAGGTTTCCCTATATG	1740
Db	6178	TCAGATGAGACCCCTACAAAATAGTGAACACAGATAGAGAAAGAGGTTTCCCTATATG	6237
QY	1741	TAATTTGTGTGMAAGTTCTGTGATCTGTCAGTTCAAGAGTTAAGAAAACTACCGGT	1800
Db	6238	TAATTTGTGTGMAAGTTCTGTGATCTGTCAGTTCAAGAGTTAAGAAAACTACCGGT	6297
QY	1801	TGTAGATGACCAAGAGAGATATACGGGTAGAACGGTAAAGAGCGCCCTCAATATGC	1860
Db	6298	TGTAGATGACCAAGAGAGATATACGGGTAGAACGGTAAAGAGCGCCCTCAATATGC	6357
QY	1861	GAGCGAGGCTTACAAACCTCGGTTCTACCGGTTACCGCAACAGTCCCTCAATCATGAGAC	1920
Db	6358	GAGCGAGGCTTACAAACCTCGGTTCTACCGGTTACCGCAACAGTCCCTCAATCATGAGAC	6417
QY	1921	CGCCCGCTTACCAAGTTGCGTTAGAGATGATGMAAGAGAGCAAAAATACTACGCGC	1980
Db	6418	CGCCCGCTTACCAAGTTGCGTTAGAGATGATGMAAGAGAGCAAAAATACTACGCGC	6477
QY	1981	TTGATATTTCCGGAATGCAATCTTATCTTAAACAGTAGTACCTTGCTATATCTGAGCC	2040
Db	6478	TTGATATTTCCGGAATGCAATCTTATCTTAAACAGTAGTACCTTGCTATATCTGAGCC	6537
QY	2041	TCCCTTTTATATAGCATGAGGGGCTAGACACACTTAGCGATCTTGTAGGCAATCCGACATAGG	2100
Db	6538	TCCCTTTTATATAGCATGAGGGGCTAGACACACTTAGCGATCTTGTAGGCAATCCGACATAGG	6597
QY	2101	ATTTCCAGGGGAGAGAAAGATTACATCTACACTGGTTCATTCAGATGTAGTAGAT	2160
Db	6598	ATTTCCAGGGGAGAGAAAGATTACATCTACACTGGTTCATTCAGATGTAGTAGAT	6657
QY	2161	AGGATATATTAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATGTTAAATCTAGACACACA	2220
Db	6658	AGGATATATTAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATGTTAAATCTAGACACACA	6717
QY	2221	ATTATGAACGCAATPACATCTCTCTCTTATCAGATTATGAGAGCTGCACAAACAAGTGGG	2280
Db	6718	ATTATGAACGCAATPACATCTCTCTCTTATCAGATTATGAGAGCTGCACAAACAAGTGGG	6777
QY	2281	TGGGGGGGACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA	2340
Db	6778	TGGGGGGGACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA	6837
QY	2341	GATGATGCTAGTAGATGATCACAATCAATTCATCCCTCTGCATTTTCAAGAACATCTGAATTTT	2400
Db	6838	GATGATGCTAGTAGATGATCACAATCAATTCATCCCTCTGCATTTTCAAGAACATCTGAATTTT	6897
QY	2401	ATCCCGGCGCTTACTACAGATCAAGATTGCACTGCAATACCCCTCATTTTGA CATAGTGTCT	2460
Db	6898	ATCCCGGCGCTTACTACAGATCAAGATTGCACTGCAATACCCCTCATTTTGA CATAGTGTCT	6957
QY	2461	ACCAATTAATCTGTACACCACTAAATGTATATTTGTGTGATGACAGAGATCACTCAATTTCA	2520
Db	6958	ACCAATTAATCTGTACACCACTAAATGTATATTTGTGTGATGACAGAGATCACTCAATTTCA	7017
QY	2521	TATCAGTATTTAGCACTTGTTGTGTCTCCGACATCTGCAACAGGGAGGGTATTTCTTTTCT	2580
Db	7018	TATCAGTATTTAGCACTTGTTGTGTCTCCGACATCTGCAACAGGGAGGGTATTTCTTTTCT	7077
QY	2581	ACTCGCGTTTCATCAACCTGAGCAACCCAAAATCGGAAGTCTTGCAAGTGTAGTGTCA	2640
Db	7078	ACTCGCGTTTCATCAACCTGAGCAACCCAAAATCGGAAGTCTTGCAAGTGTAGTGTCA	7137
QY	2641	ACTCCCTCGGGTTGTGATATGTGTGTCTCGAAAGTACAGGAGACAGAGGAAGAAATAT	2700
Db	7138	ACTCCCTCGGGTTGTGATATGTGTGTCTCGAAAGTACAGGAGACAGAGGAAGAAATAT	7197

OY		2701	AACCTCAGCTGTCCTTAAGCCGAATGTACTATGGGAGGTTAAGGTTTCAGACGGCACTAACAC	2768
Dd		7198	AACTCAGCTGTCCTTAAGCCGAATGTACTATGGGAGGTTAAGGTTTCAGACGGCACTAACAC	7257
OY		2761	GAAAGAACCAGTAAAGTACAACAATTATCGGGGACCTGGGGGCCAACTACCCAGAGTA	2820
Dd		7258	GAAAAGACCTAGATGTACAACACTTTATCGGGGACCTGGGGGCCAACTACCCAGAGTA	7317
OY		2821	GGGGGTGGANTCTTTATTTATGACAGCCGGGTATGTTCTCACTACGAGAGGTTAAAAACC	2880
Dd		7318	GGGGGTGGATCTTTATTTATGACAGCCGGGTATGTTCTCACTACGAGAGGTTAAAAACC	7377
OY		2881	AATTCACTCCAGTGACACTGTATCAGAGAAGGGAATAATGTGANTATCAAGCCATACAAATGAC	2940
Dd		7378	AATTCACTCCAGTGACACTGTATCAGAGAAGGGAATAATGTGANTATCAAGCCATACAAATGAC	7437
OY		2941	ACATGCCCATGTAGACAAGACTACACAGTTCCGATTTGCGATTAAGCCCTGGA	3000
Dd		7438	ACATGCCCATGTAGACAAGACTACACAGTTCCGATTTGCGATTAAGCCCTGGA	7497
OY		3001	CGGTTTGGTGGAAACGCATACAGCAGGCTATCTTATCTATCAAGAGTGTCAAATCCTTA	3066
Dd		7498	CGGTTTGGTGGAAACGCATACAGCAGGCTATCTTATCTATCAAGAGTGTCAAATCCTTA	7557
OY		3061	GCGCAAGACCCGGTAGCTGACTGTACCGGCCAACACAGTCACTATGGGGCCGGAAGGC	3120
Dd		7558	GCGCAAGACCCGGTAGCTGACTGTACCGGCCAACACAGTCACTATGGGGCCGGAAGGC	7617
OY		3121	AGAAATTCACAGTAGGACATCTCATTCTTGTATCAAGAGGTCATCATACCTTCT	3180
Dd		7618	AGAAATTCACAGTAGGACATCTCATTCTTGTATCAAGAGGTCATCATACCTTCT	7677
OY		3181	CCCCGGTATTATATNCCATGACAGTCAGCAACAAAACAGCACCTCTTCATAGTCTTAT	3248
Dd		7678	CCCCGGTATTATATNCCATGACAGTCAGCAACAAAACAGCACCTCTTCATAGTCTTAT	7737
OY		3241	ACATTCAATGCTTCACTCGGCCAGTAGTATCCCTTGCCAGGCTTCAGCAAGATCCCC	3300
Dd		7738	ACATTCAATGCTTCACTCGGCCAGTAGTATCCCTTGCCAGGCTTCAGCAAGATCCCC	7797
OY		3301	AACCTGCTGTTATCTCGAGCTTATACAGATCCATATCCCCTATCTATAGAAACC	3358
Dd		7798	AACCTGCTGTTATCTCGAGCTTATACAGATCCATATCCCCTATCTATAGAAACC	7855
<hr/>				
RESULT 6				
AY225110		15186 bp	RNA linear	VRL 04-MAR-2003
LOCUS	AY225110	Newcastle disease virus strain HB92 isolate Va, complete genome.		
DEFINITION	AY225110			
ACCESSION	AY225110.1	GI:28824865		
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	Zhang,C.Y.			
TITLE	Complete sequence for HB92 strain of Newcastle disease virus unpublished			
JOURNAL	2 (bases 1 to 15186)			
REFERENCE	Pan,Z.S., Chen,Y.D., Wen,G.Y. and Zhang,C.Y.			
AUTHORS	Direct Submission			
JOURNAL	Submitted (23-JUN-2003) Institute of Virology, Department of Life Science, Wuhan University, Wuhan, Hubei 430072, China			
REFERENCE	3 (bases 1 to 15186)			
AUTHORS	Shao,H.B., Yang,J. and Xiong,Z.L.			
TITLE	Submitted Submission			
JOURNAL	Submitted (23-JUN-2003) Institute of Animal Husbandry and Veterinary Science, Hubei Academy of Agricultural Science, Wuhan, Hubei 430209, China			
FEATURES				
			Location/Qualifiers	

source	1. .15186 /organism="Newcastle disease virus" /mol_type="genomic RNA" /strain="H92" /isolate="V4" /db_xref="taxon:11176" 122. .1591 /gene="NP" 122. .1591 /gene="NP" /product="nucleocapsid protein" /protein_id="AA046779.1" /db_xref="GI:28824866" /translation="MSSVFDEYEQLAAGRPNAGHGGEKSTLKVDVPEFTLNSDD PEDRMSFVFCRLRAVSEDANKPLRQGLISLCSHSQVMNHVALAKQNEATLAVL EIGFANGTGFQNNRSGVSEERARFAMIGLSEPRACNGTPTAGADEADAPDITD TLRRILSLQAVVTVAKAMTAYETADESERPRINXKMOGRVOKKYLIVPVCSSTIQ LTRQSLAVRIFLVSELKRGHNTGCTSTYTNLVGDVSTYIKNTGLTALFLTKYGIN TKTSALALSLISDIQRMKQMLRYRMKGADAPYTLIGSDOMSFAPEAQLYSFA MGMAVLDKGTGKYQFARDFMWTSFMRIGVEYAOAGSSINEDMAELKUTPARBGL AAAOQVSEETSIDMPTQGVLTGLSEGSQALOGSSNRSQGPBAGDETQFLDL MRAVANSRREAPNRQGTPOSGPPTGSPGSDNDTMGY" 1887. .3074 /gene="P" 1887. .3074 /gene="P" /product="phosphoprotein" /protein_id="AA046781.1" /db_xref="GI:28824868" /translation="MAFTDAEIDELFETSGTVIDNITTAQGRPAETVSGSAIPQGT KAVLSAAMEKSGSIQPPASQNDPQRSDSKQPTBQETTPHDSPPATSAQPPQIARD EADTQRTGASNSILMLDKLSNKSNAKGPWSPOEGNHQPTQOQSGSPGPHNS QBRQNVKAPAGNQTGDTVNTAYHGBESQLSGATPHALRSQSDNTLVSADHQ PBRFVYQAMSMWEALISQVSKDYQGLDYLKQTSSTPKMRSSTIQGLKTVAVWEAL GMKILDPGCANISLSLDLNAVRSNHLVLSGPDPPPTTQGGEMALNKLSQVPHP SELIKPATYACGPDIGVEKDTVRALINRPMHPSSAKLKLSDNAAGSIEETRIKRLA LNG" 3230. .4384 /gene="M" 3230. .4384 /gene="M" /codon_start=1 /product="matrix protein" /protein_id="AA046784.1" /db_xref="GI:28824871" /translation="MDSRRITGLYFDSTLRSSNLAPPIYLQDTGDKQOLAPRYRQ RLDSWDSKEDSVFTTYGFIQVGENEATVGMINDPKRELSTAYLCSGVFNVGD LVELARACLTMVVTCKKSANTERIVSVVQAQVLOSCEVANKSSVNAVKVAPK EKIPSGSTLEVKNFVSLTVPRDQVYKIPTAAPKVGSSSLHNALVTTIDVEDPYS PLVKSLSKDSGVYANLFLHGFMSITVKGKQVTPKLEKIRRLDLSVGLSDVGP SVLVKAGARIKILAPFPSSSGTAPRIANASPVAKILMSQTRACLSAVYITIQAGTQ RAVAVTDHDEVSTKLEKHTIAKNPEFK" 4544. .6205 /gene="F" 4544. .6205 /gene="F" /codon_start=1 /product="fusion protein" /protein_id="AA046783.1" /db_xref="GI:28824870" /translation="MGSRSSTKNDPAPMMLTIRVALVLSICIPANSIDGRPLAAAGIV TQKAVNIVTSSQGTIIVKLPLPKDXEACAKAPLDAYNRITLTTLTGLGSGIRI QESVYTSGGRGQRLIGALIGVALGYATAQITRAAALIOAKONANITLKESTIA TNEAHEVTDGLSLAVAGVMOQFVNDQNKTAQELDCIKIAQOVEEVLNLYTELT TVSGPQITSPALNKLTIQALYNLAGNMDYLTGLGANNQSLISGSLITGPNIIY DSOGLGIVTLPSVGNLNMRATVLETLSVSTRGFASALVKAVTQVGSVBEID NCTCIETDLQCTRIATVPMSPGIVSGISGNTSACVSKTEGALTPTMYTIKGSVA NCKCTTCRCVNPBGITSONYGENSLIDKQSCVLTSGITLISGSGFDYQKNISIT QDSCVITITGNLDISTELGNVNSISNALNKESSNRKLDKYNKVLJSTSALITIVLT IISLVFGIISLILIACLMYKOKAQOKTLLWLNNTDQMBATTKM" 6412. .8145	CDS	/gene="HN" 6412. .8145 /gene="HN" /codon_start=1 /product="hemagglutinin-neuraminidase" /protein_id="AA046782.1" /db_xref="GI:28824869" /translation="MRAVSVQVALLENDREARAKTWLIRIRLITFLVTWTLASVAST LVSNGASTPSNLVGIPTIRISRAEKITSTLIGSNQDVDRIRYQVALLSPALAKTEET LNNALTSLSAYQIAGNANSGWAPIHDPDVIIGIIGKELIVDDASDVTSFSAEQEHL NFIAPATTSIGGCTRISEFDMSATYCYTHNVILISGCRDHSYSOYLAVGLRTSATGR VFPSTILRSINLDPIDONRSCSVSATPLGCDMLCSKTETEEDYNSAVPRMYGRIGR FDCQVHEKQIDVNTLREGDWANYRGVCGGSFIRISVWFSSYIGKLKPSRPDTYQEGY VYIKRINDTPEDEDIOTIRAKSSYKRGGRGRIQQAIIISIKVTSIGSDPVTITVP NTVTLWKAEGRIILVTGSHPLVORGSSYFSPALLVPTVSNKATLHSPYFNATRP GSLIPQASARCPMPCTGVYTDYPLPYRNHTLRGVGTMLDGVORLNPASAVFOS TSBSRIITRVSSSTKAAYTSTGCFKVKYKNTKYCLISAEISNTLFGSFRIVPLVEIL KDDGVREARSG" 8381. .14995 /gene="L" 8381. .14995 /gene="L" /codon_start=1 /product="large polymerase protein" /protein_id="AA046780.1" /db_xref="GI:28824867" /translation="MASSGERAREHQIILPESHLSFVLVHKLLIYWKLTGLPLPDEC DPDHLILSRQMKKILLESASPDTERMTLGRVHQTLNHSKITGVLRCLBELASIE VPSTNFKRKIEKKIQHNTRYGELFRLCTHYEKLSSMSNNVPRSEFNSIRTD PAPFMSKMSITKPAWLHIKQIORHLIVARTSAAKLVTLTHKVGQVTPBELVAV THTDENKFTCLTQELVLYADMMEDGMVNTISTAHRLSESKEIDDLIRVDALAK DLGNQYDVVALNEGFRYAGVOLBPSGTAGCPFAPNLOELKDTLIGLPKRIABEV THAIVTSPLEONQAAEMCLRLWHPFLSERIAKAVRSQCAPKAVDFMDITLV LSFFGKTIINGYRKKAGVAPRYKVLIVYKQIOLADABAEISHIMLEYKLSAF EFPCELYEYDITNLSMFLKOKAIAHPDNLAEFRRLISEDKIKYKATSTNRLSI EPLSESDPYKMEVYLTLEYLRDQNVAYSRLKKEVYVNGRIEPAKLEKLRNCOV MAEGILADQIAPFQNGVIGDSISLTKYKMLASGLSPNSKKRITDCEKRVANSCH DQSKRRNRVATITTDLOKTCINWRYQTKLAHALNQMLGPHFEWTHLDMOT MFGVDPNPSPDPTDCDSLRVPNDIYIVSARGIIGLQCKLFTWLSIAIQLAAAS HCRVACVQGDNQVIAVTRVSRDSDSEVMTQLHQASDNFPEKLHVNHLIGNLAD RETRSDTFPIYSKRIEFGALISQVLYKNSKTLVLSGDSERYNSCANIATTLAD CENGLPKDFCYLYNGLMSVCQYTFDSFSTITNSHNSQSWIEDISFVSVYLTAPQ LGSLNLIQYSRLYTRNIGDPTTAPAEIRKLEAVGLSLSIMNIIILTRPGNDWBL CNDPYSFNEFTVASPNVLKQHTQRLVLETCSNPVLSGVTEDNEBEKLABELNQ AMVHPRVAAHMEASSIGRRKQIQGLVDITNYIKALTRRPLGRIKRLMIIVNSM AEFLPDDVFSSNSNHPVLSNMCSLTLDVAAANRSVPLTGGRKILIGENPDTIELY EGEILSVSGGCTRCDSGDEQTFWHLPSNIELTDRTSKNPMRPIYGSKTQBRAS LAKIAHMSPHVKAALASASVLTWAGDNVNMTRALTLIAKRCNVSEVRLISPLPT AGNLQHRLDGITQMTTPASLYRVSEYIHISDSORLPTBEGYKESGVYQOIMLIG LSLIESLFPMTTTRTDEITLHLSKFSCTIRAPAVAPPELLGMAELRTVSNKFM YDPSPVSEGDPAFLDIALIFGSYELNLESYCTIRELMNIISSQGLIGQSVASVDEDT IKNDALIVYNTNMNISEAONSQVIRFEYAALEVLVLDSCYQLYLRVRLGDNVILM SDIYKNMPEGILSNIAATISHPIHSHLHVAVGVNHGSHQGLADTDIRMSGAKLVSC TRRVYSGLYAGNKYDILFESVLDNISEKQILISPLCYLTATFTRERIPKIRGIS AEERCSVLEIYLLSDAVKPLSSBOVSSINSPIVTPPALVYMSKSLMLIREBER DVTIALLFPOQLBEPLVODIGARVADPTROPAPFLQGLDISAPRYAFTLSVOH SEHTPMPDEDDYLVYLFRCIGTASSWYASHLISVEVRCARHGLIABSGGAI MSLLELVHPHETIYYNTLFEENMPPORHGPPTQGLVYVVRNLOAEVPCBDFQ EPRPIMRENTRESDLTSDKAVGYTASVLPVRSVLSLHCDIEIPGSGOILLDOLATN SLIAMSAREGGVYIIKVIYAKGYIRHLLMNLTPCSTCKYIISNGVACSGDCSYIV FVNGYRGKPTFVEHVRMAKTLVQKHGHTLKSDEITLRLFSORRATVDIISNPLP RLIKFLRKNIDTALILEAGQPVAPFCASISVTRILADTQMTQIASHIDIVINSVLP EASGLADIVLFTPLPNLSTGDKKRTSLKQCTQIOLVETIIGLREVLNIDVGVNSIV LKMISLIEDIIPRTYIKRSTCKRYLSKISLIGITKLEMFPDTSLLVYTRAQQFYKMT IGNAVKGYINCS"	gene	ORIGIN	Query Match Best Local Similarity 99.5%; Score 3342; DB 13; Length 15186; Matches 3348; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	1 ACGGGTGAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTTCCAGACC 60 
--------	---	-----	--	------	--------	--	--

Dh 4498 ACGGTTAGAAAGATTCTGGAATCCGGTTGGCCCTTCAAGGTGCAAGATGGGCTCAAGATC 4457  
Qy 61 TTCTACCAAGAACCCAGACACCTATGATGCTGACTATCCGGATTGCGCTGGCACTGAATTG 120  
Dh 4558 TTCTACCAAGAACCCAGACACCTATGATGCTGACTATCCGGATTGCGCTGGCACTGAATTG 4617  
Qy 121 CATCTGTCCGGCAAACTTCATTGATGGCAAGGCTCTTGGCACTGCAAGAAATTGGTTAC 180  
Dh 4618 CATCTGTCCGGCAAACTTCATTGATGGCAAGGCTCTTGGCACTGCAAGAAATTGGTTAC 4677  
Qy 181 AGGAGCAAAAGCCCTCAACATATACCTCATCCCAAGAGATCAATCATAGTTAAGCT 240  
Dh 4678 AGGAGCAAAAGCCCTCAACATATACCTCATCCCAAGAGATCAATCATAGTTAAGCT 4737  
Qy 241 CCTCCCAATCTGGCCCAAGATAAGAGGCACTGTGCAAAAGCCCTTGGATGCTATCAA 300  
Dh 4738 CCTCCCAATCTGGCCCAAGATAAGAGGCACTGTGCAAAAGCCCTTGGATGCTATCAA 4797  
Qy 301 CAGGACATTGACCACTTTGCTCAACCCCTTTGTACTTATCCGTAGATTAACAAGTGC 360  
Dh 4798 CAGGACATTGACCACTTTGCTCAACCCCTTTGTACTTATCCGTAGATTAACAAGTGC 4857  
Qy 361 TGTGACATCATCTGAGAGGGGGAGACAGGGGCGCTTATAGCGCCCATTTATGGCGGTGT 420  
Dh 4858 TGTGACATCATCTGAGAGGGGGAGACAGGGGCGCTTATAGCGCCCATTTATGGCGGTGT 4917  
Qy 421 GGGCTTTGGGGTTGGCACTGCGCCGACAAATPAAGCGCGCACTCTGATTAACAAGCAA 480  
Dh 4918 GGGCTTTGGGGTTGGCACTGCGCCGACAAATPAAGCGCGCACTCTGATTAACAAGCAA 4977  
Qy 481 ACAAAATGCTGCCAACATCTCTCGACTTAAAGAGAGCATTTGCGCAACAAATGAAGCTGT 540  
Dh 4978 ACAAAATGCTGCCAACATCTCTCGACTTAAAGAGAGCATTTGCGCAACAAATGAAGCTGT 5037  
Qy 541 GCATGAGGTCACTGACGGATTATTCGCACTTAGCGATGGCAATTGGGAATAGCGACATT 600  
Dh 5038 GCATGAGGTCACTGACGGATTATTCGCACTTAGCGATGGCAATTGGGAATAGCGACATT 5097  
Qy 601 TGTAAATGACCAATTTAATAAAACAGCTCAGGAATTAGCTGCATCAAAATTTGACAGCA 660  
Dh 5098 TGTAAATGACCAATTTAATAAAACAGCTCAGGAATTAGCTGCATCAAAATTTGACAGCA 5157  
Qy 661 AGTTGTGTAGAGTCAACCTGTACCTAACCGAATTGACTACAGTATTCGGACCAAAAT 720  
Dh 5158 AGTTGTGTAGAGTCAACCTGTACCTAACCGAATTGACTACAGTATTCGGACCAAAAT 5217  
Qy 721 CACTTCACTGTCTTAAACAAAGCTGACTATTGAGCACTTTACATCTAGTGGTGA 780  
Dh 5218 CACTTCACTGTCTTAAACAAAGCTGACTATTGAGCACTTTACATCTAGTGGTGA 5277  
Qy 781 TATGATTACTTAATTGACTAAGTTAGGTAGGGGAACAATCACTCAGCTCATTAATCGG 840  
Dh 5278 TATGATTACTTAATTGACTAAGTTAGGTAGGGGAACAATCACTCAGCTCATTAATCGG 5337  
Qy 841 TAGCGGCTTAATCAACCGGTAAACCTATTCTATACGACTCAAGACTCAACTCTTGGGTAT 900  
Dh 5338 TAGCGGCTTAATCAACCGGTAAACCTATTCTATACGACTCAAGACTCAACTCTTGGGTAT 5397  
Qy 901 ACAAGTAACCTTACCTTACAGTGGGAACTTAATATATATGCTGCCACTTAATTGGAAC 960  
Dh 5398 ACAAGTAACCTTACCTTACAGTGGGAACTTAATATATATGCTGCCACTTAATTGGAAC 5457  
Qy 961 CTTATCCGTAAAGCAACAACGGGGATTTCCTCGGCACTTGCCTCAAAAGTGGAGACA 1020  
Dh 5458 CTTATCCGTAAAGCAACAACGGGGATTTCCTCGGCACTTGCCTCAAAAGTGGAGACA 5517  
Qy 1021 GGTCCGTTCTGTGATAGAAGACTTGACACTCATCTGATATAGAACTGACTTGAATTT 1080  
Dh 5518 GGTCCGTTCTGTGATAGAAGACTTGACACTCATCTGATATAGAACTGACTTGAATTT 5577  
Qy 1081 ATATTTGACAGAATTAAGTAACTGTTCCCTATGTCCCTGGTATTTATTTCTGCTTGAAGCG 1140  
Dh 5578 ATATTTGACAGAATTAAGTAACTGTTCCCTATGTCCCTGGTATTTATTTCTGCTTGAAGCG 5637

Qy 1141 CAATACGTGGCCCTGTATGTATCTCAAAAGCCGAAGGGCACTTACTACCATATCATGAC 1200  
Dh 5638 CAATACGTGGCCCTGTATGTATCTCAAAAGCCGAAGGGCACTTACTACCATATCATGAC 5697  
Qy 1201 TATCAAAAGTTCACTGATCCGCAACCTGCAAGATGACCAACATGTAGTGTAAACCCCC 1260  
Dh 5698 TATCAAAAGTTCACTGATCCGCAACCTGCAAGATGACCAACATGTAGTGTAAACCCCC 5757  
Qy 1261 GGGTATCATATCCGCAAACTATGAGAGAGCGGTCTCTAATAGATTAACAATCATGCA 1320  
Dh 5758 GGGTATCATATCCGCAAACTATGAGAGAGCGGTCTCTAATAGATTAACAATCATGCA 5817  
Qy 1321 TGTTTATCCTTAGCGGGATPACTTTAAGGCTCACTGGGGAAATTCATGTATCTATCA 1380  
Dh 5818 TGTTTATCCTTAGCGGGATPACTTTAAGGCTCACTGGGGAAATTCATGTATCTATCA 5877  
Qy 1381 GAAGAAATATCTCAATACAAATTTCTAAGATTAATAAGGCAATCTGATATCTCAAC 1440  
Dh 5878 GAAGAAATATCTCAATACAAATTTCTAAGATTAATAAGGCAATCTGATATCTCAAC 5937  
Qy 1441 TGAGCTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAAATTAAGTAAAGAAAGCA 1500  
Dh 5938 TGAGCTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAAATTAAGTAAAGAAAGCA 5997  
Qy 1501 CAGAAAATAGACAAAGTCAATGTCAAACTGACTAGCAATCTGCTCATTAACCTATAT 1560  
Dh 5998 CAGAAAATAGACAAAGTCAATGTCAAACTGACTAGCAATCTGCTCATTAACCTATAT 6057  
Qy 1561 CGTTTATCATCATATCTCTGTTTGGTATPACTTAAGCTGATTCAGACATGCTACT 1620  
Dh 6058 CGTTTATCATCATATCTCTGTTTGGTATPACTTAAGCTGATTCAGACATGCTACT 6117  
Qy 1621 AATGTACAGCAAAAGCGCAACAAAAACCTTATTAAGCTTGGGAATATATCTAGA 1680  
Dh 6118 AATGTACAGCAAAAGCGCAACAAAGCTTATTAAGCTTGGGAATATATCTAGA 6177  
Qy 1681 TCAGATGAGGCCACTACAAAAATGTGAACACAGATGAGAAAGCAAGGTTCCCTAATAG 1740  
Dh 6178 TCAGATGAGGCCACTACAAAAATGTGAACACAGATGAGAAAGCAAGGTTCCCTAATAG 6237  
Qy 1741 TAATTTGTGGAAGTTCTGTGTACTGTCAAGTTCAAGATTAAGAAAAAATCAACGGT 1800  
Dh 6238 TAATTTGTGGAAGTTCTGTGTACTGTCAAGTTCAAGATTAAGAAAAAATCAACGGT 6297  
Qy 1801 TGTAGATGACCAAAAGGACGATATATAGGGTGAACGATTAAGAGAGCGCCCTCAATTGC 1860  
Dh 6298 TGTAGATGACCAAAAGGACGATATATAGGGTGAACGATTAAGAGAGCGCCCTCAATTGC 6357  
Qy 1861 GAGCCAGGCTTCAACAACCTCGTTCTACCGCTTACCGGCAACAGTCTCATATGAGAC 1920  
Dh 6358 GAGCCAGGCTTCAACAACCTCGTTCTACCGCTTACCGGCAACAGTCTCATATGAGAC 6417  
Qy 1921 CGCGCGTTAGCCAAAGTTGCGTTAGAGATGATGAAGAGAGGCAAAATACATGCGGC 1980  
Dh 6418 CGCGCGTTAGCCAAAGTTGCGTTAGAGATGATGAAGAGAGGCAAAATACATGCGGC 6477  
Qy 1981 TTGATATCCGGAATGGAATCTTATCTTAAACAGTATGAGCCTTGCGTAATCTGTAGCC 2040  
Dh 6478 TTGATATCCGGAATGGAATCTTATCTTAAACAGTATGAGCCTTGCGTAATCTGTAGCC 6537  
Qy 2041 TCCCTTTATATAGCATGGGGCTAGACACCTAGCACTTTGAGCATACCGACTAGG 2100  
Dh 6538 TCCCTTTATATAGCATGGGGCTAGACACCTAGCACTTTGAGCATACCGACTAGG 6597  
Qy 2101 ATTTCCAGGCGAGAAAGAAATTAATCATCTACCTTGGTTCAATCAAGATGTATGAT 2160  
Dh 6598 ATTTCCAGGCGAGAAAGAAATTAATCATCTACCTTGGTTCAATCAAGATGTATGAT 6657  
Qy 2161 AGGATATATTAAGCAAGTGGCCCTGAGTTCCTGGTGAATTTGTTAAATCACTGAGACCA 2220  
Dh 6658 AGGATATATTAAGCAAGTGGCCCTGAGTTCCTGGTGAATTTGTTAAATCACTGAGACCA 6717



Qy	2222	ATTATGAAGCAAATA	CACTCTCTCTTA	CTGATTAATGAGCGTGC	CAACAGTGGG	2280
Db	6718	ATTATGAAGCAATA	CATCTCTCTTA	CTGATTAATGAGCGTGC	CAACAGTGGG	6777
Qy	2281	TGGGGGGCACCA	TATCCATGACCAGATTATATGAGGGGAT	TAGCGAAGAACTCATGTA		2340
Db	6778	TGGGGGGCACCA	TATCCATGACCAGATTATATGAGGGGAT	TAGCGAAGAACTCATGTA		6837
Qy	2341	GATGATGTA	GTGATGTCAATCATATCTATCCCTTCGATTT	CANAAACATCGAATTTT		2400
Db	6838	GATGATGTA	GTGATGTCAATCATATCTATCCCTTCGATTT	CANAAACATCGAATTTT		6897
Qy	2401	ATCCCGCGCCCTA	CTACAGAGTACGGTTGCACTGCAATACCTCATTTG	ACATGATGCT		2460
Db	6898	ATCCCGCGCCCTA	CTACAGAGTACGGTTGCACTGCAATACCTCATTTG	ACATGATGCT		6957
Qy	2461	ACCCATTACTGCTA	CACCATATGTAATATTTGTCGATGACAGATCA	CTCATTTCA		2520
Db	6958	ACCCATTACTGCTA	CACCATATGTAATATTTGTCGATGACAGATCA	CTCATTTCA		7017
Qy	2521	TATCAGTATTTAG	CACTTGCTGTCTCGGACATCTGCACAGGAGGATTTCTTTCT			2580
Db	7018	TATCAGTATTTAG	CACTTGCTGTCTCGGACATCTGCACAGGAGGATTTCTTTCT			7077
Qy	2581	ACTCTGCGCTTCC	ATCACTCTGCACACCCCAAAATCCGAAATCTT	GACAGTGTAGTGA		2640
Db	7078	ACTCTGCGCTTCC	ATCACTCTGCACACCCCAAAATCCGAAATCTT	GACAGTGTAGTGA		7137
Qy	2641	ACTCCCTGGGTTGT	ATATGCTGTGCTCGAAAGTCA	CGAGACAGAGAAAGATAT		2700
Db	7138	ACTCCCTGGGTTGT	ATATGCTGTGCTCGAAAGTCA	CGAGACAGAGAAAGATAT		7197
Qy	2701	AACTCAGCTGTCC	CTACCGGAGTGTATCATGAGAGGTTAGGGTTGCAGCGCCATGATCAC			2760
Db	7198	AACTCAGCTGTCC	CTACCGGAGTGTATCATGAGAGGTTAGGGTTGCAGCGCCATGATCAC			7257
Qy	2761	GAAAAGACCTAG	ATGTCAACATTAATCCGGGACTGGGTGGCCAACTACCCAGGATTA			2820
Db	7258	GAAAAGACCTAG	ATGTCAACATTAATCCGGGACTGGGTGGCCAACTACCCAGGATTA			7317
Qy	2821	GGGGGTGGAATCTTT	TAATGACACGCGCGATAGGTTCTCAGTCTACGAGGGTTAAACCC			2880
Db	7318	GGGGGTGGAATCTTT	TAATGACACGCGCGATAGGTTCTCAGTCTACGAGGGTTAAACCC			7377
Qy	2881	AAATTCACCCAGTGA	CACTGTACAGGAAGGAAATATGTATATACAGCGATACATGAC			2940
Db	7378	AAATTCACCCAGTGA	CACTGTACAGGAAGGAAATATGTATATACAGCGATACATGAC			7437
Qy	2941	ACATGCCCAATG	AGCACAATCCAGATTGCAATGCGCAAGTCTTGGTATTAAGCTTGA			3000
Db	7438	ACATGCCCAATG	AGCACAATCCAGATTGCAATGCGCAAGTCTTGGTATTAAGCTTGA			7497
Qy	3001	CGGTTTGGTGGG	AAACGATACAGCAGGCTATCTATCATACAGGTGTCAACATCTTA			3060
Db	7498	CGGTTTGGTGGG	AAACGATACAGCAGGCTATCTATCATACAGGTGTCAACATCTTA			7557
Qy	3061	GGCGAAGACC	CGGTACTGACTGTACCGCCCAACACATGTACA	CTCATGSGGGCCGAAAGC		3120
Db	7558	GGCGAAGACC	CGGTACTGACTGTACCGCCCAACACATGTACA	CTCATGSGGGCCGAAAGC		7617
Qy	3121	AGAAATCTCA	CAGTAGGACATCTCATTTCTTGATCAACGAGGGTCATCATCTTCTCT			3180
Db	7618	AGAAATCTCA	CAGTAGGACATCTCATTTCTTGATCAACGAGGGTCATCATCTTCTCT			7677
Qy	3181	CCCGGCTTATTA	TATCTCTATGACAGTCAACAAACAGGCACTTCAATGTGCTTAT			3240
Db	7678	CCCGGCTTATTA	TATCTCTATGACAGTCAACAAACAGGCACTTCAATGTGCTTAT			7737
Qy	3241	ACATTAAGGCTTCA	CTCGGACAGGTATATCCCTGCGAGGCTTACAGAAATGCCCC			3300
Db	7738	ACATTAAGGCTTCA	CTCGGACAGGTATATCCCTGCGAGGCTTACAGAAATGCCCC			7797
Qy	3301	AACTCGTGTGTA	CTAGAGTCTATACAGATTCATATCCCTTAATCTTCTATAGAAACC			3358

DB	7798	AAACGGTGTATTGAGTCTATACAGATCCATATCCCTTAATCTTATAGAAACC	7855
RESULT 7			
LOCUS	AY845400	15186 bp	RNA linear VRL 17-MAR-2005
DEFINITION	Newcastle disease virus strain Lasota, complete genome.		
ACCESSION	AY845400		
VERSION	AY845400.2	GI:61621428	
KEYWORDS			
SOURCE	Newcastle disease virus		
ORGANISM	Vitruves; Paramyxoviridae; Paramyxovirinae; Avulavirns.		
REFERENCE	1 (bases 1 to 15186)		
AUTHORS	Bu,Z., Ge,J., Hu,S. and Wen,Z.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-DEC-2004) Harbin Veterinary Research Institute, Chinese Academy of Agricultural Sciences, 427 Maquan Street, Nangang, Harbin 150001, China		
REFERENCE	2 (bases 1 to 15186)		
AUTHORS	Bu,Z., Ge,J., Hu,S. and Wen,Z.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-MAR-2005) Harbin Veterinary Research Institute, Chinese Academy of Agricultural Sciences, 427 Maquan Street, Nangang, Harbin 150001, China		
REMARK	Sequence update by submitter		
COMMENT	On Mar 17, 2005 this sequence version replaced gi:56799463.		
FEATURES	Location/Qualifiers		
SOURCE	1. 15186		
	/organism="Newcastle disease virus"		
	/mol_type="genomic RNA"		
	/strain="Lasota"		
	/db_xref="taxon:11176"		
gene	122..1591		
	/gene="NP"		
CDS	122..1591		
	/gene="NP"		
	/codon_start=1		
	/product="nucleocapsid protein"		
	/protein_id="AAJ0676.1"		
	/db_xref="GI:56799464"		
	/translation="MSVFPPEYEOQLAAOTRPNAGHGGEGKSTLKVDVPEVPLTNSPD PEDWSSVVFCLRLAVSEDAKKPLRQCALISLCSHSQVNRNHALAKGNERTLAVL EIDDFANGTPOFNRRSGVSEERQRFAMLIGSLPRACNSGTPVLTAGAEADAEDLTD TLIEHLSIAQVWVYAKAMTAYETADESETRINKYMOQGRVQKYLFLVCRSTIO LTIHSLAVRIFLVSELKRGKNTAGGTYNLNVDVDSYIRNTGLTAFELTLCYGIN TKHSALSLISGDIQCKMLRLYRKMGNAAPMTLIGSDMSFAPAEVADLSPFA MGASVUDKGTGKQFPARDPMSYSPRLSGYVNAQCSSINEMAAELIKTPAPRL AAAQRVSEETSIDMPTQGVGLTBSGSQLQCGSRSGQFPAGDGEFTQFLDL MRAVANSREAPNSAQGTPOSGPPTPGSDNDTDWGY"		
	1887..3074		
gene	/gene="P"		
CDS	1887..3074		
	/gene="P"		
	/codon_start=1		
	/product="phosphoprotein"		
	/protein_id="AAJ0677.1"		
	/db_xref="GI:56799465"		
	/translation="MARTFPAKIDELFETSGTVINDITTAQGPARTVGSALPOGKT KVLASAMEKSGISOPASQDNPBRODRSDQSTPBTBQTHDPSAPSADPOPPRNSD EAVDTQRTAGSINSLLMLDLKSNKSSNARKGWSFQBSNNHORPTQOCSQPSRGNS QEPQONQKAPGNOGTDVNTAYHGWEEBQLSAGATPALRQSDNTLVASDVQ PQVFOVAMSMMEALISQVSKVDYQDLVLKOTSSIPMARSIOQLKTSVAVNEAL GMKTLIPGCANISLSLSDLRVAVRSHPVLVSGSDPEPYTQGGEMALNTLQDPVHP SELIKRPTACGPDIGVEKDTVRLALINRPMHPSSAALLSKDAAGSIEIRIKIRLA LNG"		
	3290..4384		
gene	/gene="M"		
CDS	3290..4384		
	/gene="M"		
	/codon_start=1		

/product="matrix protein"  
/protein\_id="AAW30678.1"  
/db\_xref="GI:56799466"  
/translation="MDSRRITGLFYDEASHSSNLLAPPIVLQGTGDKQKQIAPOYRIQ  
RLDLMDSKEDSVITITTYGFIPOVGENEATVGMIDDKREILSAAMLGSGVNTQD  
LILBAPACLTMIYCKKSATTEBMVSUYOAPVOYLAKSSSYNAVYKVP  
EKIPGSGTLEKVPFSLTVPPKQVYKIPAAVLKVGSSILNLAHTVTTINVEIDPS  
PLVSLSKSDSGYYANLFLHGLMTTVDRKQKVTFKLEKRIKSLDLSVGLSDVILP  
SVAVKAGARTKLIAPFSSSGTACYPIDANSPQAVKILWSQTLCSRSVKIIIOAGTQ  
RAVAVTADHEVTSTLEKGHILAKNPFKK"  
4544. .6205  
/gene="F"  
4544. .6205  
/gene="F"  
/codon\_start=1  
/product="fusion protein"  
/protein\_id="AAW30679.1"  
/db\_xref="GI:56799467"  
/translation="MGSRPSTKNAPMMLITRVALVLSCTCPANSDIGRPLAAQIVY  
TGDAAVNIYTSBQTSIIIVKLPLPDKKACAPAPLAYNRILTTLPLPGDSIRI  
QESVTVSGGROGLIGAILGGVALGYATAQIAPAAALIOAKQNAANIILAKESIAA  
TNEAVHEVTGSLQAVAGKMOQFVNDOLKTAQELDCIKIAQVGEINLYTELT  
TVGPOITSPALNLTIOALYNLAGMDVLTFLGVGNOLSLISGSLITGPIIY  
DSQTLGIRVTLPSVGNLNMRTYIETLSVSTRGPASALYKVTYQVGSYVEID  
TSYCIETDLDLCTRIYTFMSPGSIYCLSGNTSACMYSKTEGALTTPYMTIKSVIA  
NCKWTCRCVNPGLIISQNYGEAVSLDKQSCNVLISGQITLRLSGFEDVYQKNI  
QDSQVILITGNLIDSTELGANNVNSISNLAFLKESNRKLDKYNVLITSTALITVYLT  
IISLFGIILSLIACVLYKQKQKTLMLGNNTLDQMATTGM"  
6412. .8145  
/gene="HN"  
6412. .8145  
/gene="HN"  
/codon\_start=1  
/product="hemagglutinin-neuraminidase"  
/protein\_id="AAW30680.1"  
/db\_xref="GI:56799468"  
/translation="MDRAVSQVALENDERBAKNTWLLIFRIALLFTVTVAISVASL  
LYMAGSTPDLVGIPTNRSRABEKITSTIGSNQDVDRYKQVADLSPALAKTEET  
INMAITSLYOINGAANSQMGALIHDPDIYIGIKELIYDDALSTFSPASQELH  
NFIAPATGSGCTRIIPSGMATHYCYTHNVILISGGRDHSYQVLAFLYRSATGR  
VFESTLARSINLDTQNRKSCSVATPLGCMILCKRTYETSEEDNSAVPTRMHGRIG  
FDQYHEKDLVLTLLFGDMVANTPGVGGSFIDSRVFSYVYGKLPSPEDVYQEGKT  
VIKRYNDQTPDEQYQIRMARSSYKPRFGKRIQQAIIISIKVSTLSDGPVLTVP  
NTYTLMGAEGRILTVGSHFLYQSGSSYFPALYPTVSNKTLTISPYTFNAFTPP  
GSIICQASARCPNDCVTGYTDPHPLIFYRHNTLRGVEGMLDVCQARLNPASVFP  
TSRSRIIRVSSSTKAYTSTCKVKVTKTKYCLSLAIISNLTIFGFRIVPLVELL  
KDGCVREARSG"  
8381. .1495  
/gene="L"  
8381. .1495  
/gene="L"  
/codon\_start=1  
/product="large polymerase protein"  
/protein\_id="AAW30681.1"  
/db\_xref="GI:56799469"  
/translation="MASSGPERAHEHQLIPESHLSPLVYKHLKYKLTGLPLPDEC  
DPIHLISRWKKILIESAPDTERMIKLGAVHOTLHNSRITGVHPRCLBELANE  
VPDSTKPKRIEKKIQIHNRXGELPTRLCTHIEKLLSSMSNVPRESPEISRTD  
PAWFHSMSTAKPAMLIHQIQRHLNVAAPTSANKLYMLTHKQOVVTPPELVVY  
THTNENKFTLQELVLMYADMMEGRMVNIISTVAHLSEKIDILLRLIDALAK  
DLNOVDVSLMEGFAYGAVQDLPEPQAGDFPAPNLOELKQILIGLIPNDIABEV  
THAIATVSGLEONQAEMLCLRLMGPILRESIRIAKRAVSGCAKPMDFPMLIYQV  
LSFPKGTILINGYRKXAGVPRYKVDITIKYIGQLHADAASITSHDMLMEYSISL  
EPEPCIEPDVYTNLSMFLKAKIAHPNDMLASFRRLISEQDKYKKEATSTRRLI  
EPLSNDPDKMEYLTLEYLRKDNVAISYLKEKXVYNGIIFAKLTKKLCNV  
MAEGILADQIAPFQNGVIOGDISLTKSMAMSQLSFNSNKRRIIDCKERVSNRNH  
DPKSKNRVATPTITDLOKYCLMRYQTIKLFMAHINOGLPHFPEWILHRLMDT  
MTMGDPNPSPDPTDCLSRVPNDIYIVARGGIBELCOKQMTMISIIAIIOLAAAS  
HCYVACMVQGDNOVIATRVSDSPENMLTOLHOSDNPEKELIHVNLIIGNIKD  
RETRISDPTFYISKRIKQDAIISQVYKNSKLVYVGDSDSENTWNSCANIYATVATL  
CENGLPDKFCYILNYSVQTYFDSFSTINNSHPLNQSWIEDISFVSYVTPAQ  
LGGISNQYRLYTRNIGDPGTAFABIQPLEAVGLISPMINILIRPQGDWMSL  
CNDPYSNFETVASPINILKKHTRRVIFETCSNPLISGVHTEDEAEKALAEFLIAG

EVTHPRVAHALMEASSVGRKQIOLGVDYTNTRYKIALTRPLGKILMRYVYSSMH  
AMFPRDVFSSSRNHPPLVSSNMCSTLADYARRRSPLTGKRIKLVSPDITELV  
EGEILSVSGCTRCDSDEQFQTPMPLPSNLELTDTCRPMRVPYSGSKQIERAA  
LAKIAHMSPVKALRASVLYIMAYGQNDVMVMTALIASRCVNLIELYLLPLPT  
AGNLOHRLLDGIOTMFTPLASVLYCHLFTFYPMILKQCSLKESKRGMMFNRVLLG  
LSLIESIPMTAPRTYDEITLHLSKSSCCIRAPVAPPELGLVPELIRVTSNKM  
YDPSRSGECPARLDLIAIFKSYELNIESYPIELMNLISISSGLIQOSVYSYEDTS  
IKDAILIYONTRNWSIEAQNSDVNRLEFAALEVNLNSTQLYLHVRGDNILVM  
GDLYKNMGILSNIAATI SHPVHSLHAAVGNHDSHQLOAPDIEIEMSAKLVSQ  
TRAVISGLYSGNKYDLPLPSVLDNLNEMKQILSRKCTGYIVLFAATREIPKRGLT  
TKKCSIIPTEYLSDAVKPLSPPOVSIMSPNITFPAPYVMSRLNIREBDR  
DTILVILPPOBPLPSPNODIGARVDDPTROBARLOELDLAPARVAFITSLQI  
PELTSPPBEDYLYRI.FRCIGTASSWYKASHLSIPBRCAHNGSLYIAESGAL  
MSLLELHPHETIYNTLFSNEMNPQRHFGPTLQFNSVYVRNLDAEYTKQGFVQ  
EPRPLMNTESDITSDKAVGYITTSAPVRSVSLHCDIETPQSGNQSLLDQALIN  
FLVAMHSVREGGVYIIVLYAMGYFPHLNMALFPCSTKGYILSGYACAGDMDCIYV  
PWYLGSPFTEHVEVMKATLVORHETILSKSPDELUTLTFEORORDVILSSPP  
RLIKYLRKNDITALEAGQPVPRPCASISVSTLANITOTIOLIASHDVYRVIYM  
BASQDLADYIPLFTPVNLSTDKKRTSLKQCTROILEVTLIGLREVNLRKQIDISLE  
LKQMIISMEDILPRTYLNKSTCPKYLKAVLIGITLKKEMFTDVSVLYLTPAQKPYMT  
IGNAVNGYNSCDS"

ORIGIN

Query Match	99.4%; Score 3337.2; DB 13; Length 15186;
Best Local Similarity	99.6%; Pred. No. 0;
Matches 3345; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
Oy 1	ACGGGTGAAGATTCTGATCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60
Db 4498	ACGGGTGAAGATTCTGATCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 4557
Oy 61	TTCTACCAAGAACCCACACCTATGATGCTGACTATCCGGGTTGCGCTGCACTGAGTTG 120
Db 4558	TTCTACCAAGAACCCACACCTATGATGCTGACTATCCGGGTTGCGCTGCACTGAGTTG 4617
Oy 121	CATCTGTCGGCAAACTTCATTGATGCGAGGCTCTTGACAGCTGCAAGAAATTGCGTTAC 180
Db 4618	CATCTGTCGGCAAACTTCATTGATGCGAGGCTCTTGACAGCTGCAAGAAATTGCGTTAC 4677
Oy 181	AGGAGCAAAAGCGGTCAACATATATGACCTATCCAGACAGGATCAATCATAGTTAAAGCT 240
Db 4678	AGGAGCAAAAGCGGTCAACATATATGACCTATCCAGACAGGATCAATCATAGTTAAAGCT 4737
Oy 241	CTCTCCGAATCTGCCCAAGATTAAGAGGATGTGCGAAAGCCCTTGGATGATACAA 300
Db 4738	CTCTCCGAATCTGCCCAAGATTAAGAGGATGTGCGAAAGCCCTTGGATGATACAA 4797
Oy 301	CAGGACATTGACCACTTGTGCTACCCCCCTTGGTGACTTATCCGTAGATCAAGAGTC 360
Db 4798	CAGGACATTGACCACTTGTGCTACCCCCCTTGGTGACTTATCCGTAGATCAAGAGTC 4857
Oy 361	TGNGACATCAATCGAGAGGGGGGAGACAGGGGCGCTTATAGGGCGCATTTATGGCGGTG 420
Db 4858	TGNGACATCAATCGAGAGGGGGGAGACAGGGGCGCTTATAGGGCGCATTTATGGCGGTG 4917
Oy 421	GGCTCTTGGGGTTGCAACTGCCCGCAAAATATACAGCGCGCGCAAGCTGTGATCAAGCCAA 480
Db 4918	GGCTCTTGGGGTTGCAACTGCCCGCAAAATATACAGCGCGCGCAAGCTGTGATCAAGCCAA 4977
Oy 481	ACAAATGCTGCCAATCTCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGCGTGT 540
Db 4978	ACAAATGCTGCCAATCTCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGCGTGT 5037
Oy 541	GCATGAGGTCACTGACCGGATTAATCCGCACTAGACGTGGCAATTGGGAAGATGCGAGATT 600
Db 5038	GCATGAGGTCACTGACCGGATTAATCCGCACTAGACGTGGCAAGTGGGAAGATGCGAGATT 5097
Oy 601	TGTTATGACCAATTTATATATAACAGCTCAGAAATTTGATCGATCAAAATTTGACAGCA 660
Db 5098	TGTTATGACCAATTTATATATAACAGCTCAGAAATTTGATCGATCAAAATTTGACAGCA 5157
Oy 661	AGTTGATGAGAGCTCAACCTGTACCTTAACCGAATTGACATCAATTTGGACCACAAAAT 720
Db 720	AGTTGATGAGAGCTCAACCTGTACCTTAACCGAATTGACATCAATTTGGACCACAAAAT 720

Db 5158 AGTTGGTGAAGACTCAACCTGTAACCTAACCAGAAATTGACCTACAGTATTCCGACCACAAAAT 5217  
Qy 721 CACTTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGGAAA 780  
Db 5218 CACTTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGGAAA 5277  
Qy 781 TATGATTAATTATGACTAAGTTAGGTGAGGAAACAATCACTCAGCTCATTAATCGG 840  
Db 5278 TATGATTAATTATGACTAAGTTAGGTGAGGAAACAATCACTCAGCTCATTAATCGG 5337  
Qy 841 TACCGGCTTATACCCGGTAAACCTTATCTATACGACTCAAGCTCAACCTTGGGGTAT 900  
Db 5338 TACCGGCTTATACCCGGTAAACCTTATCTATACGACTCAAGCTCAACCTTGGGGTAT 5397  
Qy 901 ACAGGTAACTCTACCTTCAGTCGGGAACTTAATAATATGCGGCCACTACTTGGAAAC 960  
Db 5398 ACAGGTAACTCTACCTTCAGTCGGGAACTTAATAATATGCGGCCACTACTTGGAAAC 5457  
Qy 961 CTATTCGGTAAGCAACAACGAGGAAATTTGCTCGGCACTTGCCCAAAAGTGTGACACA 1020  
Db 5458 CTATTCGGTAAGCAACAACGAGGAAATTTGCTCGGCACTTGCCCAAAAGTGTGACACA 5517  
Qy 1021 GGTTCGGTCTGTGTATGAGAAACCTTGACACTCTCATCTGTATAGAACTGACTTAAGATT 1080  
Db 5518 GGTTCGGTCTGTGTATGAGAAACCTTGACACTCTCATCTGTATAGAACTGACTTAAGATT 5577  
Qy 1081 AATATTGACAAGAAATAGTAAGTTCCCTATGTCCCTGCTGATTTATTTCTGCTTGACGG 1140  
Db 5578 AATATTGACAAGAAATAGTAAGTTCCCTATGTCCCTGCTGATTTATTTCTGCTTGACGG 5637  
Qy 1141 CAATACGTGGCCCTGATATGTAACCTCAAAAGACGGAAGCGCACTTATACCATATCATGAC 1200  
Db 5638 CAATACGTGGCCCTGATATGTAACCTCAAAAGACGGAAGCGCACTTATACCATATCATGAC 5697  
Qy 1201 TATCAAAAGGTTCACTCATCCGCAACCTGCAAGATGACAAACATGTGAGTGTGAAAACCCCC 1260  
Db 5698 TATCAAAAGGTTCACTCATCCGCAACCTGCAAGATGACAAACATGTGAGTGTGAAAACCCCC 5757  
Qy 1261 GGGTATCATATGCGCAAACTATGGAAGAGCGGTGCTCTAATAGATTAACAATCATGACAA 1320  
Db 5758 GGGTATCATATGCGCAAACTATGGAAGAGCGGTGCTCTAATAGATTAACAATCATGACAA 5817  
Qy 1321 TGTTTTATCCTTAGCGGGATTAACCTTTAAGGCTCAGTGGGAAATTCGATGTAATTATCA 1380  
Db 5818 TGTTTTATCCTTAGCGGGATTAACCTTTAAGGCTCAGTGGGAAATTCGATGTAATTATCA 5877  
Qy 1381 GAAGATATCTCAATACAAGATTCTCAAGTAATATAACAGGCACTCTTGATATCTCAAC 1440  
Db 5878 GAAGATATCTCAATACAAGATTCTCAAGTAATATAACAGGCACTCTTGATATCTCAAC 5937  
Qy 1441 TGAAGCTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAAATTAAGTGAAGAAACAA 1500  
Db 5938 TGAAGCTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAAATTAAGTGAAGAAACAA 5997  
Qy 1501 CAGAAAACCTAGACAAGTCAATGTCAAACTGACTAGACAATCTGCTCTCAATTACCTATAT 1560  
Db 5998 CAGAAAACCTAGACAAGTCAATGTCAAACTGACTAGACAATCTGCTCTCAATTACCTATAT 6057  
Qy 1561 CGTTTGGACTATCATATCTCTGTTTGGTATATCTTAACTGATCTTGAAGTGAAGAAACAA 1620  
Db 6058 CGTTTGGACTATCATATCTCTGTTTGGTATATCTTAACTGATCTTGAAGTGAAGAAACAA 6117  
Qy 1621 AATGTCAACGAAAGGCGCAACAAAACCTTATATGCTTGGGAATTAATCTATAGA 1680  
Db 6118 AATGTCAACGAAAGGCGCAACAAAACCTTATATGCTTGGGAATTAATCTATAGA 6177  
Qy 1681 TCAGATGAGACCACTACAAAATGTGAACAACAGATGAGAACGAAAGTTTCCCTAATAG 1740  
Db 6178 TCAGATGAGACCACTACAAAATGTGAACAACAGATGAGAACGAAAGTTTCCCTAATAG 6237  
Qy 1741 TAAATTTGTGAAAAGTTCTGGTACTCTGTCAATTCAAGAGTTAAGAAAACCTACCGGT 1800  
Db 6238 TAAATTTGTGAAAAGTTCTGGTACTCTGTCAATTCAAGAGTTAAGAAAACCTACCGGT 6297

Qy 1801 TGTATATGACCAAAAGCAATATACGGGTGAACCGTAAAGAGAGCCGCCCTCAATTGC 1860  
Db 6298 TGTATATGACCAAAAGCAATATACGGGTGAACCGTAAAGAGAGCCGCCCTCAATTGC 6357  
Qy 1861 GAGCGAGGCTTCAACAACCTCGTTCACCGCTTCAACGCAACAAGTCTCAATCATGAGAC 1920  
Db 6358 GAGCGAGGCTTCAACAACCTCGTTCACCGCTTCAACGCAACAAGTCTCAATCATGAGAC 6417  
Qy 1921 CGCGCGTTATAGCAAGTTGCGTTATGAGAAATGATGAAGAAGGCAAAAATATACATGCGGC 1980  
Db 6418 CGCGCGTTATAGCAAGTTGCGTTATGAGAAATGATGAAGAAGGCAAAAATATACATGCGGC 6477  
Qy 1981 TTGATATTCGGGATTTGCAATCTTATTTTAAAGTATGACCTTTGGCTATATCTGTAGCC 2040  
Db 6478 TTGATATTCGGGATTTGCAATCTTATTTTAAAGTATGACCTTTGGCTATATCTGTAGCC 6537  
Qy 2041 TCCCTTTATATATAGCAATGCGGGGCTAGACACCTAGGCACTTGTATAGGCAATACGACCTAGG 2100  
Db 6538 TCCCTTTATATATAGCAATGCGGGGCTAGACACCTAGGCACTTGTATAGGCAATACGACCTAGG 6597  
Qy 2101 ATTTCCAGGCGAGAAAGAAAGATTACATCTACCTTGTTCATCAATCAAGATGATAGAT 2160  
Db 6598 ATTTCCAGGCGAGAAAGAAAGATTACATCTACCTTGTTCATCAATCAAGATGATAGAT 6657  
Qy 2161 AGGATATATAGCAAGTGGCCCTTGAAGTCTCCGTTGGCAATTTGTTAAATCTGAGACCA 2220  
Db 6658 AGGATATATAGCAAGTGGCCCTTGAAGTCTCCGTTGGCAATTTGTTAAAMCTGAGACCA 6717  
Qy 2221 AATATAGAGCAATPAACATCTCTCTCTTATCAATTAATGAGCTGCAACCAAGTGGG 2280  
Db 6718 AATATAGAGCAATPAACATCTCTCTCTTATCAATTAATGAGCTGCAACCAAGTGGG 6777  
Qy 2281 TGGGGGCGACCTATCCATGACCCAGATTAATATAGGGGGGATTAAGCAAAAGTCAATTGA 2340  
Db 6778 TGGGGGCGACCTATCCATGACCCAGATTAATATAGGGGGGATTAAGCAAAAGTCAATTGA 6837  
Qy 2341 GATGATGCTATGATGTACATCATATTCATCCCTCTGCAATTTCAAGAACTCTGAATTT 2400  
Db 6838 GATGATGCTATGATGTACATCATATTCATCCCTCTGCAATTTCAAGAACTCTGAATTT 6897  
Qy 2401 ATCCCGCGGCTACTACAGGATGAGGTGCACTGCAATPACCTCATTTGACATGAGTGT 2460  
Db 6898 ATCCCGCGGCTACTACAGGATGAGGTGCACTGCAATPACCTCATTTGACATGAGTGT 6957  
Qy 2461 ACCCATTAATGCTACACCCATTAATGTAATATTTCTGATGACAGATCACTCATTTCA 2520  
Db 6958 ACCCATTAATGCTACACCCATTAATGTAATATTTCTGATGACAGATCACTCATTTCA 7017  
Qy 2521 TATCAGTATTTAGCACTTGGTGTGCTCCGCAACTCTGCAACAGGAGGTAATCTTTTCT 2580  
Db 7018 TATCAGTATTTAGCACTTGGTGTGCTCCGCAACTCTGCAACAGGAGGTAATCTTTTCT 7077  
Qy 2581 ACTCTGCTTCCATCAACCTGGAAGACACCCAAATTCGGAAGTCTTGCAATGGAAGTGA 2640  
Db 7078 ACTCTGCTTCCATCAACCTGGAAGACACCCAAATTCGGAAGTCTTGCAATGGAAGTGA 7137  
Qy 2641 ACTCCCGTGGGTTGTGATATGCTGTGCTCGAAAGTCAAGGACAGAGAAAGATTAAT 2700  
Db 7138 ACTCCCGTGGGTTGTGATATGCTGTGCTCGAAAGTCAAGGACAGAGAAAGATTAAT 7197  
Qy 2701 AACTCAGCTGTCCCTACGCGGATGTATCATGGAAGTTAGGGTTTCAAGCGCCAGTACAC 2760  
Db 7198 AACTCAGCTGTCCCTACGCGGATGTATCATGGAAGTTAGGGTTTCAAGCGCCAGTACAC 7257  
Qy 2761 GAAAAGGACCTTAATGTCAACAATTAATTCGGGGACTGGGTGCGCAACTCAAGGAGTA 2820  
Db 7258 GAAAAGGACCTTAATGTCAACAATTAATTCGGGGACTGGGTGCGCAACTCAAGGAGTA 7317  
Qy 2821 GGGGGTGGATCTTTTATTTGACAGCGCGTATGGTCTCACTTAACGAGGTTAAACCC 2880  
Db 7318 GGGGGTGGATCTTTTATTTGACAGCGCGGTAATGGTCTCACTTAACGAGGTTAAACCC 7377



QY 2881 AATTCAACCCGTCACATCTGTACAGAGGAAATATGTGATATATCAAGCGATACAAATGAC 2940  
DB 7378 AATTCAACCCGTCACATCTGTACAGAGGAAATATGTGATATCAAGCGATACAAATGAC 7437  
QY 2941 ACATGCCCATGATGAGCAAGAATAACCATTCGAATGAGCCAAAGTCTTGATTAAGCTTGA 3000  
DB 7438 ACATGCCCATGATGAGCAAGAATAACCATTCGAATGAGCCAAAGTCTTGATTAAGCTTGA 7497  
QY 3001 CGGTTGGTGGGAAACGATACAGACAGGCTATCTTATCTATCAAGGTGTCAACATCTTTA 3060  
DB 7498 CGGTTGGTGGGAAACGATACAGACAGGCTATCTTATCTATCAAGGTGTCAACATCTTTA 7557  
QY 3061 GCGGAAGACCCGGTACTGATCTGTACCGCCCAACACAGTCACTCATGAGGGCCGAAGGC 3120  
DB 7558 GCGGAAGACCCGGTACTGATCTGTACCGCCCAACACAGTCACTCATGAGGGCCGAAGGC 7617  
QY 3121 AGAATCTCACAGTAAAGGAGACATCTCATTTCTGTATCAAGAGGGTCATCATCTTCTCT 3180  
DB 7618 AGAATCTCACAGTAAAGGAGACATCTCATTTCTGTATCAAGAGGGTCATCATCTTCTCT 7677  
QY 3181 CCGCGCTTATTAATCTCTATGACAGTACAGCAACAAACAGCCACTTTCATAGTCTTAT 3240  
DB 7678 CCGCGCTTATTAATCTCTATGACAGTACAGCAACAAACAGCCACTTTCATAGTCTTAT 7737  
QY 3241 ACATTCAGTCCCTTCACTCCGCCAGTATATCCCTTCCAGGCTTCAAGCAAGTCCCC 3300  
DB 7738 ACATTCAGTCCCTTCACTCCGCCAGTATATCCCTTCCAGGCTTCAAGCAAGTCCCC 7797  
QY 3301 AACTCGGTGTCTCTGAGTCTATACAGATCCATATCCCTTAATCTTATAGAAACC 3358  
DB 7798 AACCCTGTGTCTCTGAGTCTATACAGATCCATATCCCTTAATCTTATAGAAACC 7855

RESULT 8  
AF375823 15186 bp RNA linear VRL 06-NOV-2001  
DEFINITION Newcasttle disease virus strain B1 isolate Takaki, complete genome.  
ACCESSION AF375823  
VERSION AF375823.1 GI:14190062  
KEYWORDS  
SOURCE  
ORGANISM  
Newcasttle disease virus B1  
Newcasttle disease virus B1  
Virusess; sRNA negative-strand viruses; Mononegavirales;  
Paramyxoviridae; Paramyxovirinae; Avulaviruses.

REFERENCE  
AUTHORS Nakaya, T., Crois, J., Park, M.S., Nakaya, Y., Zheng, H., Sagreera, A.,  
Villat, E., Garcia-Sastre, A. and Palese, P.  
TITLE Recombinant Newcasttle disease virus as a vaccine vector  
JOURNAL J. Virol. 75 (23), 11868-11873 (2001)  
PUBMED 11689668  
REFERENCE 2 (bases 1 to 15186)  
AUTHORS Nakaya, T., Garcia-Sastre, A. and Palese, P.  
TITLE Direct Submission  
JOURNAL Submitted (02-MAY-2001) Microbiology, Mount Sinai School of  
Medicine, One Gustave Levy Place, New York, NY 10029, USA  
FEATURES  
source  
1. 15186  
/organism="Newcasttle disease virus B1"  
/viation  
/mol\_type="genomic RNA"  
/strain="B1"  
/isolate="Takaki"  
/db\_xref="taxon:139270"  
56..1792  
/gene="NP"  
56..1792  
/gene="NP"  
/product="nucleocapsid protein"  
122..1591  
/gene="NP"  
/codon\_start=1  
/product="nucleocapsid protein"  
/protein\_id="AAK5547.1"

CDS

gene  
mRNA  
CDS

/db\_xref="GI:14190063"  
/translation="MSSVFPDEYBOLLAAOTRPNGAHGGEKSTLKYDVPVETLNSD  
PERMRSPVVECLAIYSEDANKPLROGALLSLICSHSQWNRHVYALAKONEATLAVL  
ELDGFANGTPOFNRRSGVSEERAEQREAMIGSLPRACSNGTPTVACAGEDAPEDITD  
TLERLISIQOAVWTVAKAMTAYETLDESETRIRINKMOQGRVQKYLIPVCSSTIQ  
LTIROSIAVRIPLVSELKRGNTAGSTYVNLGVDVDSYIRNTGLFAPFLTKYGN  
TKTISALASLSIDGIOMKQMLRYRKGNAPYMTLLGSDMSFAPAEAYOLYSKA  
MGAAVTDKSTGKYQAPARDPMSTISFWMILGYEYAOAGSSINEMAAELKILTPARGL  
AALAAVSEVTSIDMFTQOVGVLTGISEGSGQLQAGSNRSQGPBAAGGETOFLDL  
MRAVANSREAPNSAQTPQSGPPPPGSDNDTDMGY"  
1804..3244  
/gene="P"  
/product="phosphoprotein"  
1887..3074  
/gene="P"  
/codon\_start=1  
/product="phosphoprotein"  
/protein\_id="AAK5548.1"  
/db\_xref="GI:14190064"  
/translation="MAFTDAEIDELFETSGTVIDNIIITAQKPAETVGSALPQSKT  
KVLAAWEKSGSIQPPASODNLDRODSIDQSPTEPQTTPHDSPATSAQPPQATD  
EAYDTOLRTGANSILIMDLKLSNKSNAKGPMSRPOEGRHQPQQCSQPSRGS  
OERLQNVKAPRNOCTDNTATYAHGWEESOLASGAPHALRSROSDMTLVASDHO  
PVDFOVAMSMGALISQRYSKYDQDLVLKQTSSTPMARSETQQLKTSVAMENAL  
GMKMLIDPPGANISLSLDLAVASHPLVSGPDSPPYVTOGEMALNKLSQPVPH  
SELIKPATACGPDIQVETDVRALIMSRPMPSSAKLSLIDAGSIIETRIKRLA  
LNG"  
3256..4487  
/gene="W"  
3256..4487  
/gene="W"  
/product="matrix protein"  
3290..4384  
/gene="W"  
/codon\_start=1  
/product="matrix protein"  
/protein\_id="AAK5549.1"  
/db\_xref="GI:14190065"  
/translation="MDSRTGLYFDSAHSSNLAAPVILQDTGDKKOIAPORYIO  
RLDSMDSKDSVETITTYGRIFQVGNBETAGMIDKPKBELSAAALICGVSNTGD  
LVELARACLTMTYTCKKSAATNEMVSUVOAPOVLQSCVYANKYSVNAVKVKAAP  
EKIPGSGTLEKYNFVSLIVPKDVKYKIPAAVLKISGSSLYNALAVTINVEDPRS  
PLVSKLEKSDSGYANLFLHGLMTVDRKGVTFPKLEKIRSLDLSVGLSVLGP  
SLVVKRAGARTKILAPFSSSGTACPIANASPOVAKILWSQTCILRSVKLIIDAGTQ  
RAVAVTADHEVTSKLEKHTLAKYVFKK"  
4498..6279  
/gene="F"  
4498..6279  
/gene="F"  
/product="fusion protein"  
4544..6205  
/gene="F"  
/codon\_start=1  
/product="fusion protein"  
/protein\_id="AAK5550.1"  
/db\_xref="GI:14190066"  
/translation="MGSRPSTKPNPAPMLLITRVALVLSICPANSIDORPLAAGIIV  
TGDRAVNTISSQSGSIYVLLPPLPDKACACAPLDAYNRLLTTLTLPDGSIRRI  
QESVTSIGGRQKRLIGLVALGVATAQITAAALIOAKMANIILAKESIAA  
TNEAVHEVTDLSQLAVAGMOQFVDFNKTAQELDKIAQOVGVELNLVTELT  
TVFPGQITSPALNKLTIDALYNLAGNMDDYLITLGLGNNOLISGLITGPNILY  
DSOTOLGIVTLPSPVGNLNNMRATYLETLSVTRGFSALVPRKVVQVGVSEILD  
TSYCIETDLDLYCIRIYVTPMSPGIVYCLSGNTSACVSKTEGALTTPYMTIKGSVIA  
NCKRTTCRCNPPGISIQNYGNAVSLIDKOSCVLSIGLITRLISGEDVDYVKNISII  
QDSQVITITGNDISTELGNVNSISNALNKLEBSNRDLKRYNVLTSLSALITTYVLT  
IISLVFGLISLLIACILMYRQKAAQKTLMLGNNTLDQMRATYTK"

gene  
mRNA

gene  
mRNA  
CDS

CDS  
6412..8145  
/gene="HN"  
/codon\_start=1  
/product="hemagglutinin-neuraminidase"  
/protein\_id="AAK5551.1"  
/db\_xref="GI:14190067"  
/translation="MDRAVQVLALENDERAKNTWLLIFPAILLFTVTLTASVSL  
LYEMGASTPDLVGIPTIRISRAEKLITSLGSDVDVDRITYQVLAESPLALNTET  
INNAITSLAYQINGAANNQMGAPIHDPYIGIGKELIYDASDVTSYPSPAFQEBL  
NPIAPPTGSGCTRIPEFDMSATHYCTHANVILSGCDHSHSHQYLALGVLPATSR  
VFPSLTSLINDPTONRKSCSVATPLGCMCLCSKATEEEDNVSVPTRMWRGLG  
PDCQYHEKDLDTTLEBDWANTPVGCGSGFIDSRWFSPYSGIKPTPBDYQEGY  
VITKRYNDTCPEEDQYIRMAKSYKFGGKRIQQAIIISIKVTSLSGDPVLTVP  
NVTWLGAEGRILTVGSHFLYQSGSSYFSPALLYPTWSDKATLTLSPYTAFTBP  
GSIIPCASARCPNSCVGYTDPYPLIFRNHTLIRGVGTMIDGEOARLNPASVFPSS  
TSRSRITRVSSSIIKAAVTTSTCPKVKTKYCTLSIAEISNTLFGSFRIVPLVEIL  
KDGQVREASG"  
8370..15073  
/gene="L"  
8370..15073  
/product="large polymerase protein"  
/gene="L"  
8381..14995  
/codon\_start=1  
/product="large polymerase protein"  
/protein\_id="AAK5552.1"  
/db\_xref="GI:14190068"  
/translation="MASSGPRAHQIILPESHLSPLVGHKLLYWKLTGLPLPDC  
DPEHLISRWKMKILBSASPDTERMKLGAHVHQTLLHNSRITGVLPRLCELANIE  
VPSTNPKRIEKKIQHNTRYGELFRLTTHIEKLKLGMSNVNRPSEFSSIRVD  
PAFPMKSTAKFAMHLKIQIORHLIQAARTSAANKLMLTHKQVQVTELVV  
THNENKFTCLQELVLMVADMMGDMVNIISTVAHLSLSEKIDILIDALAK  
DIONOVYDVVSLMBGFAYGAVOLLEPSTGAPFANOLEIKDILIGLIPNIAESV  
THAIATVPSGLEQQAEMLCILRMCHPLIESRIAKAYRSQMGKRWDPMTIDQY  
LSFPGKITNGYRKQAGVPRVAVDTTYKRVIGQLADABESHDIMLEYSLSL  
BEPFCLEYPVNTLSPMLKDKAIAPNDMLASFRNLSEDKHAKATSTNRLL  
EFLSNDPDEYKEMEYLTLEYLADNVASYSLEKEVNGRIFAKLTCKLMQCY  
MAFGILADOIAPPEQNGVIOISLTKSLMAMSGFNSNKRITDCKRVSQRNH  
DPSKRRRVATPTITDIOKYLNMRYOTIKLPAHAINOLMIPHEPMIILMDTT  
MFGDPENPSDPTDCLSRVNDIITYVARGGIBELCQKMTMISAIITQAAARS  
HCRVACWQGDNOVIAVTRVRSDDSEWVLTQHQSDNPFKEHLHVNHLIGHNLND  
RETRSDPTFIYAKRIFKDGAIIISOYKNSKLVLVGSDISENTVSSCANISVAVL  
CENGLPDKFCYLIANYMSCVQTFDESEFSTNNSHPLDMSIEDISFVSYLTPAQ  
LGLSLNOYSLRYTRNIGDPGTTAFARIKRLAVGLISPNIRNTLIRPQDGMASL  
CNPYSPNEETVASPNIVLKHQOVLPFCNSPBLSGVTHENEAERKALAEILNO  
EVHPRVAAHMEASVGRKKIQGLVDITNTVIKALTRPLGIKLWKIVNTSMH  
AMLPFDVSSSSNHPVLSNMCSTLADARNRSPVLTGAKILIGVNPDTIELV  
EGEILSVGGCTCDSGDEQFTWFLPNSIELTDDTSKNPMRPVLYGSKTORBRAS  
LAKIAHMSPHVKAARASVLIWAGDNEVMTALTIASRCVNLLEYRLSLPLPT  
AGLQHRIDGDIQMTPTPASIVRSPYHIHNSDSORLFTBEGVKEGNVYVQOIMLIG  
LSLIESIFPMTTRTYDEITLHLSKFSCCIRAPVAVPELLIGVARELATVNSKEM  
YDPSVEGDFPARLDLAIKFSYELANESYPTIEIMNLISISGKLIGQSVSYDEBTS  
IKNDALIVYDNTNRMISEANSDVRLFEYAALEVLLDCSQOLYLRDLNDIVLM  
GDYIKMFGILLINIAATISHPVHSRLAHVGLVNHGSLADTDEIEMSAKLLVSC  
TRVITSGLYGKCYDLFPVLDONEMKOLISRCCTCYLTAFATREIPIKRLGT  
AEEKSLTEYILSDAKVCDIGARVODTPRPAALIGELDISAPARYATFISQIH  
DTLIALIFPOEPLIEPVSODIGARVODTPRPAALIGELDISAPARYATFISQIH  
BELTSPNEEDYLRVYLRGIGTASSWSVASHLSVPERCAHNGSLVLASGQAF  
MSLLELHPHEITLYNTLPSENNMPQRHGPPTQJLNSVNNLQAEVTKDQFQ  
EPRFLRENTESDITSDAKVGYTASVPRSVSLHCDIEIPGSOISLDDALAV  
SLIAMSVERGGVYIKVLYAMGYFHLNLMLFAPGCTKYTLTSSORRARDIISSEY  
FWNGYLGPPFVHEVVMAKTIVORHGLTISKDEITLFTLSORRARDIISSEY  
RLIKYLRKNTIDTALIEAGQVPRPCAESIVSTLANITQITQIASHIDIVISVYM  
EAGGLADIVLFTFPYNLSTGKRITSLKQCTROIIEVTLIGLREVENLAKIGDITSLV  
LKGMSIEDILPRTYLRKSTCPKYLKAVIGITKLKEMFTDTSVLYLTRAQOKRYMKT  
IGNAVKGYNSCDS"

ORIGIN  
Query Match 98.5%; Score 3308.4; DB 13; Length 15186;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 3327; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy	1	ACGGGTGAAGATTCTGATCCCGGTTGGGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60
Db	4498	ACGGGTGAAGATTCTGATCCCGGTTGGGCCCTCCAGGTGCAAGATGGGCTCCAGACC	4557
Qy	61	TTTACCAAGAACCCACACCTTATGATGCTACTATCCGGGTTGGCGCTGCACTGAGTTG	120
Db	4558	TTTACCAAGAACCCACACCTTATGATGCTACTATCCGGGTTGGCGCTGCACTGAGTTG	4617
Qy	121	CATCTGTCGGCAAACTCCATTGATGAGAGGCGCTCTTGACCTGACAGAAATTGCTTAC	180
Db	4618	CATCTGTCGGCAAACTCCATTGATGAGAGGCGCTCTTGACCTGACAGAAATTGCTTAC	4677
Qy	181	AGGAGCAAAACCGGTCAACATACACTCATCCAGACAGATCAATCATAGTTAGCT	240
Db	4678	AGGAGCAAAACCGGTCAACATACACTCATCCAGACAGATCAATCATAGTTAGCT	4737
Qy	241	CTTCCGGAATCTGCGCAAGATTAAGAGGATGAGGAAAGCCCTTGGATGATCA	300
Db	4738	CTTCCGGAATCTGCGCAAGATTAAGAGGATGAGGAAAGCCCTTGGATGATCA	4797
Qy	301	CAGGACATTGACACCTTGTGCTCAACCCCTTGGTGACTTATCCGTAGATACAAAGTC	360
Db	4798	CAGGACATTGACACCTTGTGCTCAACCCCTTGGTGACTTATCCGTAGATACAAAGTC	4857
Qy	361	TGTGACTCATCTGAGAGGGGGAGACAGGGGCGCTTATAGGGCCATTATGGCGGTGT	420
Db	4858	TGTGACTCATCTGAGAGGGGGAGACAGGGGCGCTTATAGGGCCATTATGGCGGTGT	4917
Qy	421	GGCTTTGGGGTTGCAACCTGCGCCACAAATACAGGGGCGGCGCTGTGATCAAGCCA	480
Db	4918	GGCTTTGGGGTTGCAACCTGCGCCACAAATACAGGGGCGGCGCTGTGATCAAGCCA	4977
Qy	481	ACAAAATGCTGCCAAACATCTCCGACTTAAGAAGAGCATTCGCCCAACATGAGCTGT	540
Db	4978	ACAAAATGCTGCCAAACATCTCCGACTTAAGAAGAGCATTCGCCCAACATGAGCTGT	5037
Qy	541	GCAATGAGTCACTGACGAGATTATCGCAATGACGTGCGCATGTTGGGAATGACAGATT	600
Db	5038	GCAATGAGTCACTGACGAGATTATCGCAATGACGTGCGCATGTTGGGAATGACAGATT	5097
Qy	601	TGTTAATGACCAATTTAATAAAACAGTCAAGAAATTTAGATGCAAAATTTGACAGCA	660
Db	5098	TGTTAATGACCAATTTAATAAAACAGTCAAGAAATTTAGATGCAAAATTTGACAGCA	5157
Qy	661	AGTTGGGTGAGACTCAACCTGATACCTTAACGAATTTGACTAGATTTGGACCACAAT	720
Db	5158	AGTTGGGTGAGACTCAACCTGATACCTTAACGAATTTGACTAGATTTGGACCACAAT	5217
Qy	721	CACCTTCACTGCTTTAAACAAGCTGACTATTACAGGCACTTTACAACTGAGTGGA	780
Db	5218	CACCTTCACTGCTTTAAACAAGCTGACTATTACAGGCACTTTACAACTGAGTGGA	5277
Qy	781	TATGATTTACTTATTTGACTAAGTTAGGTGTAAGGAAACAATCACTGAGCTATTAACTCGG	840
Db	5278	TATGATTTACTTATTTGACTAAGTTAGGTGTAAGGAAACAATCACTGAGCTATTAACTCGG	5337
Qy	841	TAGGGGCTTAATACCGGTAAACCTTATTATACAGACTCAAGACTCAACTCTTGAGTAT	900
Db	5338	TAGGGGCTTAATACCGGTAAACCTTATTATACAGACTCAAGACTCAACTCTTGAGTAT	5337
Qy	901	ACAGGTAACTCTACCTTCACTCGGAAACCTTAATAATATGCTGCCACTTATTTGAAAC	960
Db	5398	ACAGGTAACTCTACCTTCACTCGGAAACCTTAATAATATGCTGCCACTTATTTGAAAC	5457
Qy	961	CTTATCCGTAGACAAACGAGGGATTTGCTCGGCACTTGTCCAAAATGGTGGACACA	1020
Db	5458	CTTATCCGTAGACAAACGAGGGATTTGCTCGGCACTTGTCCAAAATGGTGGACACA	5517
Qy	1021	GCTCGGTTCTGTATGAAAGAACTTGAACCTGATCTGATATGAACTGACTTAACTT	1080
Db	5518	GCTCGGTTCTGTATGAAAGAACTTGAACCTGATCTGATATGAACTGACTTAACTT	5577
Qy	1081	ATATTGTACAAGATAGTAACTTCCCTATGTCCTCGTATTAATCTGCTTGACGG	1140

|||||  
Db 5578 ATATTTGACAGAAATAGTAAGTTCCTTATGTCCCTGGTATTTTACTCTCTGAGGG 5637  
Qy 1141 CAATACGCGGCTGTATGTACTCAAAAGCCGAAGCGCATTACTACCATCATGAC 1200  
Db 5638 CAATACATCGGCTGTATGTACTCAAAAGCCGAAGCGCATTACTACCATCATGAC 5697  
Qy 1201 TATCAAGGTTCACTCATCGCAACTGCAAGATGACAATGTAGATGTGTAACCCGCC 1260  
Db 5698 TATCAAGGCTCACTCATCGCAACTGCAAGATGACAATGTAGATGTGTAACCCGCC 5757  
Qy 1261 GGGATCATATCGCAAACTATGAGAGCCGTGTCTTAATAGATAACATCATGCA 1320  
Db 5758 GGGATCATATCGCAAACTATGAGAGCCGTGTCTTAATAGATAACATCATGCA 5817  
Qy 1321 TGTTTATCTTAGCGGGATATACTTTAAAGGCTCAGTGGGAAATTCATGTAATTACA 1380  
Db 5818 TGTTTATCTTAGCGGGATATACTTTAAAGGCTCAGTGGGAAATTCATGTAATTACA 5877  
Qy 1381 GAAGAATATCTCAATACAAAGATTCTCAATATATATACAGCAATCTTGAATCTCAAC 1440  
Db 5878 GAAGAATATCTCAATACAAAGATTCTCAATATATATACAGCAATCTTGAATCTCAAC 5937  
Qy 1441 TGAGCTTGGGAATGTCAAACTCGATCATATGCTTGAATATAGTTAGAGAAAGCA 1500  
Db 5938 TGAGCTTGGGAATGTCAAACTCGATCATATGCTTGAATATAGTTAGAGAAAGCA 5997  
Qy 1501 CAGAAACTGACAAAGTCATGTCAACTGACATGTCATCTGCTCATTTACTTATAT 1560  
Db 5998 CAGAAACTGACAAAGTCATGTCAACTGACATGTCATCTGCTCATTTACTTATAT 6057  
Qy 1561 CGTTTGACTATCATATCTCTGTTTGTGTATCTTAGCTGATTTCTAGCATCTACT 1620  
Db 6058 CGTTTGACTATCATATCTCTGTTTGTGTATCTTAGCTGATTTCTAGCATCTACT 6117  
Qy 1621 AATGTACAAAGCAAAAGCGCAAAACCTTATATGCGTTGGGAATTAATCTTGA 1680  
Db 6118 AATGTACAAAGCAAAAGCGCAAAACCTTATATGCGTTGGGAATTAATCTTGA 6177  
Qy 1681 TCGATAGAGCCACTCAAAATGTGACACAGATGAGAACAAAGGTTTCCCTAATAG 1740  
Db 6178 TCGATAGAGCCACTCAAAATGTGACACAGATGAGAACAAAGGTTTCCCTAATAG 6237  
Qy 1741 TAAATTTGTGAAGTTCTGTGTAGTCTGTCACTTCAAGAGTTAAGAAAACTACCGGT 1800  
Db 6238 TAAATTTGTGAAGTTCTGTGTAGTCTGTCACTTCAAGAGTTAAGAAAACTACCGGT 6297  
Qy 1801 TGTAGATGACCAAGAGAGATATACGGGTAGAACGGTAAAGAGCGCCCTCAATTGC 1860  
Db 6298 TGTAGATGACCAAGAGAGATATACGGGTAGAACGGTAAAGAGCGCCCTCAATTGC 6357  
Qy 1861 GAGCGAGGCTTCAACACTCGGTTCTACCGGTTACCGGACAAAGTCTCTCATATGAGAC 1920  
Db 6358 GAGCGAGGCTTCAACACTCGGTTCTACCGGTTACCGGACAAAGTCTCTCATATGAGAC 6417  
Qy 1921 CGGCGGTTAGCCAAAGTTGCGTTAGAGATGATGAGAAAGAGGCAAAAAATACATGCGGC 1980  
Db 6418 CGGCGGTTAGCCAAAGTTGCGTTAGAGATGATGAGAAAGAGGCAAAAAATACATGCGGC 6477  
Qy 1981 TGTATATTCGGGATTTGCAATCTTATTTCTTAAACAGTATGACTTGGCTATATCTGTAGCC 2040  
Db 6478 TGTATATTCGGGATTTGCAATCTTATTTCTTAAACAGTATGACTTGGCTATATCTGTAGCC 6537  
Qy 2041 TCCCTTTATATAGCATGGGGCTAGCACACTTACGATCTTGTAGGATACCGACTAGG 2100  
Db 6538 TCCCTTTATATAGCATGGGGCTAGCACACTTACGATCTTGTAGGATACCGACTAGG 6597  
Qy 2101 ATTTCAGGGGCAAGAAAGATTACATCTACCTGCTTCCATCAAGATGTAGTAT 2160  
Db 6598 ATTTCAGGGGCAAGAAAGATTACATCTACCTGCTTCCATCAAGATGTAGTAT 6657  
Qy 2161 AGGATATATAGCAAGTGGCCCTTGAAGTCTCGTTGGCATTTAAATATGAGACCA 2220  
|||||

Db 6658 AGGATATATAGCAAGTGGCCCTTGAAGTCTTCCATTTGGCATTTGTAATATCTAGACCA 6717  
Qy 2221 ATTATGAACGCAATACATCTCTCTTATGAGTTATGAGGTGCAACACAGTGGG 2280  
Db 6718 ATTATGAACGCAATACATCTCTCTTATGAGTTATGAGGTGCAACACAGTGGG 6777  
Qy 2281 TGGGGGGCACTATTCATGACCCAGATTTATATAGGGGGATATGGCAAGAACTCATGTA 2340  
Db 6778 TGGGGGGCACTATTCATGACCCAGATTTATATAGGGGGATATGGCAAGAACTCATGTA 6837  
Qy 2341 GATGATGTAGTATGTCACATTCATTCCTCTGCAATTTCAAGAACTCTGAATTTT 2400  
Db 6838 GATGATGTAGTATGTCACATTCATTCCTCTGCAATTTCAAGAACTCTGAATTTT 6897  
Qy 2401 ATCCCGGCGCTTACAGATACAGATGCACTGCAATACCCATTTGACATGAGTCT 2460  
Db 6898 ATCCCGGCGCTTACAGATACAGATGCACTGCAATACCCATTTGACATGAGTCT 6957  
Qy 2461 ACCCATTACTGCTACCCCATTAATGTATATGTCTGTGATGCAAGATCACTCATTTCA 2520  
Db 6958 ACCCATTACTGCTACCCCATTAATGTATATGTCTGTGATGCAAGATCACTCATTTCA 7017  
Qy 2521 TATCAGATTTAGCACTTGTGTGTCTCCGACATCTGCAACAGGGAGGTATCTTTTCT 2580  
Db 7018 CATCAGATTTAGCACTTGTGTGTCTCCGACATCTGCAACAGGGAGGTATCTTTTCT 7077  
Qy 2581 ACTCTGCGTTCCATCAACTGAGACAGACCCAAATCGGAAGTCTTGCACTGTGATGCA 2640  
Db 7078 ACTCTGCGTTCCATCAACTGAGACAGACCCAAATCGGAAGTCTTGCACTGTGATGCA 7137  
Qy 2641 ACTCCCTGGTGTGTATGTGTGTCTGAAAGTCAACGAGACAGAGAAAGATTTAT 2700  
Db 7138 ACTCCCTGGTGTGTATGTGTGTCTGAAAGTCAACGAGACAGAGAAAGATTTAT 7197  
Qy 2701 AACTCAGCTGTCCCTACCGGATGTACATGGAGGTTAGGTTGACGCGCACTACAC 2760  
Db 7198 AACTCAGCTGTCCCTACCGGATGTACATGGAGGTTAGGTTGACGCGCAATATAC 7257  
Qy 2761 GAAGAAGCACTAGATGTCAACAATTTTGGGGAGTGGGTGGCCAACTACCGAGAGTA 2820  
Db 7258 GAAGAAGCACTAGATGTCAACAATTTTGGGGAGTGGGTGGCCAACTACCGAGAGTA 7317  
Qy 2821 GGGGGTGAATCTTTTATGACGCGCGGTATGTTTCTCAGTCTACGAGGTTAAACC 2880  
Db 7318 GGGGGTGAATCTTTTATGACGCGCGGTATGTTTCTCAGTCTACGAGGTTAAACC 7377  
Qy 2881 AATTCACCCAGTGCACCTGTACAGAAAGGAAATATGTGATATCAAGCCTTACAAATGAC 2940  
Db 7378 AATTCACCCAGTGCACCTGTACAGAAAGGAAATATGTGATATCAAGCCTTACAAATGAC 7437  
Qy 2941 ACATGCCAGATGAGCAAGACTACAGATTGGAATGGCAAGTCTTGGTATTAAGCTGGA 3000  
Db 7438 ACATGCCAGATGAGCAAGACTACAGATTGGAATGGCAAGTCTTGGTATTAAGCTGGA 7497  
Qy 3001 CGGTTTGTGGGAAACGATACAGAGGCTATCTTATCTATCAAGGTCTCAACATCTTAA 3060  
Db 7498 CGGTTTGTGGGAAACGATACAGAGGCTATCTTATCTATCAAGGTCTCAACATCTTAA 7557  
Qy 3061 GGGCAAGCCCGGTATGCTGTACCGCCCAACACAGTCACTCATGAGGGCCGGAAGGC 3120  
Db 7558 GGGCAAGCCCGGTATGCTGTACCGCCCAACACAGTCACTCATGAGGGCCGGAAGGC 7617  
Qy 3121 AGAATTTCTACAGTAGGAGACATCATTTCTGTATGACAGAGGTCATCATCTTCTCT 3180  
Db 7618 AGAATTTCTACAGTAGGAGACATCATTTCTGTATGACAGAGGTCATCATCTTCTCT 7677  
Qy 3181 CCCCGTTAATTTATTCCTATGACAGTACAGAACAAACAGCACTTTCATATGCTTAT 3240  
Db 7678 CCCCGTTAATTTATTCCTATGACAGTACAGAACAAACAGCACTTTCATATGCTTAT 7727  
Qy 3241 ACATTCATATGCTTCACTCGGCGAGTATGATCCTTGGCAGGCTTACGCAAGATGCCCC 3300  
Db 7728 ACATTCATATGCTTCACTCGGCGAGTATGATCCTTGGCAGGCTTACGCAAGATGCCCC 7797

Cyt	3301	AACTCGGTGTATCMGAGAGCTCATGCACATCCATGCCCAATCCTCTATAGAACC	3358
Dn	7798	AACTCGTGTATTGAGACTTAACAGATCCATATCCCCTAATCTTCTATGAACC	7855
RESULT_9			
LOCUS	AF309418	15186 bp	RNA linear VRL 02-DEC-2000
DEFINITION	Newcastle disease virus B1, complete genome.		
ACCESSION	AF309418		
VERSION	AF309418.1	GI:11527326	
KEYWORDS	.		
SOURCE	Newcastle disease virus B1		
ORGANISM	Virusae; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirus.		
REFERENCE	1 (bases 1 to 15186)		
AUTHORS	Sellers,H.S. and Seal,B.S.		
TITLE	Complete sequence for the B1 strain of Newcastle disease virus unpublished		
JOURNAL	2 (bases 1 to 15186)		
REFERENCE	Sellers,H.S. and Seal,B.S.		
AUTHORS	Direct Submission		
TITLE	Submitted (28-SEP-2000) U.S. Department of Agriculture/Agriculture Research Services, Southeast Poultry Research Laboratory, 934 College Station Road, Athens, GA 30605, USA		
JOURNAL	Location/Qualifiers		
FEATURES	1..15186		
source	/organism="Newcastle disease virus B1"		
	/mol_type="Genomic RNA"		
	/strain="B1"		
	/db_xref="taxon:139270"		
gene	56..1792		
	/gene="NP"		
CDS	122..1591		
	/gene="NP"		
	/codon_start=1		
	/product="nucleocapsid protein"		
	/protein_id="AAC36987.1"		
	/db_xref="GI:11527331"		
	/translation="MSSVFDIEQLLAQTRPENGAGGEGKSTLKVDVPYFTLNSDDPEDWSEFVFCLRIAVSEDANKPRQGALISLSHSGVMNHNHALGKNQEAFLAVLEIDFPANGTPQFNRRSGVSEBERAQRFMIASGLPASCNGTFPTLAGAEADAPEDITDLEILSLQAOAVNTAKAMPAVEADESERIRINKVMQGRVOKTYLLPVCGSTIOTLRLOSIAVRFLVSWELTKRGNTAGTGSTYYNIKGVDSYRNRGTALFPLIKVGINTKSIALAISLSDEDTQKKOLRLYRKKGDAAPMTLLGSDSDMSPPAPEAQCYSPRWGMVAIVDKGTGYQFAKDFMSTSFMLGVEYAAQGSINEDWAELKUTTPARRRELAAAQRVSEVTSSIDMPHOQVGVTLSEGGSQALOGGSNNSSOCPPEAGDGETOFDLDMRAVANSMREARLEANAQGTPOGPPPTPGPSODNDTWGY"		
gene	1804..3244		
	/gene="P"		
CDS	1887..3074		
	/gene="P"		
	/codon_start=1		
	/product="phosphoprotein"		
	/protein_id="AAC36983.1"		
	/db_xref="GI:11527332"		
	/translation="MATPTDAEIDELPETSGTVINDITTAGKPAETVGRSAIQCKTKVSAAMEKHGSIOPPASQDNPDFKDSDSKQSTPEQTTPHDSPATSADQPPTQATDEAVDTLRTGASNLSLLMDKLSNKSNNAKGPWSFQEGNHORPTQQSQSPSRGNSQERPNQOVKAAPGNQGDVNTAYHGOWEEQSLSAGATPHGRSKQSNNTPEVSADHPHQPDVFOVMAINSMEGISQSVASKVAYQVDLVFKOTSILPMMGSELIOGLKTFAVAWEANLFGMKMTLDPGCANSSISLSDLRAVARSHVLVSGPDSPPYIOGGEAMLNLKSQVPHRPSELIKRPTACGCPDIGVERDYRALINSRPMPHPSASALKSLKDAAGSIBETIKIKRLALNG"		
gene	3256..4487		
	/gene="M"		
CDS	3290..4384		
	/gene="M"		
	/codon_start=1		
	/product="matrix protein"		
	/protein_id="AAC36981.1"		

gene  
CDS  
4498..6279  
/gene="F"  
4544..6205  
/gene="F"  
/codon\_start=1  
/product="fusion protein"  
/protein\_id="AAG36978.1"  
/db\_xref="GI:11527329"  
/translation="MGSRPFTKNPAPMLITRVALVSLICPANSIDGRPFAAGIVV  
TGDKNVITYTSQTSIIIVKLPLNPKDKECAAPADYARNTLTTLTPGDSIRH  
QESVYTSGGKGRGLIGAIIGVALVQAFATQAPAAALIQAKQANAILILKESIAA  
TNEAVEHTDGLSOLAVAGMOQFVNDQPKTQOEIDCIQAGQVEINLYTELTL  
TFGQSTIPLNPKITTOALYNLAGMNDYLTTLTGIGNOLSLISGLITGNPIIV  
DSQDTLAIQVTLPSVGNLMKRTYLETLESTTRGPASALYKVTYQVSVIEID  
TSYCIETDLDIYLCRIYTFPWSFGIYSLDSNTACMSKTEGALTYTPMTIKSVIA  
NCKMTKCVNPFGIISQNYEAVSLIDKQSCENSLGGLTLRSGEDVYQNIISD  
QDSQYIINGNDLITSTELGNVANSISNMLNKEBENRKLDKNVNLTSTSLITYIVLT  
ISLVFGLSILACLYLMYKQAKQKTLMLGNNTLDQMRATTK"

gene  
CDS  
6321..8132  
/gene="HN"  
6412..8145  
/gene="HN"  
/codon\_start=1  
/product="hemagglutinin-neuraminidase"  
/protein\_id="AAG36979.1"  
/db\_xref="GI:11527328"  
/translation="MDRAVSQVALENBEREAKNTWLIPIRALIFLVYLAISVASL  
LYSWASQFSPSLVGIPTRIISRAEKITSTLSDNDDVDRIYKOVALSPALNLTETTT  
IMNATLTSYQINGANNSGWGAHPHDVYIGIGIKELIYDADSVTSFYPASQEH  
NFIPIPTTSGSCSTRIIPSEFDMGATRYCYTHNVILSGCRDHSYSOYALAGVLTATGR  
VEFTSLRISINDLDTQNRKSCVSATPLGCDMLCSKATETPEEDYNSAPFTMGVGRGLG  
FDQGVHEHDLVTTLFGDMVAVNPYGGGSPIDSRVPEYGGKLPNSPPTVOEGKRY  
VLYKRYNDTCDEBDYQIRMAKSSYKRRRPGKRIQQALISIKYTSIGEDPVUTVPR  
NVTILMGAEGRILVGTISHFLYQKGSSTFSPALLYPMIVSKRTLHSPTFNATPR  
GSIPOASARPNSCVGVYDYPVPLFYRNHTLRGFGTMLDDEQARLNPAVSAPFOS  
TSRSITITVSSSSIKAAVTTSTCFKVVNTKTYCLSLAEISNTLFGFEPRLVPLVEITIL  
KDDGREARSG"

gene  
CDS  
8370..15073  
/gene="L"  
8381..14995  
/gene="L"  
/codon\_start=1  
/product="large polymerase protein"  
/protein\_id="AAG36980.1"  
/db\_xref="GI:11527329"  
/translation="WASGEPRAEHQIILPESHLSPLVYKHLLYKKLTGLPLPDEBC  
VDFDILSRQWKKLIESASPDTERMIKLGRAVHQTLNHSKITGVLPRLCEELANTE  
PAPFMFSKSTAKPAMLIHQIQRHLIYAATPRANAKLVMLTRGVQFPTPLVVV  
THTNENKTKCTLOELVMTYADMEGRMVNIISTYAHLSISEKIDILRLDALAK  
DLGNVYDVVSLMGFAAGVQLPESTGAPDFANIDELQDILGLPNDIAESV  
THAIRVSGEONQOAMCULRLMGPRLBSRTIAKARSQMCARMDPMDILOV  
LSFEGGIIINERYRKNAGWPRVAVDTYKGVYIQIADSAEISHDMLREYSLAL  
EFBPCIEBDPVTNLSPMLKDAIHPNDNMLSPRNLISDQCKHYKATSTNRLLI  
EFLSENDDEPYKMEVYLTLEEDNVAVSYSLKEKVKNGNIIPAKLTRKLANCOV  
LGGSLGPGCYLLYRNGIDPGETFAEIKRLBAEGLSPINMTNLTIRPGRNGAMLO  
CNDPSRPFETVVASPNTVYKHTQRYLPFCNSNDLISCTEENDEAEKRLAEELNGL  
EVIHPRVAHATMEKSSYGRKKOGLDVTYTYTKATLTPRPGIKRTKMLIYVSSNH  
AMLPRDDVFSSSRNHPVSSNMCSLTLDIARRRSPLTPGKIKLGVSNPDTIELV

EGELISVSGCTRCDSGDEQTFPHLSNTELTDDTSKNPWPVPIYLSKTOERBAAS  
LAKIAHNSPHVKALRASVYLIMAYGDNVMTAALTAKRCNVNLELYLLEPLPT  
AGNQHRLDGIQTMTFTPASLYRCHLFTFYMILKSCSKESKREAFNRWMLG  
LSLIESJEPMTTTRDEITLHLSKSSCCREAPVAPFLPLVLRATVTSNKKM  
YDPSVSGDEPARDLAIKFSYELNLESYPIELMNILISISGLIGOSVVSYEDNS  
IKNDATIIYDNTRMWISBAONSQVRYRFEVAALEYLHRSYQIYLYLRBGDNLVLYK  
GDLTKMNPGLILSNIAATISHPVLIHSHRLAAGLVNHDSDHLADTDFEMAKLIVSC  
TRVVISGLYSGNKYDLLEPSVLDNDLNEKMQQLSRUCLYTVFATFRELPJKRLG  
AEKCSILTEYLISDAVPLSPDVSIMSPNIITFPANLYMSKSLNIIREBERD  
DTILALEPPELPPSVODIGARVDPFROPAALFOELDSAPARVDAFTSOIH  
PELTPSPBEDYIVRYLPRGIGTASSSWYKASHLSPEVRCABNGSLVABSGAT  
MSLELHVPHETIYNTLPSNKNPQHRGPTPTOFNNSVYRNLQAEVTCXGFVQ  
EPRVRENTESDLSDKAVGITSAPVRSVSLHCDIEIPESNQSLLDQALINL  
SLIAMSBSRGEGVYIKVLYAMGYFHLMLFAPCSKGLYVLSNGVACRDMCYL  
FVNGYLGPTFVEHVNRMAKTLVORHGLILSKSDEITLRLFTSORGRVDTIISPLP  
RLIKYLNKIDTALIEAGGQVPRPCAESLSTLANITQIIOIASHIDTVRYIVYM  
EABGDLDVYLPFTPNYLSDBGKRTSLKOTROIETLIGLAVENLNKIGDIIISLY  
LKMISMEDLIPLRTYLNHSTCPKYLKAVIGITLKEPMTDTSVLYLTRAQOKFTMYKT  
IGNAVKGYNSCDS"

ORIGIN

Query Match 98.4%; Score 3305.2; DB 13; Length 15186;  
Best Local Similarity 99.0%; Pred. No. 0; Mismatch 33; Indels 0; Gaps 0;  
Matches 3325; Conservative 0;

Qy	1	ACGGGTAGAAGATTCTGGATCCCGTTGGCCGCTCCAGGTGCAAGATGGGCTCCAGACC	60
Db	4498	ACGGGTAGAAGACTCTGGATCCCGTTGGCCGCTCCAGGTGCAAGATGGGCTCCAGACC	4557
Qy	61	TTTACCAAGAACCCAGACCTATGATGCTGATCTATCCGGGTGGCTGGCACTGAGTTG	120
Db	4558	TTTACCAAGAACCCAGACCTATGATGCTGATCTATCCGGGTGGCTGGATGAGTTG	4617
Qy	121	CATGTGCGGCAACCTCCATTGATGAGGCGCTCTTGCACTGAGGAATTGGGTAC	180
Db	4618	CATGTGCGGCAACCTCATTTGATGAGGCGCTTTTGCACTGAGGAATTGGGTAC	4677
Qy	181	AGGAGCAAAAGCCGTCAACATATACACTCATCCAGACAGATCAATCATGTTAAAGCT	240
Db	4678	AGGAGCAAAAGCATCAACATATACACTCATCCAGACAGATCAATCATGTTAAAGCT	4737
Qy	241	CTCTCCGAATCTGCCCAAGATTAAGAGGCAATGGTCGAAAGCCCCCTTGATGATACAA	300
Db	4738	CTCTCCGAATCTGCCCAAGATTAAGAGGCAATGGTCGAAAGCCCCCTTGATGATACAA	4797
Qy	301	CAGGACATTGACCACTTTGCTCAACCCCTTGCTGATCTATCCGTAGGATACAAAGATC	360
Db	4798	CAGGACATTGACCACTTTGCTCAACCCCTTGCTGATCTATCCGTAGGATACAAAGATC	4857
Qy	361	TGTGACTACATCTGAGGGGGGAGACAGGGGCGCTTATAGCGCATTTATGGCGGTGT	420
Db	4858	TGTGACTACATCTGAGGGGGGAGACAGGGGCGCTTATAGCGCATTTATGGCGGTGT	4917
Qy	421	GGCTCTTGGGGTTGCACTGCGGCAAAATTAACAGCGGCGCAGCTGTGATACAGCCAA	480
Db	4918	GGCTCTTGGGGTTGCACTGCGGCAAAATTAACAGCGGCGCAGCTGTGATACAGCCAA	4977
Qy	481	ACAAAATGCTGCAACATCTCTCGACTTAAAGAGAGCATTCGCGCAACCAATGAGGCTGT	540
Db	4978	ACAAAATGCTGCAACATCTCTCGACTTAAAGAGAGCATTCGCGCAACCAATGAGGCTGT	5037
Qy	541	GCATGAGTCACTGACGGATTATGCAACATAGCAGTGGCAGTTGGGGAAGATGACAGCTT	600
Db	5038	GCATGAGTCACTGACGGATTATGCAACATAGCAGTGGCAGTTGGGGAAGATGACAGCTT	5097
Qy	601	TGTTAATGACCAATTTAATAAAACAGCTCAGAAATTAAGCTGATCAAAATTTGACAGCA	660
Db	5098	TGTTAATGACCAATTTAATAAAACAGCTCAGAAATTAAGCTGATCAAAATTTGACAGCA	5157
Qy	661	AGTTGAGTGAAGCTCAACCTGTACCTTAACCGAATTGACTACATATTCCGACCACAAAAT	720
Db	5158	AGTTGAGTGAAGCTCAACCTGTACCTTAACCGAATTGACTACATATTCCGACCACAAAAT	5217

Qy	721	CATTCACTGCTTTAAACAAAGCTGACCTATTCAAGCACTTTAACAATCTAGCTGGTGAAA	780
Db	5218	CATTCACTGCTTTAAACAAAGCTGACCTATTCAAGCACTTTAACAATCTAGCTGGTGAAA	5277
Qy	781	TATGATTACTTATTTGACTAAGTGAAGTGAAGGGAACAATGAACCTCAGCTCAATTAATCGG	840
Db	5278	TATGATTACTTATTTGACTAAGTGAAGTGAAGGGAACAATGAACCTCAGCTCAATTAATCGG	5337
Qy	841	TAGCGGCTTAAATCAACCGGTAAACCTTATTTAGCACTCAGAGACTCAACTCTTGGGTAT	900
Db	5338	TAGCGGCTTAAATCAACCGGTAAACCTTATTTAGCACTCAGAGACTCAACTCTTGGGTAT	5397
Qy	901	ACAGGTAACTCTACCTTCACTGCGGAACCTTAATTAATGCGTGCACACTACTTGGAAAC	960
Db	5398	ACAGGTAACTCTACCTTCACTGCGGAACCTTAATTAATGCGTGCACACTACTTGGAAAC	5457
Qy	961	CTTATCCGTAGCAACACAGGGGATTTGGCTCGGCACTTGTCCCAAAAGTGAGACACA	1020
Db	5458	CTTATCCGTAGCAACACAGGGGATTTGGCTCGGCACTTGTCCCAAAAGTGAGACACA	5517
Qy	1021	GGTCGGTCTGTGATTAAGAACTTTGACACCTCATCTGTATAGAACTGACTTATGATTT	1080
Db	5518	GGTCGGTCTGTGATTAAGAACTTTGACACCTCATCTGTATAGAACTGACTTATGATTT	5577
Qy	1081	ATATTGTACAAAGATTAAGTAAAGCTTCCCTATGTCCTTGATTTATTCCTGAGCGG	1140
Db	5578	ATATTGTACAAAGATTAAGTAAAGCTTCCCTATGTCCTTGATTTATTCCTGAGCGG	5637
Qy	1141	CAATACGTCGGGCTGTATGTATCTCAAAAGACGGAAGCGCACTTACTACACATATAC	1200
Db	5638	CAATACGTCGGGCTGTATGTATCTCAAAAGACGGAAGCGCACTTACTACACATATATAC	5697
Qy	1201	TATCAAAAGTTCAGTCACTCGCAACTGCAAGATGACAAACATGTAGATGTGTTAAACCCCC	1260
Db	5698	TATCAAAAGTTCAGTCACTCGCAACTGCAAGATGACAAACATGTAGATGTGTTAAACCCCC	5757
Qy	1261	GGGTATCATATCGCAAAACCTATGAGAAAGCGGTCTCTTAATTAATTAATTAATCA	1320
Db	5758	GGGTATCATATCGCAAAACCTATGAGAAAGCGGTCTCTTAATTAATTAATTAATCA	5817
Qy	1321	TGTTTATCTTATAGCGGGAATTAACCTTTAAGGCTCAGTGGGGAATTCGATGTTAATCA	1380
Db	5818	TGTTTATCTTATAGCGGGAATTAACCTTTAAGGCTCAGTGGGGAATTCGATGTTAATCA	5877
Qy	1381	GAAGATATCTCAATPACAAGATCTCAAGTATATATAACAGGCAATCTTGAATCTCAAC	1440
Db	5878	GAAGATATCTCAATPACAAGATCTCAAGTATATATAACAGGCAATCTTGAATCTCAAC	5937
Qy	1441	TGACCTTGGGAATGTCAACAACCTGATCAAGTATGCTTTGAATTAAGTGAAGAAAGCA	1500
Db	5938	TGACCTTGGGAATGTCAACAACCTGATCAAGTATGCTTTGAATTAAGTGAAGAAAGCA	5997
Qy	1501	CAGAAAACCTAGACAAAGTCAATGTCAAACTGACTAGCAACATCTGCTCATTTACTTAAT	1560
Db	5998	CAGAAAACCTAGACAAAGTCAATGTCAAACTGACTAGCAACATCTGCTCATTTACTTAAT	6057
Qy	1561	CGTTTGAATCATATCTCTGTTTGGTATGATTAAGCTGANTCTAGAGATGCTACT	1620
Db	6058	CGTTTGAATCATATCTCTGTTTGGTATGATTAAGCTGANTCTAGAGATGCTACT	6117
Qy	1621	AATGTACAGCAAAAGCGCAACAAACCTTATTAATGCTTGGGAATTAATTAATCTTGA	1680
Db	6118	AATGTACAGCAAAAGCGCAACAAACCTTATTAATGCTTGGGAATTAATTAATCTTGA	6177
Qy	1681	TGAGATGAGCCCACTACAAAAATGTGAACAGATGAAGAAAGAAAGGTTTCCTTAATAG	1740
Db	6178	TGAGATGAGCCCACTACAAAAATGTGAACAGATGAAGAAAGAAAGGTTTCCTTAATAG	6237
Qy	1741	TAAATTTGGAAGGTTCTGCTAGTCTGTGAGTTCAGAGAGTAAAGAAAAAAGTACCGGT	1800
Db	6238	TAAATTTGGAAGGTTCTGCTAGTCTGTGAGTTCAGAGAGTAAAGAAAAAAGTACCGGT	6297
Qy	1801	TGTAGATGACCAAGACGATATATCGGGTAGAAAGGTTAAGAGAGCGGCCCTCAATTTGC	1860



Db	6298	TGTAGATGACCAAGAGATATACGGGTAGAGACGGTAAAGAGGGCCGCCCTCAATTGC	6357
Qy	1861	GAGCCAGGCTTCACAACCTCCGTTCTACCGCTTCACCGACAACAGTCTCAATCATGGAC	1920
Db	6358	GAGCAGACTTCACAACCTCCGTTCTACCGCTTCACCGACAACAGTCTCTCAATCATGGAC	6417
Qy	1921	CGCGCGCTTACCCAAAGTTGCGTTAGAGATGATGAAAGAGGGCAAAATATCATGGCGC	1980
Db	6418	CGCGCGCTTACCCAAAGTTGCGTTAGAGATGATGAAAGAGGGCAAAATATCATGGCGC	6477
Qy	1981	TTGATATATCCGGATTTGCAATCTTATCTTAAACAGTAGTACCTTGCGCTATATCTGTAGCC	2040
Db	6478	TTGATATATCCGGATTTGCAATCTTATCTTAAACAGTAGTACCTTGCGCTATATCTGTAGCC	6537
Qy	2041	TCCCTTTTATATAGCATGGGGGCTTAGCAACCTAGCGATCTTTGATAGCATACCACTAGG	2100
Db	6538	TCCCTTTTATATAGCATGGGGGCTTAGCAACCTAGCGATCTTTGATAGCATACCGCATAGG	6597
Qy	2101	ATTTTCAGAGGAGAAAGAAATTTTCAATCTTACACTTGGTTCCAAATCAAGATGTATAGAT	2160
Db	6598	ATTTTCAGAGGAGAAAGAAATTTTCAATCTTACACTTGGTTCCAAATCAAGATGTATAGAT	6657
Qy	2161	AGGATATATTAAGCAAGTGGCCCTTGAGTCTCCGTTGGGATGTTTAAATACAGAACACA	2220
Db	6658	AGGATATATTAAGCAAGTGGCCCTTGAGTCTCCATTTGGATTTGTTAAATCTGAAACACA	6717
Qy	2221	ATTATGAACGGATTAACATCTCTCTCTTATCAGATTAAATGAGCTGCAACCAAGTGGG	2280
Db	6718	ATTATGAACGGATTAACATCTCTCTCTTATCAGATTAAATGAGCTGCAACCAAGCGGG	6777
Qy	2281	TGGGGGGGACCTATTCATGACCCAGATTTATATAGGGGGGATAGGCAAAAGAACTCATTTGA	2340
Db	6778	TGGGGGGGACCTATTCATGACCCAGATTTATATAGGGGGGATAGGCAAAAGAACTCATTTGA	6837
Qy	2341	GATGATGCTAGTGAATGTCAACATCATTTATCCCTCTGCAATTTCAAGAACATCTGAATTTT	2400
Db	6838	GATGATGCTAGTGAATGTCAACATCATTTATCCCTCTGCAATTTCAAGAACATCTGAATTTT	6897
Qy	2401	ATCCCGGGCCTACTACAGAGTACAGGTTGCACTCGAATACCCCTCATTTGACATGAGTCT	2460
Db	6898	ATCCCGGGCCTACTACAGAGTACAGGTTGCACTCGAATACCCCTCATTTGACATGAGTCT	6957
Qy	2461	ACCCTTATCTGCTACACCCCATATGTAAATATTTGCTGGATGAGATCACTCACTTCA	2520
Db	6958	ACCCTTATCTGCTACACCCCATATGTAAATATTTGCTGGATGACAGATCACTCACTCACTCA	7017
Qy	2521	TATCAGTATTTAGCACTTGTTGTGTCTCGGACATCTGCAACAGGAGGGGTATCTTTTCT	2580
Db	7018	TATCAGTATTTAGCACTTGTTGTGTCTCGGACATCTGCAACAGGAGGGGTATCTTTTCT	7077
Qy	2581	ACTCTGCGTTCCATCAACCTGTGAGCAGACCCCAAAATCGGAAGTCTTGCACTGTGAGTGA	2640
Db	7078	ACTCTGCGTTCCATCAACCTGTGAGCAGACCCCAAAATCGGAAGTCTTGCAAGTGTGAGTGA	7137
Qy	2641	ACTCCCTCTGSGTTGTGATATGCTGTGCTCGAAAGTCAACGAGACAGAGAAAGAAATAT	2700
Db	7138	ACTCCCTCTGSGTTGTGATATGCTGTGCTCGAAAGTCAACGAGAGAGAGAAAGAAATAT	7197
Qy	2701	AACCTCAGCTGTCCCTACGCGGATGTATATGGAAGGTTAAGGTTGCAACGCGCAATATCAC	2760
Db	7198	AACCTCAGCTGTCCCTACGCGGATGTATATGGAAGGTTAAGGTTTTCGAGCGGCAATATCAC	7257
Qy	2761	GAAAGAGACCTAGATGTCAACAACATTTATCGGGGACTGGGTGGCCAACTACCCAGAGATA	2820
Db	7258	GAAAGAGACCTAGATGTCAACAACATTTATCGGGGACTGGGTGGCCAACTACCCAGAGATA	7317
Qy	2821	GGGGGTGAGATCTTTTATTTAGACAGCCGCGATATGTTCTCAGTCTACGAGGGGTAAAAACC	2880
Db	7318	GGGGGTGAGATCTTTTATTTAGACAGCCGCGATATGTTCTCAGTCTACGAGGGGTAAAAACC	7377
Qy	2881	AATTCACCCACTGACCTGTACAGGAAGGAAATGTGATATACAGCATATCAATGAC	2940

Db	7278	AATTCAACCAGGTGACACTGTATACAGGAAGGGAAAATATGTATATATCAAGGCATACAATGAC	7437
Qy	2941	ACATGCCAGATGAGCAAGACTATCAAGATTGGAATGGCCAAAGTTTGGTATAAAGCTTGG	3000
Db	7438	ACATGCCAGATGAGCAAGACTATCAAGATTGGAATGGCCAAAGTTTGGTATAAAGCTTGG	7497
Qy	3001	CGGTTTGGTGGAAAAGCATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCTTGA	3060
Db	7498	CGGTTTGGTGGAAAAGCATACAGCAGGCTATCTTATCTATCAAAAGTCAACATCTTGA	7557
Qy	3061	GGCGAACAACCCGGTACTGATCTGTATCGGCCCAACAACATCAACATCAGGGGGCCGAAGGC	3120
Db	7558	GGCGAACAACCCGGTACTGATCTGTATCGGCCCAACAACATCAACATCAGGGGGCCGAAGGC	7617
Qy	3121	AGAAATTCTCAACGTAGGAGGACATCTCATTTCTGTATGAAGAGGGGTATCAACTTCTCT	3180
Db	7618	AGAAATTCTCAACGTAGGAGGACATCTCATTTCTGTATGAAGAGGGGTATCAACTTCTCT	7677
Qy	3181	CCCGCGTTTATTTATTCCTATGACGATGAGCAACAAAACAGCACTCTTCATATGACTTAT	3240
Db	7678	CCCGCGTTTATTTATTCCTATGACGATGAGCAACAAAACAGCACTCTTCATATGACTTAT	7737
Qy	3241	ACATTCAATGCGCTTCACTCGGCGAGGTAGTATCCCTTGCAGGCTTCAGCAAGAATGGCCC	3300
Db	7738	ACATTCAATGCGCTTCACTCGGCGAGGTAGTATCCCTTGCAGGCTTCAGCAAGAATGGCCC	7797
Qy	3301	AACCTGCTGTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC	3358
Db	7798	AACCTGCTGTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC	7855

RESULT	10
AZ890002	
LOCUS	3819 bp    mRNA           linear    VRL_04-OCT-2004
DEFINITION	Newcastle disease virus turkey/USA/VGCA/89 fusion protein and hemagglutinin-neuraminidase bicistronic mRNA, complete cds.
ACCESSION	AZ890002
VERSION	
KEYWORDS	AZ89002.1    GI:33772483
SOURCE	.
ORGANISM	Newcastle disease virus viruses; segRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirus. 1 (bases 1 to 3819)
REFERENCE	Seal,B.S. Nucleotide and predicted amino acid sequence analysis of the fusion protein and hemagglutinin-neuraminidase protein genes among Newcastle disease virus isolates. Phylogenetic relationships among the Paramyxovirinae based on attachment glycoprotein sequences Func. Integr. Genomics 4 (4), 246-257 (2004) 15108051 2 (bases 1 to 3819)
JOURNAL	Seal,B.S. Direct Submission Submitted (01-MAY-2003) Agricultural Research Service, USDA, Southwest Poultry Research Laboratory, 934 College Station Road, Athens, GA 30605, USA
PUBMED	
REFERENCE	Location/Qualifiers
TITLE	1..3819
JOURNAL	/organism="Newcastle disease virus" /mol_type="mRNA" /isolate="turkey/USA/VGCA/89" /db_xref="taxon:11176"
	47...1708
	/codon_start=1 /product="fusion protein" /protein_id="AA054643.1" /db_xref="GI:33772484"
CDS	/translation="MGRSPSTKNPAPMLTLIRVALVLSICIPANSIDREPLAAGIV TGKAVVIYTSQSGSLIVKLPNLPKEAKCAPADAPRFLTLLPFGDISIRI OESVTSSGGRRGLIGALVGATPAQTAAVLIAIKOMANIILRDSIAA TNEAHVEYTQLSCLAVAGMKQFPNDQRNKTRNOELDCKIQAOVCVELNIYLTELT TVGEPTLPSALKLTIQALYNLAAGMMDLTRLGIANNOLSSLGSLITENPIFY

## CDS

DSOITLGIOTVLPISVGNINMRATYLETISVSTRGRPASALVPKVVITOVGSEIBLD  
TSYCTIDTDLDIKCTRIYVTPFISPGIYSCISNTSACMTSKTEGALTTPYILITKSSVIA  
NCKWTCRCVNPBGIIISQNTGEAVSLIDKOSCNVLSJGGITRLISGEVDVYQKNIS1  
QDSQVITITGNLIDSTELGKNVNSISNMLNKESNRKLDKNVLTLSISALITYIVLT  
IISLIFGLISLILACLYMYKQAKQKTLMLGNNTLDMQMRATQM"  
1915..3648  
/db\_xref="GI:33772485"  
/codon\_start=1  
/product="hemagglutinin-neuraminidase"  
/protein\_id="AA054644.1"  
/translation="MDRAVSOVALENDERAKNTWRLLFRIALFLTVTLAISVSL  
LYSGASTPSDLVGIPIRISRAEEKITSTGSDVDRIYKVALSPLALNTET  
IMAAITSLISVQINAAANSWGAPIHDPDIYIGIKELIYNDADYTSFYRSEODHL  
NFIWAPTRSGCTRISFSDMSATHDICSHNYLSCDHSHTSHOYTLGVARISATGR  
VPSITLSINLIDITQNRKSCSVSATPLGCDMLCSKVTEBEDSDNSAVPRMWRGLG  
FDGQYHEKDLVDITLFGDWVWNPYGVGGISIDSRVWFSYVGLKPTIPSTVDEGK  
VIYKRVNDCDEBDQYQIRMAKSSYKFGKRIQOALISIKVTSISEPVLVTEP  
NTVTLMAEGRLITVGTSHLTYORGSYSPALLIYPMVTSKRTLTLSIPYFNATP  
GSIPTCOSASRCRNSCTGVYTLPIPLIFRNHTLRGVPTMLDDEQARLNPAVSFVS  
TSCRITRVSPTSSKAAITYTSTCFKVVKNKNTCYLSIAEISNTLFGFRIVPLIVEIL  
KIDGVREARSG"

## ORIGIN

Query Match 97.7%; Score 3281.2; DB 13; Length 3819;  
Best Local Similarity 96.6%; Pred. No. 0;  
Matches 3310; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 ACGGGTGAAGAATCTGGATCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60  
DB 1 ACGGGTGAAGAATCTGGATCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60  
QY 61 TTCTACCAAGAACCCAGACACCTATGATGCTACTATCCGGGTTGCGCTGGCACTGAGTTG 120  
DB 61 TTCTACCAAGAACCCAGACACCTATGATGCTACTATCCGGGTTGCGCTGGCACTGAGTTG 120  
QY 121 CATCTGTCGGCAAACTTCATGATGGAGGCTCTTGGCACTGCAAGAAATTGGTGTTAC 180  
DB 121 CATCTGTCGGCAAACTTCATGATGGAGGCTCTTGGCACTGCAAGAAATTGGTGTTAC 180  
QY 121 CATCTGTCGGCAAACTTCATGATGGAGGCTCTTGGCACTGCAAGAAATTGGTGTTAC 180  
DB 121 CATCTGTCGGCAAACTTCATGATGGAGGCTCTTGGCACTGCAAGAAATTGGTGTTAC 180  
QY 181 AGGAGCAAAAGCGGTCAACATATACCTCATCCAGACAGGATCAATCATGTTAAAGCT 240  
DB 181 AGGAGCAAAAGCGGTCAACATATACCTCATCCAGACAGGATCAATCATGTTAAAGCT 240  
QY 241 CCTCCCGAATCTGCGCAAGATAAGAGGCAATGTCGCAAAAGCCCTTGGATGATCAAA 300  
DB 241 CCTCCCGAATCTGCGCAAGATAAGAGGCAATGTCGCAAAAGCCCTTGGATGATCAAA 300  
QY 301 CAGGACATTGACCACTTTGCTCACCCCTTGGTGACTCTATCCGTAGGATACAAAGATC 360  
DB 301 CAGGACATTGACCACTTTGCTCACCCCTTGGTGACTCTATCCGTAGGATACAAAGATC 360  
QY 361 TGTGACATCACTGGAAGGGGGGAGACAGGGGGGCTTATAGCGCCCAATTATGGCGGTG 420  
DB 361 TGTGACATCACTGGAAGGGGGGAGACAGGGGGGCTTATAGCGCCCAATTATGGCGGTG 420  
QY 421 GGCCTCTGGGGTTGCAACTGCGGCAAAATAACCGCGCGCAATTCGTGATACAAAGCAA 480  
DB 421 GGCCTCTGGGGTTGCAACTGCGGCAAAATAACCGCGCGCAATTCGTGATACAAAGCAA 480  
QY 481 ACAAATGCTGCAACATCTCCGACTTAAAGAGAGCATTCGCGCAACCAATGAGGCTGT 540  
DB 481 GCAAAATGCTGCAACATCTCCGACTTAAAGAGAGCATTCGCGCAACCAATGAGGCTGT 540  
QY 541 GCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCACTTGGGAAGATGACAGCA 600  
DB 541 GCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCACTTGGGAAGATGACAGCA 600  
QY 601 TGTAAATGACCAATTTAATAAAGAGCTCAGGAATTTGACTGATCAAAATTTGACAGCA 660  
DB 601 TGTAAATGACCAATTTAATAAAGAGCTCAGGAATTTGACTGATCAAAATTTGACAGCA 660  
QY 661 AGTTGTGTAGAGCTCAACCTGTACCTAACCGAATTGACTACAGTATTCGAGCAACAAT 720  
DB 661 AGTTGTGTAGAGCTCAACCTGTACCTAACCGAATTGACTACAGTATTCGAGCAACAAT 720

DB 661 AGTTGTGTAGAGCTCAACCTGTACCTAACCGAATTGACTACAGTATTCGAGCAACAAT 720  
QY 721 CACTTCACTGCTTTAAACAAAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGGAAA 780  
DB 721 CACTTCACTGCTTTAAACAAAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGGAAA 780  
QY 781 TATGATTAATCTATGACTAAGTAGGTGAGGAAACAATCACTGAGCTCAATTAATGG 840  
DB 781 TATGATTAATCTATGACTAAGTAGGTGAGGAAACAATCACTGAGCTCAATTAATGG 840  
QY 841 TAGGGCTTAATCAACCGGTAACCTTATTCATAGACTCAAGACTCAACTCTGGGAT 900  
DB 841 TAGGGCTTAATCAACCGGTAACCTTATTCATAGACTCAAGACTCAACTCTGGGAT 900  
QY 901 ACAGGTAACTCTACCTTCACTGAGGAACTTAATATATGCTGCGCACTTACTTGAATC 960  
DB 901 ACAGGTAACTCTACCTTCACTGAGGAACTTAATATATGCTGCGCACTTACTTGAATC 960  
QY 961 CTTATCCGTAAAGCAACCAAGGGGATTGCTCGGCACTTGTCCAAAGTGGTGAACA 1020  
DB 961 CTTATCCGTAAAGCAACCAAGGGGATTGCTCGGCACTTGTCCAAAGTGGTGAACA 1020  
QY 1021 GGTGCTTCTGTATGAGAAAGAACTTGAACCTCATCTGATGAGAACTGACTAGATTT 1080  
DB 1021 GGTGCTTCTGTATGAGAAAGAACTTGAACCTCATCTGATGAGAACTGACTAGATTT 1080  
QY 1081 ATATTGTACAAGAAATGATTAACGTTCCCTATGTCCTGATGTTTATTCCTGCTGAGCGG 1140  
DB 1081 ATATTGTACAAGAAATGATTAACGTTCCCTATGTCCTGATGTTTATTCCTGCTGAGCGG 1140  
QY 1141 CAATACGTCGGCTGTATGTAATCAAAAGACCGAAGGCGCACTTACTACCATATAC 1200  
DB 1141 CAATACGTCGGCTGTATGTAATCAAAAGACCGAAGGCGCACTTACTACCATATAC 1200  
QY 1201 TATCAAGGTTCATCTATCCGCACTGCAAGATGACAAACATGATGATGTTAAACCCGCC 1260  
DB 1201 TATCAAGGTTCATCTATCCGCACTGCAAGATGACAAACATGATGATGTTAAACCCGCC 1260  
QY 1261 GGGTATCATATCGCAAACTATGAGAGAGCGGTCTCTTAATAGATAAACAATATGCA 1320  
DB 1261 GGGTATCATATCGCAAACTATGAGAGAGCGGTCTCTTAATAGATAAACAATATGCA 1320  
QY 1321 TGTATTATCTTAAAGCGGAAATACCTTTAAGGCTCAGTGGGAAATTCAGATTAATCA 1380  
DB 1321 TGTATTATCTTAAAGCGGAAATACCTTTAAGGCTCAGTGGGAAATTCAGATTAATCA 1380  
QY 1381 GAAGAAATATCTCAATACAAATTCCTCAAGTAATTAACAGGCAATCTGATATCTCAAC 1440  
DB 1381 GAAGAAATATCTCAATACAAATTCCTCAAGTAATTAACAGGCAATCTGATATCTCAAC 1440  
QY 1441 TGACCTTGGGAATGTCAACAACCTGATCAGTATGCTTGAATTAAGTGAAGAAAGCA 1500  
DB 1441 TGACCTTGGGAATGTCAACAACCTGATCAGTATGCTTGAATTAAGTGAAGAAAGCA 1500  
QY 1501 CAGAAACTGACAAAGTCAATGTCAAATGCTAGACATCTGCTCATTAATCTATAT 1560  
DB 1501 CAGAAACTGACAAAGTCAATGTCAAATGCTAGACATCTGCTCATTAATCTATAT 1560  
QY 1561 CGTTTGAATCATATCTCTGTTTGGTATCTTAAGCTGATTTCTAGATGCTACCT 1620  
DB 1561 CGTTTGAATCATATCTCTGTTTGGTATCTTAAGCTGATTTCTAGATGCTACCT 1620  
QY 1621 AATGTACAGCAAAAGCGGCAAAAACCTTATTAAGCTTGGGAATTAATCTTGA 1680  
DB 1621 AATGTACAGCAAAAGCGGCAAAAACCTTATTAAGCTTGGGAATTAATCTTGA 1680  
QY 1681 TCAGATGAGCCCACTCAAAAATGTGAACAAGATGAGAACCAAGGTTTCCCTAATAG 1740  
DB 1681 TCAGATGAGCCCACTCAAAAATGTGAACAAGATGAGAACCAAGGTTTCCCTAATAG 1740  
QY 1741 TAAATTTGTGAAAAGTCTGTGATGCTGTCAATTCAGAGATTAAAGAAAACCTACCGGT 1800  
DB 1741 TAAATTTGTGAAAAGTCTGTGATGCTGTCAATTCAGAGATTAAAGAAAACCTACCGGT 1800

QY 1801 TGTAGATGACCAAGAGCGATATACGGGTAGAACGGTAAAGAGCGCCCTCAATTGC 1860  
DB 1801 TGTAGATGACCAAGAGCGATATACGGGTAGAACGGTAAAGAGCGCCCTCAATTGC 1860  
QY 1861 GAGCCAGGCTTACACACTCCGTTCTACCGCTTACCGGACACAGCTCTCAATCATAGAC 1920  
DB 1861 GAGCCAGGCTTACACACTCCGTTCTACCGCTTACCGGACACAGCTCTCAATCATAGAC 1920  
QY 1921 CGGCGCGTTCAGCAAGTTGCGTTAGAGATGATGAAGAGAGGCAAAAAATACATGCGCG 1980  
DB 1921 CGGCGCGTTCAGCAAGTTGCGTTAGAGATGATGAAGAGAGGCAAAAAATACATGCGCG 1980  
QY 1981 TTGATATTCGGATTCGATTCATTTATCTTAAACAGTATGACCTTGGCTATATCTGAGCC 2040  
DB 1981 TTGATATTCGGATTCGATTCATTTATCTTAAACAGTATGACCTTGGCTATATCTGAGCC 2040  
QY 2041 TCCCTTTATATATAGCATGGGGGCTAGACACCTAGCCATCTGTAGGCAATACGACATAGG 2100  
DB 2041 TCCCTTTATATATAGCATGGGGGCTAGACACCTAGCCATCTGTAGGCAATACGACATAGG 2100  
QY 2101 ATTTCCAGGCGAGAGAAAAAGATTATACATCTACCTTGGCTCAATCAAGATGATAGAT 2160  
DB 2101 ATTTCCAGGCGAGAGAAAAAGATTATACATCTACCTTGGCTCAATCAAGATGATAGAT 2160  
QY 2161 AGGATATATTAAGCAAGTGGCCCTTGAAGTCTCCGTTGGCATTTGTTAAATCTGAGACCA 2220  
DB 2161 AGGATATATTAAGCAAGTGGCCCTTGAAGTCTCCGTTGGCATTTGTTAAATCTGAGACCA 2220  
QY 2221 ATTATGAACGCATTAACATCTCTCTTATATCAAGTATTAAGAGCTGCAACACAGTGGG 2280  
DB 2221 ATTATGAACGCATTAACATCTCTCTTATATCAAGTATTAAGAGCTGCAACACAGTGGG 2280  
QY 2281 TGGGGGGGACCTATCCATGACCCAGATTTATAGGGGGGATAGGCAAGAACTCATTTGA 2340  
DB 2281 TGGGGGGGACCTATCCATGACCCAGATTTATAGGGGGGATAGGCAAGAACTCATTTGA 2340  
QY 2341 GATGATCTAGTATGATCAATCTTATCTTATCTCTGCTGCTGATTTCAAGAACATCTGAATTTT 2400  
DB 2341 GATGATCTAGTATGATCAATCTTATCTTATCTCTGCTGCTGATTTCAAGAACATCTGAATTTT 2400  
QY 2401 ATCCCGGCGCTTACTACAGATCAAGTTCGATCTCGAATACCTCTATTTGACATAGTCT 2460  
DB 2401 ATCTGGGCGCTTACTACAGATCAAGTTCGATCTCGAATACCTCTATTTGACATAGTCT 2460  
QY 2461 ACCCATTAAGCTTACCCCAATTAAGTATATGCTGAGTCAAGATCACTCATTTCA 2520  
DB 2461 ACCCATTAAGCTTACCCCAATTAAGTATATGCTGAGTCAAGATCACTCATTTCA 2520  
QY 2521 TATCAGATTTAGCACTTGTGTCTCCGACATCTGCAACAGGAGGGTATCTTTTCT 2580  
DB 2521 TATCAGATTTAGCACTTGTGTCTCCGACATCTGCAACAGGAGGGTATCTTTTCT 2580  
QY 2581 ACTTCGGCTTCATCAACTGAGACACCCAAATATCGAAGTCTTGACATGTGAGTCA 2640  
DB 2581 ACTTCGGCTTCATCAACTGAGACACCCAAATATCGAAGTCTTGACATGTGAGTCA 2640  
QY 2641 ACTTCGGCTTCATCAACTGAGACACCCAAATATCGAAGTCTTGACATGTGAGTCA 2700  
DB 2641 ACTTCGGCTTCATCAACTGAGACACCCAAATATCGAAGTCTTGACATGTGAGTCA 2700  
QY 2701 AACCTCACTGCTCCTAGCGGATGATCATAGGAGGTTAGGGTTCGACGCGCATATAC 2760  
DB 2701 AACCTCACTGCTCCTAGCGGATGATCATAGGAGGTTAGGGTTCGACGCGCATATAC 2760  
QY 2761 GAAAGAGACCTAGATGTCACAACTATTCGGGAGCTGGGTGAGCACTACCGAGAGTA 2820  
DB 2761 GAAAGAGACCTAGATGTCACAACTATTCGGGAGCTGGGTGAGCACTACCGAGAGTA 2820  
QY 2821 GGGGGTGAATCTTTTATTTAGACAGCGGATATGTTCTCAGTCTACGAGGGTTAAAAACC 2880  
DB 2821 GGGGGTGAATCTTTTATTTAGACAGCGGATATGTTCTCAGTCTACGAGGGTTAAAAACC 2880

QY 2881 AATTCCCGCAGTACCTGACAGGAAAGGAAATATGTGATATACAGCATCAATGAC 2940  
DB 2881 AATTACACCAAGTACCTGTACAGAGAGGAAATATGTGATATACAGCATCAATGAC 2940  
QY 2941 ACATGCCAGATGAGCAAGACTACAGATTGATGAGCCCAAGTCTTGATTAAGCCTGGA 3000  
DB 2941 ACATGCCAGATGAGCAAGACTACAGATTGATGAGCCCAAGTCTTGATTAAGCCTGGA 3000  
QY 3001 CGGTTGGTGGGAAAGCATACAGAGGCTATCTTATCTTAAAGTGTCAACATCTTTA 3060  
DB 3001 CGGTTGGTGGGAAAGCATACAGAGGCTATCTTATCTTAAAGTGTCAACATCTTTA 3060  
QY 3061 GGGGAGACCCGGTACTGATGATACGCGCCACAGCTCAGCTCATGAGGGGCGAAAGGC 3120  
DB 3061 GGGGAGACCCGGTACTGATGATACGCGCCACAGCTCAGCTCATGAGGGGCGAAAGGC 3120  
QY 3121 AGAATCTCAGAGGAGGACATCTCATTTCTTGATACAGAGGTCATCATCTTCT 3180  
DB 3121 AGAATCTCAGAGGAGGACATCTCATTTCTTGATACAGAGGTCATCATCTTCT 3180  
QY 3181 CCCGCGTATTTATCTTATCTGACAGTACGCAAAAAACAGCACTTTCAATGCTTAT 3240  
DB 3181 CCCGCGTATTTATCTTATCTGACAGTACGCAAAAAACAGCACTTTCAATGCTTAT 3240  
QY 3241 ACATTAAGTCTTACTCGGCGCAGGATGATCCCTTGGCCAGGCTTCAGCAAGTGGCCC 3300  
DB 3241 ACATTAAGTCTTACTCGGCGCAGGATGATCCCTTGGCCAGGCTTCAGCAAGTGGCCC 3300  
QY 3301 AACTCGTGTGTTCTGAGTCTTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358  
DB 3301 AACTCGTGTGTTCTGAGTCTTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358

## RESULT 11

A03663 3825 bp DNA linear PAT 14-Apr-2005  
LOCUS  
DEFINITION Newcastle disease virus HN and F genes.  
ACCESSION A03663  
VERSION A03663.1 GI:492839  
KEYWORDS  
SOURCE  
ORGANISM Newcastle disease virus  
Virus; ssRNA negative-strand viruses; Mononegavirales;  
Paramyxoviridae; Paramyxovirinae; Avulavirinae.

REFERENCE  
AUTHORS Bingham, R.W., Chambers, P., Emerson, P.T. and Millar, N.S.  
TITLE Newcastle disease virus gene clones  
JOURNAL Patent: EP 0227414-A 2 01-JUL-1987;  
NATIONAL RESEARCH DEVELOPMENT CORPORATION  
location/Qualifiers

## FEATURES

## source

1..3825  
/organism="Newcastle disease virus"

/mol\_type="unassigned DNA"

/db\_xref="taxon:11176"

## gene

47..1708  
/gene="F"

## CDS

47..1708  
/gene="F"

## gene

/codon\_start=1  
/protein\_id="CAA00288.1"

## CDS

/db\_xref="GI:492840"

## gene

/db\_xref="GOA:P06156"

## CDS

/db\_xref="InterPro:IPR000685"

## gene

/db\_xref="InterPro:IPR000776"

## CDS

/db\_xref="UniProt/Swiss-Prot:P06156"

## gene

/translation="MGPSTKMPVPMMLTVRYALVLSCTCPANSIDGRPLAAGIV  
TGKAVITYSQGTSLIVLPLNLPDKECAKAPLADAYNRITLITPLGDSIKRI  
QESVTSIGSRQRFIGALIGVALGVAITPAALTAALTAQONAMNITLKESTIA  
TNEAVHEVTDLSOLAVAGKQOFVNDKRAOEIGCIRIAQOVVELNIVTELT  
TVRGPTSPALKLITLQALYNLAGMDYLTKLGANNQLSLIGSGILTNPILY  
DSOTQLGIVTTPSYGNLNMATYLETLSVSTTGAFALVPKVTVOYGVSIEED  
TSCLETDLDTCTRIATVTFPMSPGITSCLSGNTSACHTSTBEALTTPPYNTIGSVIA  
NCKMTTCRCVNPPIISQNYGEAVSLIDKQSCNVSLDGIITLRLSGEDATYQKNISI



gene  
CDS  
1915..3648  
/gene="HN"  
/protein\_id="CA00289.1"  
/db\_xref="GI:492841"  
/db\_xref="GOA:P32884"  
/db\_xref="InterPro:IPR000665"  
/db\_xref="InterPro:IPR011040"  
/db\_xref="UniProt/Swiss-Prot:P32884"

OSOVIIITGNLDISTELGNVNNISNALNKBESNSKLDKXNVLTSTSLITYIVLT  
IISLVFGLISLVLAICYLMYKQKQKQKTLMLGNNTLDMQMRATTKM"  
1915..3648  
/gene="HN"  
1915..3648  
/gene="HN"  
/codon\_start=1  
/protein\_id="CA00289.1"  
/db\_xref="GI:492841"  
/db\_xref="GOA:P32884"  
/db\_xref="InterPro:IPR000665"  
/db\_xref="InterPro:IPR011040"  
/db\_xref="UniProt/Swiss-Prot:P32884"  
translation="MDRAVSQVLENDEREKNTWRLIFRIALLTVTLTASVSL  
VSMGASTPSDLVGIPTIRISRAEKITSALGSNOVDVRIKQVALSPLALNTET  
IMNATLSLVOINAGNNSGKAPIHDPFGISGKILYVDAIDVTSVPSAQBHL  
NFIPIPTGSGCTRIIPSPMSATHYCTTHVILSGCDHSHSHYALGLVLTATR  
IIPSTLSISLDTQNRKSCSVATPPLGCDMLCKVTEBEDNLSAVPTIMHGRIG  
PDQYHKKDLDTVTLFEDWVANYPGVGGSGFIIDGRWVSVYVGLKPSPSDVOGKY  
VIKRYNDTCPEDDYQIRMAKSSYKPEFGKRIQOALISIKVSTLGEDPVLTVPP  
NTYLMGAEGRILFVGTSHFLYORSSYFSPALLYPMTVSKNTLHSPYFNATPS  
GSIIPQASARCPNSCTGVYTDYPLI FYRNHTLRGVGMTLDEQARLNPSTAVPS  
TSSRITRVSSSTKAAVYTTSTCKVKVKNKTYCLTAISNTLFGFRIVPLVLEIL  
KNDGVRARSG"

## ORIGIN

Query Match 95.3%; Score 3199.6; DB 6; Length 3825;  
Best Local Similarity 97.1%; Pred. No. 0; Mismatches 99; Indels 0; Gaps 0;  
Matches 3259; Conservative 0;

Qy 1 ACGGGTGAAGATTCTGGATCCCGTTGGCCCTCCAGGTGCAAGATGGGCTCCAGAC 60  
Db 1 ACGGGTGAAGATTCTGGATCCCGTTGGCCCTCTTCTAGGTGCAAGATGGGCCCCAGACC 60  
Qy 61 TTCTACCAAGAACCCAGACCTTATGATGCTGATCTCCGGGTTGGCTGCTGAGTTG 120  
Db 61 TTCTACCAAGAACCCAGATCTTATGATGCTGATCTCCGGGTTGGCTGCTGAGTTG 120  
Qy 121 CATGTGCCGCAACTCCATTGATGGAGGCTCTTGCAGCTGACAGGAATGTGGTAC 180  
Db 121 CATGTGCCGCAACTCCATTGATGGAGGCTCTTGCAGCTGACAGGAATGTGGTAC 180  
Qy 181 AGGAGCAAAAGCCGTCAACATATACCTCATCCAGACAGAGTCAATAGTTAAAGCT 240  
Db 181 AGGAGCAAAAGCACTCAACATATACCTCATCCAGACAGAGTCAATAGTTAAAGCT 240  
Qy 241 CCTCCGAATCTGCCAAGATAGAGGCAATGTGCAAAAGCCCTTGGATGATCAAA 300  
Db 241 CCTCCGAATCTGCCAAGATAGAGGCAATGTGCAAAAGCCCTTGGATGATCAAA 300  
Qy 301 CAGGACATTTGACCACTTTGCTCAACCCCTTGGTGACTCTATCCGTAGATACAAAGTTC 360  
Db 301 CAGGACATTTGACCACTTTGCTCAACCCCTTGGTGACTCTATCCGTAGATACAAAGTTC 360  
Qy 361 TGTGACTACATCTGAGGGGGAGAGACAGGGGCGCTTATAGGCGCCATTATTTGGCGGTG 420  
Db 361 TGTGACTACATCTGAGGGGGAGAGACAGAAACGCTTTATAGGCGCCATTATTTGGCGGTG 420  
Qy 421 GGCTCTTGGGGTTGCAATGCGGCAAAATTAACAGCGGCGGAGCTGTATCAAGCCAA 480  
Db 421 GGCTCTTGGGGTTGCAATGCTGCAAAATTAACAGCGGCGGAGCTGTATCAAGCCAA 480  
Qy 481 ACAAATATGCTGCAACATCTCCGACTTAAAGAGAGCATTTGCCCAACCAATGAGGCTGT 540  
Db 481 ACAAATATGCTGCAACATCTCCGACTTAAAGAGAGCATTTGCCCAACCAATGAGGCGGT 540  
Qy 541 GCATGAGGTCAGTACGAGATTATCGAACTAGCAGTGGCAGTTGGGAAGATGACAGATT 600  
Db 541 GCATGAGGTCAGTACGAGATTATCGAACTAGCAGTGGCAGTTGGGAAGATGACAGATT 600  
Qy 601 TGTAAATGACCAATTTAATAAAAGCTCAGGAATTAGACTGCATCAAAATTTGACAGCA 660  
Db 601 TGTAAATGACCAATTTAATAAAAGCTCAGGAATTAGACTGCATCAAAATTTGACAGCA 660

Qy 661 AGTTGGTGAAGCTCAACCTGTACCTTAACCGAATTTGACTACAGATTTGGACCAAAAT 720  
Db 661 AGTTGGTGAAGCTCAACCTGTACCTTAACCGAATTTGACTACAGATTTGGACCAAAAT 720  
Qy 721 CACTTCAACCTGCTTAAACAAAGCTGACATTTACAGGCACTTTAGCAATCTAGCTGGGAAA 780  
Db 721 CACTTCAACCTGCTTAAACAAAGCTGACATTTACAGGCACTTTAGCAATCTAGCTGGGAAA 780  
Qy 781 TATGATTAATCTTATTTGACTAAGTAGGTGAGGAAACAATCACTAGCTCAATTAATCGG 840  
Db 781 TATGATTAATCTTATTTGACTAAGTAGGTGAGGAAACAATCACTAGCTCAATTAATCGG 840  
Qy 841 TAGCGGCTTAAATCAACCGGTAAACCTTATCTAATGACCTCAAGACTCAACTCTTGGGTAT 900  
Db 841 TAGCGGCTTAAATCAACCGGTAAACCTTATCTAATGACCTCAAGACTCAACTCTTGGGTAT 900  
Qy 901 ACAGGTAACTTACCTTCACTGAGGGAACCTTAATTAATGAGTGGCCACTTCTGGAAAC 960  
Db 901 ACAGGTAACTTACCTTCACTGAGGGAACCTTAATTAATGAGTGGCCACTTCTGGAAAC 960  
Qy 961 CTTATCGGTAAAGCAACCAAGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
Db 961 CTTATCGGTAAAGCAACCAAGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
Qy 1021 GGTGCGTTCTGTGATGAGAGAACTTGAACCTCATCTGATGAGAACTGAATTGATTT 1080  
Db 1021 GGTGCGTTCTGTGATGAGAGAACTTGAACCTCATCTGATGAGAACTGAATTGATTT 1080  
Qy 1081 ATATTGTACAAAGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1140  
Db 1081 ATATTGTACAAAGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1140  
Qy 1141 CAATACGTCGCGCTGTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1200  
Db 1141 CAATACGTCGCGCTGTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1200  
Qy 1201 TATCAAGGTTCACTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1260  
Db 1201 TATCAAGGTTCACTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1260  
Qy 1261 GGGTATCATATTCGCAAACTATGAGAGAACCGGTGTCTCTAATGATTAATGATTAATGATTAAT 1320  
Db 1261 GGGTATCATATTCGCAAACTATGAGAGAACCGGTGTCTCTAATGATTAATGATTAATGATTAAT 1320  
Qy 1321 TGTATTATCTTACGCGGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1380  
Db 1321 TGTATTATCTTACGCGGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1380  
Qy 1381 GAAGATATCTCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1440  
Db 1381 GAAGATATCTCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1440  
Qy 1441 TGAGCTTGGGAATGTAACCACTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1500  
Db 1441 TGAGCTTGGGAATGTAACCACTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1500  
Qy 1501 CAGGAACTGACAAAGTCAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1560  
Db 1501 CAGGAACTGACAAAGTCAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1560  
Qy 1561 CGTTTGAATCATATCTGTTTGTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1620  
Db 1561 CGTTTGAATCATATCTGTTTGTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1620  
Qy 1621 AATGTACAGCAAAAGCGCAACCAAAACCTTATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1680  
Db 1621 AATGTACAGCAAAAGCGCAACCAAAACCTTATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1680  
Qy 1681 TCAATGAGGCACTTCAAAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1740  
Db 1681 TCAATGAGGCACTTCAAAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1740

```
QY 1741 TAATTTGTGAAAAGTTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAACTACCGGT 1800
DB 1741 TAATTTGTGAAAAGTTCTGTAGTCTGTCAAGTTAAGAAAACTACCGGT 1800
QY 1801 TGTAGATGACCAAGAGCGATATACGGGTAGAACGATAGAGAGCCGCCCTCAATTGC 1860
DB 1801 TGTAGATGACCAAGAGCGATATACGGGTAGAACGATAGAGAGCCGCCCTCAATTGC 1860
QY 1861 GAGCCAGGCTTCAACACCTCCGTTCTACCGTTCAACGACCAACAGTCTCAATCATGAG 1920
DB 1861 GAGCCAGGCTTCAACACCTCCGTTCTACCGTTCAACGACCAACAGTCTCAATCATGAG 1920
QY 1921 CGGCGCCTTAGCCCAAGTTGCGTTAGAGATGATGAAAAGAGAGCAAAAAATACATGCGC 1980
DB 1921 CGGCGCCTTAGCCCAAGTTGCGTTAGAGATGATGAAAAGAGAGCAAAAAATACATGCGC 1980
QY 1981 TTGATATTCCGGAGTTGCAATCTTATTCTTAAACAGTAGAGCCTTGCGCTATATCTGAGCC 2040
DB 1981 TTGATATTCCGGAGTTGCAATCTTATTCTTAAACAGTAGAGCCTTGCGCTATATCTGAGCC 2040
QY 2041 TCCCTTTATATAGCATGAGGCGCTAGACAACCTAGCCATCTTGAGCATACCGACTAGG 2100
DB 2041 TCCCTTTATATAGCATGAGGCGCTAGACAACCTAGCCATCTTGAGCATACCGACTAGG 2100
QY 2101 ATTTCCAGGGCAGAGAAAAGATTACATCTACCTAGTTCCTCAATCAAGATATGATGAT 2160
DB 2101 ATTTCTAGGGCAGAGAAAAGATTACATCTAGCTGTGTTCCATCAAGATATGATGAT 2160
QY 2161 AGGATATATAGCAAGTGGCGCTTGAAGTCCCGTTGGCATTTGTAAATACAGACACA 2220
DB 2161 AGGATATATAGCAAGTGGCGCTTGAAGTCCCGTTGGCATTTGTAAATACAGACACA 2220
QY 2221 ATTATGACGCAATTAACATCTCTCTCTTATCAGATTATAGAGCTGCAACACAGTGG 2280
DB 2221 ATTATGACGCAATTAACATCTCTCTCTTATCAGATTATAGAGCTGCAACACAGTGG 2280
QY 2281 TGGGGGCGACCTATCCATGACCCAGATTATATAGGGGAGATAGCAAAAGACTATTGTA 2340
DB 2281 TGGGGGCGACCTATCCATGACCCAGATTATATCGGGGAGATAGCAAAAGACTATTGTA 2340
QY 2341 GATGATGCTAGTGTGATGTCATCATCTTATCCCTGTCATTTCAAGAACATCTGAATTTT 2400
DB 2341 GATGATGCTAGTGTGATGTCATCATCTTATCCCTGTCATTTCAAGAACATCTGAATTTT 2400
QY 2401 ATCCCGGCGCTACTACAGATCAGGTGCACTGGAATACCTGATTTGACATGAGTCT 2460
DB 2401 ATCCCGGCGCTACTACAGATCAGGTGCACTGGAATACCTGATTTGACATGAGTCT 2460
QY 2461 ACCCATTAAGTCTACACCCATTAATGTAATTTGTCTGAGTGCAGAGATCACTCACTCA 2520
DB 2461 ACCCATTAAGTCTACACCCATTAATGTAATTTGTCTGAGTGCAGAGATCACTCACTCA 2520
QY 2521 TATCAGATTAGACTTGTGTGCTCCGACATGCAACAGGAGGATATCTTTCT 2580
DB 2521 TATCAGATTAGACTTGTGTGCTCCGACATGCAACAGGAGGATATCTTTCT 2580
QY 2581 ACTCTGCGTTCATCAACTCTGATGAGACACCAAAATGGAAGTCTTGCAGTGAGTGA 2640
DB 2581 ACTCTGCGTTCATCAACTCTGATGAGACACCAAAATGGAAGTCTTGCAGTGAGTGA 2640
QY 2641 ACTCTCCGTGGTGTGATATGCTGTCTCGAAAGTCAACGAGACAGAGAAAGATTAT 2700
DB 2641 ACTCTCCGTGGTGTGATATGCTGTCTCGAAAGTCAACGAGACAGAGAAAGATTAT 2700
QY 2701 AACTCAGCTCTCCTTAGCGTATGCAATGAGGATAGGAGTTAGGCTTCAACGAGTACAC 2760
DB 2701 AACTCAGCTCTCCTTAGCGTATGCAATGAGGATAGGAGTTAGGCTTCAACGAGTACAC 2760
QY 2761 GAAAAGACCTAGATGTCACAACTATTTCGGGAGCTGGGTGCGCAACTACAGAGATA 2820
DB 2761 GAAAAGACCTAGATGTCACAACTATTATTGAGACTGGGTGCGCAACTACAGAGATA 2820
QY 2821 GGGGGTGAATCTTTATTGACAGCCGGTATGATTCTCAGTCTACGAGGGTTAAACC 2880
```

```
DB 2821 GGGGGTGAATCTTTATTGACGGCCGGTATGTTCTCACTACAGAGGGCTGAAACC 2880
QY 2881 AATTCAACCCAGTACACTGTACAGAGAGGAAATATGTATATACAGCATCAATGAC 2940
DB 2881 AATTCAACCCAGTACACTGTACAGAGAGGAAATATGTATATACAGCATCAATGAC 2940
QY 2941 ACATGCCAGATGACAGACACTACAGATTGCAATGGCCAAAGTCTTGTAAGCCCTGA 3000
DB 2941 ACATGCCAGATGACAGACACTACAGATTGCAATGGCCAAAGTCTTGTAAGCCCTGA 3000
QY 3001 CGGTTTGTGGGAAACGATACAGACAGGCTATCTTATCTATCAAGGTCAACATCTTA 3060
DB 3001 CGGTTTGTGGGAAACGATACAGACAGGCTATCTTATCTATCAAGGTCAACATCTTG 3060
QY 3061 GGGAGAACCCGATCTGACTGTACCGCCCAACACAGTCACTCATGSGGGCCGAAGGC 3120
DB 3061 GGGAGAACCCGATCTGACTGTACCGCCCAACACAGTCACTCATGSGGGCCGAAGGC 3120
QY 3121 AGAATCTCACAGTAGGAGACATCTCAATTTCTGTATACAGAGGTCATATCTCT 3180
DB 3121 AGAATCTCACAGTAGGAGACATCTCAATTTCTGTATCAGAGGTCATATCTCTCT 3180
QY 3181 CCGCGTTATATATCCTATGACAGTACAGCAAAACAGCCACTCTTCAATAGCTTAT 3240
DB 3181 CCGCGTTATATATCCTATGACAGTACAGCAAAACAGCCACTCTTCAATAGCTTAT 3240
QY 3241 ACATTCAGTCCCTTCACTCGGCCAGGTAGTATCCCTTGCCAGGCTTCAGCAAGTGC 3300
DB 3241 ACATTCAGTCCCTTCACTCGGCCAGGTAGTATCCCTTGCCAGGCTTCAGCAAGTGC 3300
QY 3301 AACTCGTGTGTTACTGAGTCTTATACAGATCCATATCCCTAATCTTATAGAAAC 3358
DB 3301 AACTCGTGTGTTACTGAGTCTTATACAGATCCATATCCCTAATCTTATAGAAAC 3358
```

```
RESULT 12
DQ060053 15186 bp RNA linear VRL 18-JUN-2005
LOCUS Newcastle disease virus, complete genome.
DEFINITION DQ060053
ACCESSION DQ060053
VERSION DQ060053.1 GI:67552898
KEYWORDS Newcastle disease virus
SOURCE Newcastle disease virus
ORGANISM Newcastle disease virus
REFERENCE 1. (bases 1 to 15186)
AUTHORS Wang, Z., Bao, J., Chen, J., Zhen, D., Chen, Y. and Song, C.
TITLE Genomic sequence for isolate AQI-ND026 of Newcastle disease virus
REFERENCE 2. (bases 1 to 15186)
AUTHORS Wang, Z., Bao, J., Chen, J., Zhen, D., Chen, Y. and Song, C.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2005) National Exotic Animal Disease Center,
National Animal Quarantine Institute, Ministry of Agriculture, 369
Nanjing Road, Qingdao, Shandong 266032, China
FEATURES
source
1. 15186
/organism="Newcastle disease virus"
/mol_type="genomic RNA"
/isolate="AQI-ND026"
/db_xref="taxon:11176"
/country="China"
56..1801
/gene="N"
56..1801
/gene="N"
122..1591
/gene="N"
/codon_start=1
/product="nucleoprotein"
/protein_id="A168569.1"
```



Db 4558 TTCTACCAAAACCCAAACCTATGATGCTGACGTCCGGGTCCGGTGTACGAGTTG 4617  
Qy 121 CATCTGCGGGAAACCTCAATTGATGGAGGCTCTTGAGACTGACGAATTTGGTTAC 180  
Db 4618 CATCTGCGGGAAACCTCAATTGATGGAGGCTCTTGAGACTGACGAATTTGGTTAC 4677  
Qy 181 AGGAGCAAAAGCCGTCAACATATACACCTGATCCAGACAGGATCAATCATATGTTAAGCT 240  
Db 4678 AGGAGCAAAAGCAAGTCAACATATACACCTGATCCAGACAGGATCAATCATATGTTAAGCT 4737  
Qy 241 CCTCCGAATCTGCCCCAAGATAGAGGCAATGCGCAAAAGCCCCCTTGATGATCA 300  
Db 4738 CCTCCGAACCTGCCCCAAGATAGAGGCAATGCGCAAAAGCCCCCTTGATGATCA 4797  
Qy 301 CAGGACATGACCACTTTGCTCAACCCCTTGATGATCTATCCGTAGATACAAAGATC 360  
Db 4798 CAGGACATGACCACTTTGCTCAACCCCTTGATGATCTATCCGTAGATACAAAGATC 4857  
Qy 361 TGTGACTACATCTGGAGGGGGAGACAGGGGCGCTTATAGGCGCCATTTATGGCGGTGT 420  
Db 4858 TGTATCTACATCTGGAGGGGGAGAGACAGAAACGCTTTATAGGGCCATTTATGGCGGTGT 4917  
Qy 421 GGCCTTTGGGGTTGCAATGCGCGCAAAATPACAGGGCGGCACTTGTATCAAGCCAA 480  
Db 4918 GGCCTTTGGGGTTGCAATGCTGCAAAATPACAGGGCGGCACTTGTATCAAGCCAA 4977  
Qy 481 ACAAAATGCGCAACATCTCCGCACTTAAAGAGAGATTGCGCAACCAATGAGGCTGT 540  
Db 4978 ACAAAATGCTGCGCAACATCTCCGCACTTAAAGAGAGATTGCGCAACCAATGAGGCTGT 5037  
Qy 541 GCATGAGGCTCATGACGGAATTTATCGCAATGAGGCGAGTTGGGAGATGCAAGCAATT 600  
Db 5038 GCATGAGGCTCATGAGCGAATTTATCGCAATGAGGCGAGTTGGGAGATGCAAGCAATT 5097  
Qy 601 TGTATATGACCAATTTATTAACAGCTCAGGAATTTGACTGCTCAAAATTTGACACGCA 660  
Db 5098 TGTATATGACCAATTTATTAACAGCTCAGGAATTTGAGGCTGCTCAAAATTTGACACGCA 5157  
Qy 661 AGTTGGGTGAGAGCTCAACCGTACCTAACCGAATTTGACTACAGTATTTGGACCACAAAAT 720  
Db 5158 AGTTGGGTGAGAGCTCAATCTGATCTTAACCGAATTTGACTACAGTATTTGGACCACAAAAT 5217  
Qy 721 CACTTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGGAA 780  
Db 5218 CACTTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGGAA 5277  
Qy 781 TATGATATCTTATGACTAAGTTAGGTGAGGAACTACATCACTCACTCATTAATCGG 840  
Db 5278 TATGATATCTTGTGACTAAGTTAGGTGAGGAACTACATCACTCACTCATTAATCGG 5337  
Qy 841 TAGCGGCTTATACCGGTAAACCTATTTCTAATGACTACAGACTCAACTCTTGAGGTAT 900  
Db 5338 TAGCGGCTTATACCGGCAACCTATTTCTAATGACTACAGACTCAACTCTTGAGGTAT 5397  
Qy 901 ACAGGTAATCTACTCTTCACTGCGGAACCTAATATATGCTGCGCACTTACTTGGAAAC 960  
Db 5398 ACAGGTAATCTACTCTTCACTGCGGAACCTAATATATGCTGCGCACTTACTTGGAAAC 5457  
Qy 961 CTTATCCGTAGACAAACAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
Db 5458 CTTATCCGTAGACAAACAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 5517  
Qy 1021 GGTGCGTTCTGTATAGAAACCTTGACACTCACTGATAGAACTGATTAAGTTT 1080  
Db 5518 GGTGCGTTCTGTATAGAAACCTTGACACTCACTGATAGAAACCTGATTAAGTTT 5577  
Qy 1081 ATATTGTAACAAGATAGTAAGTTCTCTATGTCCTGATATTAATCTGCTTGAGCGG 1140  
Db 5578 ATATTGTAACAAGATAGTAAGTTCTCTATGTCCTGATATTAATCTGCTTGAGCGG 5637  
Qy 1141 CAATAGCTGGGCTGTATGTACTCAAAAGACGGAAGGCGCACTTATCAACCATATCATGAC 1200  
|||||

Db 5638 CAATACATCGGCTGTATGTACTCAAAAGACCGAAGGGCACTCACTACGCCATACATGAC 5697  
Qy 1201 TATCAAAAGTTTCAATGCTATCGCAACTGCAAGATGACAAATGATGTGTAAACCCCC 1260  
Db 5698 TATCAAAAGCTCAATGCTATCGCTAATCTGCAAGATGACAAATGATGTGTAAACCCCC 5757  
Qy 1261 GGGTATCTATTCGCAAACTATGGAAGAGCCGTCTCTAATAGATTAACAATCATATGCAA 1320  
Db 5758 GGGTATCTATTCGCAAACTATGGAAGAGCCGTCTCTAATAGATTAACAATCATATGCAA 5817  
Qy 1321 TGTATATCTTATAGGCGGGATTAACCTTAAAGGCTCAGTGGGGAATTCGATTAACCTTATCA 1380  
Db 5818 TGTATATCTTATAGCGGGATTAACCTTAAAGGCTCAGTGGGGAATTCGATTAACCTTATCA 5877  
Qy 1381 GAAGAATATCTCAATACAGATTTCTCAAGTAATTAATTAACAGGCAATCTGATATCTCAAC 1440  
Db 5878 GAAGAATATCTCAATACAGATTTCTCAAGTAATTAATTAACAGGCAATCTGATATCTCAAC 5937  
Qy 1441 TGAAGTTGGGAATGTCAACCACTGATCAATATGCTTTGATTAATTAAGGAAAGCAA 1500  
Db 5938 TGAAGTTGGGAATGTCAACCACTGATCAATATGCTTTGATTAATTAAGGAAAGCAA 5997  
Qy 1501 CAGAAAATGACAAAGTCAATGTCAACTGATGACATGCTGCTCAATTAACCTATAT 1560  
Db 5998 CAGAAAATGACAAAGTCAATGTCAACTGATGACATGCTGCTCAATTAACCTATAT 6057  
Qy 1561 CGTTTGTACTATCATATCTCTGTTTGGTATACCTTACCTGATATCTGACATGCTACT 1620  
Db 6058 CGTTTGTACTATCATATCTCTGTTTGGTATACCTTACCTGATATCTGACATGCTACT 6117  
Qy 1621 AATGTACAGCAAAAGGCGCACAAAACCTTATTAATGCTTGGGAATTAATCTGAGA 1680  
Db 6118 AATGTACAGCAAAAGGCGCACAAAACCTTATTAATGCTTGGGAATTAATCTGAGA 6177  
Qy 1681 TCAAGTAGAGCACTACAAAAATGTGAACACAGATGAGGAAGGAAGTTCCCTAATAG 1740  
Db 6178 TCAAGTAGAGCACTACAAAAATGTGAACACAGATGAGGAAGGAAGTTCCCTAATAG 6237  
Qy 1741 TAAATTTGTGAAAGTTCTGTAGTCTGTCAAGTTCAAGAGTTTAAAGAAAATCAACGGT 1800  
Db 6238 TAAATTTGTGAAAGTTCTGTAGTCTGTCAAGTTCAAGAGTTTAAAGAAAATCAACGGT 6297  
Qy 1801 TGTATATGACCAAAAGACATATACGGGTGAACGGTGAAGAGGCGCCCTCAATTCG 1860  
Db 6298 TGTATATGACCAAAAGACATATACGGGTGAACGGTGAAGAGGCGCCCTCAATTCG 6357  
Qy 1861 GAGCGAGGCTTCAACCTCCGTTCAACGCTTCAACCGACAAAGCTCCTCAATCATGAGAC 1920  
Db 6358 GAGCGAGGCTTCAACCTCCGTTCAACGCTTCAACCGACAAAGCTCCTCAATCATGAGAC 6417  
Qy 1921 CGCGCGTTAGCAAGTTGCGTTAGAGAAATGATGAAGAGGCAAAATAACATGCGCG 1980  
Db 6418 CGCGCGTTAGCAAGTTGCGTTAGAGAAATGATGAAGAGGCAAAATAACATGCGCG 6477  
Qy 1981 TGTATATTCGGGATTTGCAATCTTATCTTAACAGTATGACCTTGGCTATATCTGATGCC 2040  
Db 6478 TGTATATTCGGGATTTGCAATCTTATCTTAAAGTATGACCTTAGCTACATCTGTAGGCC 6537  
Qy 2041 TCCCTTTTATATAGCAGTGGGGCTAGACACCTAGAGCACTTGTAGGCAATACGACGTAAGG 2100  
Db 6538 TCCCTTTTATATAGCAGTGGGGCTAGACACCTAGAGCACTTGTAGGCAATACGACGTAAGG 6597  
Qy 2101 ATTTCCAGGCGAGAAAGAAATTAACATCTACACTTGGTTCCATCAAGATGTATAGAT 2160  
Db 6598 ATTTCCAGGCGAGAAAGAAATTAACATCTGCACTTGGTTCCATCAAGATGTATAGAT 6657  
Qy 2161 AGGATATATAGCAAGTGGCCCTTGAATCTCCGTTGCACTTGTAAATCTGAGACACA 2220  
Db 6658 AGGATATATAGCAAGTGGCCCTTGAATCTCCGTTGCACTTGTAAACATGAGACATCA 6717  
Qy 2221 ATTTAGAGCGCAATTAATCTCTCTCTATCAATTAATGAGACTGCAAAACAAGTGGG 2280  
Db 6718 ATTTAGAGCGCAATTAATCTCTCTCTATCAATTAATGAGACTGCAAAACAAGTGGG 6777

Qy	2281	TTGGGGGGGACCTATCCATGACAGCCAGATTATATAGGGGGGAATAGGCAAGACCTATTGTA	2340
Db	6778	TTGGGGGGGACCTATCCATGACAGCCAGATTATATAGGGGGGAATAGGCAAGACCTATTGTA	6837
Qy	2341	GATGATGCTGATGATGTCACATCAATTCATCCCTGTCATTTCAAGAACATCTGAATTTT	2400
Db	6638	GATGATGCTGATGATGTCACATCAATTCATCCCTGTCATTTCAAGAACATCTGAATTTT	6897
Qy	2401	ATCCCGGCGCCTACTACAGATCAGGTTTGCACTCGAATACCTTCATTTGACATAGTGTCT	2460
Db	6898	ATCCCGGCGCCTACTACAGATCAGGTTTGCACTCGAATACCTTCATTTGACATAGTGTCT	6957
Qy	2461	ACCCATTACTGCTACACCCATAAATGTAATATGTCTGGAATGACAGATCACTCAATTTCA	2520
Db	6958	ACCCATTACTGCTACACCCATAAATGTAATATGTCTGGAATGACAGATCACTCAATTTCA	7017
Qy	2521	TATCAGATATTAGACATGCTGTGTGTCTCCGACATCTCGAACAGGAGGGATTCCTTTCT	2580
Db	7018	TATCAGATATTAGACATGCTGTGTGTCTCCGACATCTCGAACAGGAGGATTCCTTTCT	7077
Qy	2581	ACTCTGCGTTTCCATCAACCTGAGACGACACCCAAAATCGAAGTCTTGCAGTGTAGTGTCA	2640
Db	7078	ACTCTGCGTTTCCATCAACCTGAGATGACACCCAGATCGGAAGTCTTGCAGTGTAGTGTCA	7137
Qy	2641	ACTCCCTCGGTTGTGATATGCTGTGCTCGAAAGTCACAGAGACAGAGGAAGAAATAT	2700
Db	7138	ACTCCCTTAGGTTGTGATATGCTGTGCTCGAAAGTCACAGAGACAGAGGAAGAAATAT	7197
Qy	2701	AACTCAGCTGTCCCTAAGCGGATGGTACATGAGGATTAAGGATTCGACGGCCAGTACAC	2766
Db	7198	AACTCAGCTGTCCCTAAGCCTATGGTACATGAGGATTAAGGATTCGACGGCCATACAC	7257
Qy	2761	GAAGAGGACCTAGATGTTCACAACAATTAATCGGGGACTGGGTGGCCAACTACCCAGAGTA	2820
Db	7258	GAAGAGGACCTAGAGTCAACAATTAATTTGAGGACTGGGTGGCCAACTACCCAGAGTA	7317
Qy	2821	GGGGGTGGATCTTTTATTTAGCAAGCCGGTATAGTTCCTAGTCTACAGAGGTTAAACC	2888
Db	7318	GGGGGTGGATCTTTTATTTAGCAAGCCGGCTATAGTTCCTAGTCTACAGAGGCTGAACC	7377
Qy	2881	AATTCACCCAGTGAACCTGTACAGGAAGGAAATATGTGATATCAACGATACATATGAC	2948
Db	7378	AATTCACCCAGTGAACCTGTACAGGAAGAAATATGTATATATACAGCATCAATATAC	7433
Qy	2941	ACATGCCCAGATGAGACAGACTACCAATTCGAAATGGCCAACTTCGTATTAAGCTTGA	3000
Db	7438	ACATGCCCAGATGAGACAGACTACCAAGATCCGAATGGCCAACTTCGTATTAAGCCGG	7497
Qy	3001	CGGTTTGGTGGGAAACGCTACAGCAGGCTATCTTATCTATCAGAGTCTCAACTCTTA	3066
Db	7498	CGGTTTGGTGGGAAACGCTATCAGCAGGCTATCTTATCTATCAGAGTCTCAACTCTTG	7557
Qy	3061	GGCGAAGACCCGGTATCTGATACCGGCCAAACAGTCAACATAGGGGGCGGAAAGC	3120
Db	7558	GGCGAAGACCCAGTATCTGATACCGGCCAAACAGTCAACATAGGGGGCGGAAAGC	7617
Qy	3121	AGAAATCTCAGATGAGGACATCTCATTTCTTGTAATCAAGAGGGTCACTCACTTCTCT	3180
Db	7618	AGAAATCTCAGATGAGGACATCTCATTTCTTGTAATCAAGAGGGTCACTCACTTCTCT	7677
Qy	3181	CCCGGTTATTATATCTTATGACAGTCAAGCAACAAACAGCCACTCTTCATATGTCCTTAT	3240
Db	7678	CCCGGTTATTATATCTTATGACAGTCAAGCAACAAACAGCCACTCTTCATATGTCCTTAT	7733
Qy	3241	ACATTCAATGCTTCACTCGGCGCAGATAGTATCCCTTGCCAGGGCTTCAGCAAGAGCCCC	3300
Db	7738	ACATTCAATGCTTCACTCGGCGCAGATAGTATCCCTTGCCAGGGCTTCAGCAAGAGCCCC	7797
Qy	3301	AACTCGTGTGTAATCGAGGCTATACATCAATCAATATCCCTTAATCTTATATGAAGCC	3358
Db	7798	AACTCGTGTGTAATCGAGGCTATACATCAATCAATATCCCTTAATCTTATATGAAGCC	7855

LOCUS	EO1252	3825 bp	DNA	linear	PAT 29-SEP-1997
DEFINITION	EO1252	Synthetic DNA encoding Newcastle disease virus (NDV) protein.			
ACCESSION	EO1252				
VERSION	EO1252.1	GI:2169511			
KEYWORDS	JP 1987163693-A/1.				
SOURCE	JP 1987163693-A/1.				
ORGANISM	synthetic construct				
REFERENCE	other sequences; artificial sequences.				
AUTHORS	1 (bases 1 to 3825)				
TITLE	Richiyado,U.B., Fuiritsupu,C., Piltaa,T.E. and Neiru,S.M.				
JOURNAL	NEWCASTLE DISEASE VIRUS GENE CLONE Patent: JP 1987163693-A 1 20-JUL-1987;				
COMMENT	NATL RES DEV CORP				
OS	Artificial gene				
OC	Artificial sequence; Genes.				
OS	Newcastle disease virus (NDV)				
PN	JP 1987163693-A/1				
PD	20-JUL-1987				
PF	18-DEC-1986 JP 1986302719				
PR	18-DEC-1985 GB 85 8531147, 14-APR-1986 GB 86 8609037, PR				
15-JUL-1986 US 86 865765					
PI	RICHYADO UOOKAA BINGAMU, FUIRITSUPU CHIYANBAZU, PI				
TANREI EMASON,					
PI	NEIRU SUTSUMAMATO MIRPA				
PC	C12N15/00,C12N1/20//A61K39/17,C12P21/02,(C12N1/20,C12R1:19);				
CC	strandedness: Double;				
CC	topology: Linear;				
CC	hypothetical: No;				
CC	anti-sense: No;				
CC	*source: strain=Bodet-C;				
FH	Key	Location/Qualifiers			
FH	3'UTR	1..47			
FT	CDS	join(48..1708),(1915..3648)			
FT		/product='Newcastle disease virus (NDV)			
FT		protein'			
FT	5'UTR	3649..3825			
FT	mRNA	1..3825			
FT	exon	1..1708			
FT	intron	1709..1914			
FT	exon	1915..3825.			
FEATURES					
SOURCE	1..3825	Location/Qualifiers			
ORIGIN		/organism="synthetic construct"			
		/mol_type="genomic DNA"			
		/db_xref="taxon:32630"			
Query Match	95.2%;	Score 3196.4;	DB 6;	Length 3825;	
Best local similarity	97.0%;	Pred. No. 0;			
Matches 3257;	Conservative	0;	Mismatches 101;	Indels 0;	Gaps 0;
Db	1	ACGGGTAGAAAGATTCTGGATCCCGGTGGCGCCCTCCAGAGTGAAGATGGGCTCCAGAC	60		
Qy	1	ACGGGTAGAAAGATTCTGGATCCCGGTGGCGCCCTCCAGAGTGAAGATGGGCTCCAGAC	60		
Db	61	TTCTACCAAGAACCCAGTACCTTAAGATGCTGACATCTCGAATCGCGCTGTAAGTGG	120		
Qy	61	TTCTACCAAGAACCCAGTACCTTAAGATGCTGACATCTCGAATCGCGCTGTAAGTGG	120		
Db	121	CATCTGTCGGGCAAACTCATTGATGAGGAGGAGCTCTTGCGGCTCAGGAATTTGGTAACT	180		
Qy	121	CATCTGTCGGGCAAACTCATTGATGAGGAGGAGCTCTTGCGGCTCAGGAATTTGGTAACT	180		
Db	181	AGGAGACAAAGCCGTCAACATATACCTCTACCCAGACAGAGATCAATCATATGTTAACT	240		
Qy	181	AGGAGACAAAGCCGTCAACATATACCTCTACCCAGACAGAGATCAATCATATGTTAACT	240		
Db	241	AGGAGACAAAGCCGTCAACATATACCTCTACCCAGACAGAGATCAATCATATGTTAACT	240		
Qy	241	AGGAGACAAAGCCGTCAACATATACCTCTACCCAGACAGAGATCAATCATATGTTAACT	240		



Dh 241 CTTCCCAACCTGCCCCAAGATTAAGAGGCAATGTCGAAAGCCCCCTTGATGCAATACA 300  
Qy 301 CAGGACATTTGACCACTTTGTCTACCCCCCTTGTAAGTCTATCCGTAGATACAAAGATC 360  
Dh 301 CAGGACATTTGACCACTTTGTCTACCCCCCTTGTAAGTCTATCCGTAGATACAAAGATC 360  
Qy 361 TGTGACTTACATCTGAGAGGGGGAGACAGGGGGCCCTTATAGGCGCATTAATGGCGGT 420  
Dh 361 TGTGACTTACATCTGAGAGGGAGAGACAGAAACGCTTTATAGCGCCCATTAATGGCGGT 420  
Qy 421 GGCTCTTGGGGTTGCACTGCGGCAAAATACAGCGCGCGCAGCTCGATACAAAGCAA 480  
Dh 421 GGCTCTTGGGGTTGCACTGCGGCAAAATACAGCGCGCGCAGCTCGATACAAAGCAA 480  
Qy 481 ACAAAATGCTGCGCAACATCTCCGACTTAAGAGAGCATGGCCGCAACCAATGAGGCTGT 540  
Dh 481 ACAAAATGCTGCGCAACATCTCCGACTTAAGAGAGCATGGCCGCAACCAATGAGGCGT 540  
Qy 541 GCATGAGGTCACTGACGGATTATGCAACTAGCAGTGGCAGTTGGAGAGATGACAGATT 600  
Dh 541 GCATGAGGTCACTGACGGATTATGCAACTAGCAGTGGCAGTTGGAGAGATGACAGATT 600  
Qy 601 TGTTAATGACCAATTTAATAAAACAGCTCAGGAATTTAGACTGCAATCAAAATTTGACAGCA 660  
Dh 601 TGTTAATGACCAATTTAATAAAACAGCTCAGGAATTTAGACTGCAATCAAAATTTGACAGCA 660  
Qy 661 AGTTGATGAGAGCTCAACCTGTACTTAAACGAAATTTGACAGTAATTCGAGCCACAAT 720  
Dh 661 AGTTGATGAGAGCTCAACCTGTACTTAAACGAAATTTGACAGTAATTCGAGCCACAAT 720  
Qy 721 CACTTCACTGCTTTAAACAAAGCTGACTATTCAGGCACTTTAACAATGAGTGTGAAA 780  
Dh 721 CACTTCACTGCTTTAAACAAAGCTGACTATTCAGGCACTTTAACAATGAGTGTGAAA 780  
Qy 781 TATGGAATTAATTTAGCTAAGTAGGAGGAGAAATCAATCAGCTCATTAATTCG 840  
Dh 781 TATGGAATTAATTTAGCTAAGTAGGAGGAGAAATCAATCAGCTCATTAATTCG 840  
Qy 841 TAGCGGCTTATCAACCGGTAAACCTTATTTCTATACAGCTCAAGCTCAATCTTGGGTAT 900  
Dh 841 TAGCGGCTTATCAACCGGTAAACCTTATTTCTATACAGCTCAAGCTCAATCTTGGGTAT 900  
Qy 901 ACAAGTAATCTTACCTTCAAGTGGGAAACCTTAATTAATATGCGTCACTTCTTGAAC 960  
Dh 901 ACAAGTAATCTTACCTTCAAGTGGGAAACCTTAATTAATATGCGTCACTTCTTGAAC 960  
Qy 961 CTTATCCGTAAAGCAACCAAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
Dh 961 CTTATCTGTAAAGCAACCAAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
Qy 1021 GGTGCGTTCTGTGATAGAAAGCTTGACACTTATCTGTATAGAAACTGACTTAGATT 1080  
Dh 1021 GGTGCGTTCTGTGATAGAAAGCTTGACACTTATCTGTATAGAAAGCTTAGATT 1080  
Qy 1081 AATATGTACAAAGATAGTAACGTTCCCTATGTCCCTGTATTTATCTGCTTGAACGG 1140  
Dh 1081 AATATGTACAAAGATAGTAACGTTCCCTATGTCCCTGTATTTATCTGCTTGAACGG 1140  
Qy 1141 CAATACGTCGGCTGTATGTATCTCAAGACGAAAGGGGCACTTCTACACCATATGAGAC 1200  
Dh 1141 CAATACGTCGGCTGTATGTATCTCAAGACGAAAGGGGCACTTCTACACCATATGAGAC 1200  
Qy 1201 TATCAAAAGTTCACTGACGCAACCTGACAGATGACAAACATGTATGATGTAAACCCCC 1260  
Dh 1201 TATCAAAAGTTCACTGACGCAACCTGACAGATGACAAACATGTATGATGTAAACCCCC 1260  
Qy 1261 GGGATATCATATCGCAAAACTATGAGAGAGCGGTCTCTAATAGATTAAGCAATCATGCAA 1320  
Dh 1261 GGGATATCATATCGCAAAACTATGAGAGAGCGGTCTCTAATAGATTAAGCAATCATGCAA 1320  
Qy 1321 TGTTTTATCTTATAGCGGGATTAATTTAAGGCTCAGTGGGAAATTCGATCAACTTATCA 1380  
Dh 1321 TGTTTTATCTTATAGCGGGATTAATTTAAGGCTCAGTGGGAAATTCGATCAACTTATCA 1380

Qy 1381 GAAGAAATATCTCAATACAGATTTCTCAAGTAAATATAACAGGCAATCTGATATCTCAAC 1440  
Dh 1381 GAAGAAATATCTCAATACAGATTTCTCAAGTAAATATAACAGGCAATCTGATATCTCAAC 1440  
Qy 1441 TGAAGTTGGGAATCTCAACATCTGATCACTAATGCTTTGAATTAAGTAAAGGAAAGCAA 1500  
Dh 1441 TGAAGTTGGGAATCTCAACATCTGATCACTAATGCTTTGAATTAAGTAAAGGAAAGCAA 1500  
Qy 1501 CAGAAACTAGACAAAGTCAATGCAATGCAACTGACACTGACATCTGCTCATTAATCTATAT 1560  
Dh 1501 CAGAAACTAGACAAAGTCAATGCAATGCAACTGACACTGACATCTGCTCATTAATCTATAT 1560  
Qy 1561 CGTTTGTACTATCATATCTCTGTTTGTGATATCTAGCTGAGTTCTACATGCTACCT 1620  
Dh 1561 CGTTTGTACTATCATATCTCTGTTTGTGATATCTAGCTGAGTTCTACATGCTACCT 1620  
Qy 1621 AATGTACAAACAAAGGCGCAACAAAACCTTATTAATGCTTGGGAAATTAATCTTGA 1680  
Dh 1621 AATGTATTAACAAAGGCGCAACAAAACCTTATTAATTAATGCTTGGGAAATTAATCTTGA 1680  
Qy 1681 TCAGATGAGAGCACTACAAAAATGTGACACAGATGAGGAAAGAGGTTCCCTAATAG 1740  
Dh 1681 TCAGATGAGAGCACTACAAAAATGTGACACAGATGAGGAAAGAGGTTCCCTAATAG 1740  
Qy 1741 TAAATTTGTGAAAGTTCTGATGCTGTGAGTTCAAGATTAAGAAATACTACCGGT 1800  
Dh 1741 TAAATTTGTGAAAGTTCTGATGCTGTGAGTTCAATTCGAGAGTTAGAAATACTACCGGT 1800  
Qy 1801 TGTATGATGACCAAAAGACATATACGGGTAGAACGTTAGAGAGGCGCCCTCAATTTGC 1860  
Dh 1801 TGTATGATGACCAAAAGACATATACGGGTAGAACGTTAGAGAGGCGCCCTCAATTTGC 1860  
Qy 1861 GAGCAGGCTTCAACACTCGTTCTTACCGCTTCAACGCAACAGTCTCAATCATATGAC 1920  
Dh 1861 GAGCAGGCTTCAACACTCGTTCTTACCGCTTCAACGCAACAGTCTCAATCATATGAC 1920  
Qy 1921 CGGCGCTTACCAAGTTGCGTTAGAGAAATGATGAAAGAGGCAAAAATACATGCGC 1980  
Dh 1921 CGGCGCTTACCAAGTTGCGTTAGAGAAATGATGAAAGAGGCAAAAATACATGCGC 1980  
Qy 1981 TTTGATATTCGGATTTGCAATCTTATTTCTTAACAGTATGACTTTGCTATATCTGTAGCC 2040  
Dh 1981 TTTGATATTCGGATTTGCAATCTTATTTCTTAACAGTATGACTTTGCTATATCTGTAGCC 2040  
Qy 2041 TCCCTTTTATATGACATGCGGGCTAGACACACTAGGACTTGTAGGACATACCGACTAGG 2100  
Dh 2041 TCCCTTTTATATGACATGCGGGCTAGACACACTAGGACTTGTAGGACATACCGACTAGG 2100  
Qy 2101 ATTTCCAGGCGAGAGAAAGATTTACATCTTACCTTGTTCATCAATCAAGATGTAGAT 2160  
Dh 2101 ATTTCTTAGGCGAGAGAAAGATTTACATCTTACCTTGTTCATCAATCAAGATGTAGAT 2160  
Qy 2161 AGGATATATTAAGCAATGCGCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGA 2220  
Dh 2161 AGGATATATTAAGCAAGTGGCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGA 2220  
Qy 2221 AATATGAGCAATTAACATCTCTCTTATCAGATTAATGAGCTGCAACACAGTGG 2280  
Dh 2221 AATATGAGCAATTAACATCTCTCTTATCAGATTAATGAGCTGCAACACAGTGG 2280  
Qy 2281 TGGGGGCGACCTATTCATGACCCAGATTAATAGGGGGGATAGGCAAGAACTCATTTGA 2340  
Dh 2281 TGGGGGCGACCTATTCATGACCCAGATTTATAGGGGGGATAGGCAAGAACTCATTTGA 2340  
Qy 2341 GATGATGCTATGATGATCATATCTTATCCTTGTGACATTTCAAGAACTTGAATTTT 2400  
Dh 2341 GATGATGCTATGATGATCATATCTTATCCTTGTGACATTTCAAGAACTTGAATTTT 2400  
Qy 2401 ATCCGCGCGCTTACTACAGGATCAAGGTTGCACTGGAATTCCTTCAATTTGACATGAGTCT 2460  
Dh 2401 ATCCGCGCGCTTACTACAGGATCAAGGTTGCACTGGAATTCCTTCAATTTGACATGAGTCT 2460

Qy	2461	ACCATTACTGCTACACCCCAATATGTAATATTGCTGGATGCAAGATCACTCACTTCA	2520
Db	2461	ACCCATTACTGCTACACTCATATATGTAATATTGCTGGATGCAAGATCACTCACTCA	2520
Qy	2521	TATCAGATTAGACCTTGGTGTCTCCGACATCTGCAACAGGAGGCTTCTTCTTCT	2580
Db	2521	CATCAGATTAGACCTTGGTGTCTCCGACATCTGCAACAGGAGGATATCTTCTTCT	2580
Qy	2581	ACTCTGCGTTCATCAACCTTGACGACACCCAAATCGGAAGTCTTGCAGTGTAGTCA	2640
Db	2581	ACTCTGCGTTCATCAACCTTGACGACACCCAAATCGGAAGTCTTGCAGTGTAGTCA	2640
Qy	2641	ACTCTGCGTGTGTATATCTGTCTCGAAAGTCAACGACAGACAGAGAAAGATTAT	2700
Db	2641	ACTCTGCGTGTGTATATCTGTCTCGAAAGTCAACGACAGACAGAGAAAGATTAT	2700
Qy	2701	AACCTGCTGTCCTAGCGGATGTAACATGGAGAGTTAGGTTGACAGGCGCAGTACAC	2760
Db	2701	AACCTGCTGTCCTAGCGGATGTAACATGGAGAGTTAGGTTGACAGGCGCAGTACAC	2760
Qy	2761	GAAGAAGACCTAGATGTCACAACTTATTCGGGAGCTGGTGGCACTACCCAGAGTA	2820
Db	2761	GAAGAAGACCTAGATGTCACAACTTATTTAGAGACTGGTGGCACTACCCAGAGTA	2820
Qy	2821	GGGGGTGATCTTTTATTTAGACGCGCGGTATGTTCTCAGTCTACGAGGGTTAAACC	2880
Db	2821	GGGGGTGATCTTTTATTTAGACGCGCGGTATGTTCTCAGTCTACGAGGGCTGAACC	2880
Qy	2881	AATTCAACCCAGTGCACCTGTACAGAAAGGAAATGTGATATTCAGACCTTAAATAC	2940
Db	2881	AATTCAACCCAGTGCACCTGTACAGAAAGGAAATGTGATATTCAGACCTTAAATAC	2940
Qy	2941	ACATGCCAGATGACAAAGATCAACAGTCCGAATGGCCAAAGTCTTGTATTAAGCCG	3000
Db	2941	ACATGCCAGATGACAAAGATCAACAGTCCGAATGGCCAAAGTCTTGTATTAAGCCG	3000
Qy	3001	CGGTTTGTGGGAAACGATACAGAGGCTATCTTATCTATCAAGTGTCAACATCTTCA	3060
Db	3001	CGGTTTGTGGGAAACGATACAGAGGCTATCTTATCTATCAAGTGTCAACATCTTCA	3060
Qy	3061	GGCGAAGACCGGATGCTGATACCGGCCAACACAGTCACTCATGAGGGCCGAAAGC	3120
Db	3061	GGCGAAGACCGGATGCTGATACCGGCCAACACAGTCACTCATGAGGGCCGAAAGC	3120
Qy	3121	AGATTCTCACAGTAGGAGCATCTCATTTCTTGTATCAACAGAGGGTCACTACTCTCT	3180
Db	3121	AGATTCTCACAGTAGGAGCATCTCATTTCTTGTATCAACAGAGGGTCACTACTCTCT	3180
Qy	3181	CCCGCTTATATATCTATGACAGTCAAGCAAAACAGCCACTTTCATATGCTTAT	3240
Db	3181	CCCGCTTATATATCTATGACAGTCAAGCAAAACAGCCACTTTCATATGCTTAT	3240
Qy	3241	ACATTCAATGCTTCACTCGGCGAGTAGTATCCCTTGGCCAGGCTTCAAGAGTCCCC	3300
Db	3241	ACATTCAATGCTTCACTCGGCGAGTAGTATCCCTTGGCCAGGCTTCAAGAGTCCCC	3300
Qy	3301	AACCTGCTGTATCTGAGTCTATACAGATCATATCCCTTAATCTTATAGAAC	3358
Db	3301	AACCTGCTGTATCTGAGTCTATACAGATCATATCCCTTAATCTTATAGAAC	3358

## RESULT 14

AY289000

4552 bp mRNA linear VRL 04-OCT-2004

Newcastle disease virus chicken/USA/Roakin/48 fusion protein and

hemagglutinin-neuraminidase b1c1stronic mRNA, complete cds.

AY289000

AY289000.1 GI:33772477

KEYWORDS

Newcastle disease virus

Newcastle disease virus

Paramyxoviridae; Paramyxovirinae; Avulavirus.

REFERENCE 1 (bases 1 to 4552)  
 AUTHORS Seal, B.S.  
 TITLE Nucleotide and predicted amino acid sequence analysis of the fusion protein and hemagglutinin-neuraminidase protein genes among Newcastle disease virus isolates. Phylogenetic relationships among the Paramyxovirinae based on attachment glycoprotein sequences

JOURNAL J. Virol. 74(4):2462-2471 (2000)  
 PUBMED 1108051  
 REFERENCE 2 (bases 1 to 4552)  
 AUTHORS Seal, B.S.  
 TITLE Direct Submission

Submitted (01-MAY-2003) Agricultural Research Service, USDA, Southeast Poultry Research Laboratory, 934 College Station Road, Athens, GA 30605, USA

FEATURES  
 Location/Qualifiers

## CDS

## CDS

1..4552  
 /organism="Newcastle disease virus"  
 /mol\_type="mRNA"  
 /isolate="chicken/USA/Roakin/48"  
 /db\_xref="taxon:11176"  
 47..1708  
 /codon\_start=1  
 /product="fusion protein"  
 /protein\_id="AA054639.1"  
 /db\_xref="GI:33772478"  
 /translation="MGPRPSTKPTPMMLTVRVALVLSICIPANSIDGRPIAAGIV  
 TGDKAVNIYSSQSGSIIIVKLLPMLPKDKECAAPADAVNRKTLTLPLGDSIRRI  
 OESVTTSGRRKRFIGALIGGVAFVATRAQAPADAAIOAKONAAITLTKESIAA  
 TNAVHEVTGDSOLAIVAGMOQFVNDQFKTLOEACIRIAOVGVETLVLTELT  
 TVRGPQITSPALNKLTHALYNLAGMDVLTFLGIGNNDSLSLSGLTSGLTIVLT  
 DSQQLGIDVLTLPVSNLNNRATYLETLSVSTTRPASLVKRVTVQSVBELD  
 TSYCIETDLDLYCRIVTFPMSPGIVYLSGNTSACVSKTEGALPTPKSVIA  
 NCKMTTCRCVNPGLIISQNGEAVSLIDKOSCNLSLDGITLRSGEADATYQKRSI  
 ODSQVITLGNLDISTELGNVNSISNLNLEENSLDKRVNVLGTSLSALITVILT  
 IISVPRGILSLVLAICYIMYKQKQKQKTLMLGNNTLDMQRTTKM"  
 1915..3648  
 /codon\_start=1  
 /product="hemagglutinin-neuraminidase"  
 /protein\_id="AA054640.1"  
 /db\_xref="GI:33772479"  
 /translation="MDRTVSGVAMLENDERAKNTWRLIFRIATLLTLYVTLATVAST  
 VTSWGAISPSDLVGIPTIRISAEKTKTSALGSNDVDRIYKOVALSPPLALMTETT  
 IMNAITLSIYQINMAANNISGMAPIHDPDFIGKGLIVDDADVTFSYSAQOHL  
 NFIPAPPTGSGCIRIPFSDMSATVCTYTHAIISSGCRDHSYQYLAIGVLTATGR  
 IFESTLASINDPQNSCSVSATPAGCMDCSKTETBEDYNSAVPLTMVRELG  
 FDCQYHEKDI.DVTLTFEDWVANYRGVGGSSIFDSRWFSYVGLKPNSPDTVEKY  
 VIYKRYNDTEPDEDDIYIRAKSSYKRGRRGKRIQQAIIISIKVSTLSGEBPULVFP  
 NTVTLMGABEGRILTVGSHFLDYQSSYFSPALYPMVTSKRTILHSPTFNATRP  
 GSIIPQASARCPSNCSVTGYTDYPLIFRNHTLRGVFTMLDGEQRLNPASAVFDS  
 TSSRLIRTVSSSTKAYTTSCTCFKVKVTKMYCLISIAEISNTLFGSFRIVPLIVEIL  
 KNGVREARSG"

## ORIGIN

Query Match 95.0%; Score 3190; DB 13; Length 4552;  
 Best local similarity 96.9%; Pred. No. 0;  
 Matches 3253; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

Qy	1	ACGGGTAGAGATTCTGATCCCGGTTGGCGCCTCCAGGTGCAAGATGGGCTCAGACC	60
Db	1	ACGGGTAGAGATTCTGATCCCGGTTGGCGCCTTCTAGGGTGCAAGATGGGCCCAAGACC	60
Qy	61	TTCTACCAAGAACCCAGACCTATGATGCTGATATCCGGTTCGGCTGACACTGAGTTG	120
Db	61	TTCTACCAAGAACCCAGACCTATGATGCTGATATCCGGTTCGGCTGACACTGAGTTG	120
Qy	121	CATCTGTCGGGCAAACTTCATTGAGCAGGCTCTTTCAGCTGCAGGAATTGGTTAC	180
Db	121	CATCTGTCGGGCAAACTTCATTGAGCAGGCTCTTTCAGCTGCAGGAATTGGTTAC	180
Qy	181	AGAGAGCAAAAGCCCTCAACATATACCTCATCCCAAGAGATCATATGTTAAGCT	240
Db	181	AGAGAGCAAAAGCAATATACCTCATCCCAAGAGATCATATGTTAAGCT	240

QY 241 CTTCCGAACTCTGCCAAGATTAAGAGCACTGTCGAAAGCCCCCTTGATGCATCA 300  
| | | | |  
Db 241 CTTCCCAACCTGCGCAAGATTAAGAGGCACTGTGCGAAAGCCCCCTTGATGCATCA 300  
QY 301 CAGGACATTGACACTTTGCTCACCCCTTGATGACTCTATCGGTAGATCAAGAGTC 360  
| | | | |  
Db 301 CAGGACATTGACACTTTGCTCACCCCTTGATGACTCTATCGGTAGATCAAGAGTC 360  
QY 361 TGTGACTACACTTGGAGGGGGAGACAGGGGCGCTTATAGCGCCATTAATTTGCGGTGT 420  
| | | | |  
Db 361 TGTGACTACACTTGGAGGGGGAGACAGAAAGCTTTATAGCGCCATTAATTTGCGGTGT 420  
QY 421 GGCCTTTGGGGTGCACCTGCGCACAATTAACGCGCGCGAGCTGTGATCAAGCCAA 480  
| | | | |  
Db 421 GGCCTTTGGGGTGCACCTGCTGCAAAATTAACGCGCGCGAGCTGTGATCAAGCCAA 480  
QY 481 ACAAATGCTGCGCAACATCCCTCGCATTTAAAGAGACATTTGCGCAACCAATGAGGCGT 540  
| | | | |  
Db 481 ACAAATGCTGCGCAACATCCCTCGCATTTAAAGAGACATTTGCGCAACCAATGAGGCGT 540  
QY 541 GCATGAGGTGACATGACGGAATTAACGCACTAGACAGTGGGAAATGACAGAGTT 600  
| | | | |  
Db 541 GCATGAGGTGACATGACGGAATTAACGCACTAGACAGTGGGAAATGACAGAGTT 600  
QY 601 TGTATATGACCAATTAATAAAACAGCTCAGGAATTAAGGCTGACAGAAATTTGACAGCA 660  
| | | | |  
Db 601 TGTATATGACCAATTAATAAAACAGCTCAGGAATTAAGGCTGACAGAAATTTGACAGCA 660  
QY 661 AGTTGAGTGAAGTCAACCTGTACTTAACGAATTAAGTCAATTAATTCGGAACCAAAAT 720  
| | | | |  
Db 661 AGTTGAGTGAAGTCAACCTGTACTTAACGAATTAAGTCAATTAATTCGGAACCAAAAT 720  
QY 721 CACTTCACTGCTTTAAACAAAGCTGACTATTCAGGCACTTTTACATCTAGCTGTGAAA 780  
| | | | |  
Db 721 CACTTCACTGCTTTAAACAAAGCTGACTATTCAGGCACTTTTACATCTAGCTGTGAAA 780  
QY 781 TATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840  
| | | | |  
Db 781 TATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840  
QY 841 TAGGGGCTTAATCAACGGGTAACTTCTATAGACTCAAGCTCAACTCTTGGGGTAT 900  
| | | | |  
Db 841 TAGGGGCTTAATCAACGGGTAACTTCTATAGACTCAAGCTCAACTCTTGGGGTAT 900  
QY 901 ACAGGTAACTCTACTTCACTGCGGGAACCTTAATTAATTAATTAATTAATTAATTA 960  
| | | | |  
Db 901 ACAGGTAACTCTACTTCACTGCGGGAACCTTAATTAATTAATTAATTAATTAATTA 960  
QY 961 CTTATCCGTAAAGCAACCAAGGGGATTTGCTCGGCACTTGTCCCAAAAGGTGAGACA 1020  
| | | | |  
Db 961 CTTATCCGTAAAGCAACCAAGGGGATTTGCTCGGCACTTGTCCCAAAAGGTGAGACA 1020  
QY 1021 GGTTCGCTTCTGTGATTAAGAACTTGAACCTCTACTCTGTATTAAGAACTGAATTA 1080  
| | | | |  
Db 1021 GGTTCGCTTCTGTGATTAAGAACTTGAACCTCTACTCTGTATTAAGAACTGAATTA 1080  
QY 1081 ATATTGTACAAAGATTAAGTATGCTTCCCTATGTCCTGATTAATTCCTGAGCGG 1140  
| | | | |  
Db 1081 ATATTGTACAAAGATTAAGTATGCTTCCCTATGTCCTGATTAATTCCTGAGCGG 1140  
QY 1141 CAATAGCTGGGCTGTATGTATCTCAAAAGACCGAAGGCGCACTTAACACATATCATGAC 1200  
| | | | |  
Db 1141 CAATAGCTGGGCTGTATGTATCTCAAAAGACCGAAGGCGCACTTAACACATATCATGAC 1200  
QY 1201 TATCAAAAGTTCAGTCACTGCGCAACTGCAAGATGAACAATGTATGTATTAACCCCC 1260  
| | | | |  
Db 1201 TATCAAAAGTTCAGTCACTGCGCAACTGCAAGATGAACAATGTATGTATTAACCCCC 1260  
QY 1261 GGGATCATATGCGAAACTATGAGAAGCGGTCTCTAATAGATTAACATCATGCAA 1320  
| | | | |  
Db 1261 GGGATCATATGCGAAACTATGAGAAGCGGTCTCTAATAGATTAACATCATGCAA 1320  
QY 1321 TGTTTATCTTAGGCGGGAATTACTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 1380  
| | | | |

Db 1321 TGTTTATCTTAGACGGGAATTACTTTAAGGCTCAGTGGGGAATTCGATGCATTAATCA 1380  
| | | | |  
QY 1381 GAAGAAATATCTCAATACAAAGATTTCTCAAGTAATTAATAACAGGCAATCTGTATCTCAAC 1440  
| | | | |  
Db 1381 GAAGAAATATCTCAATACAAAGATTTCTCAAGTAATTAATAACAGGCAATCTGTATCTCAAC 1440  
QY 1441 TGAGCTTGGGAATGTCAACAACTCGATCAAGTAATGCTTTGAATTAAGTAAAGAAACAA 1500  
| | | | |  
Db 1441 TGAGCTTGGGAATGTCAACAACTCGATCAAGTAATGCTTTGAATTAAGTAAAGAAACAA 1500  
QY 1501 CAGAAACTAGCAAAAGTCAATGTCAACCTGACAGCAATCTGCTCTCATTAATTAAT 1560  
| | | | |  
Db 1501 CAGAAACTAGCAAAAGTCAATGTCAACCTGACAGCAATCTGCTCTCATTAATTAAT 1560  
QY 1561 CGTTTGAATCATATCTCTGTTTGTGATTAATTAAGCTGATTAATTAAGTCAATGCTACT 1620  
| | | | |  
Db 1561 CGTTTGAATCATATCTCTGTTTGTGATTAATTAAGCTGATTAATTAAGTCAATGCTACT 1620  
QY 1621 AATGTACAAAGCAAAAGCGGCAACAAACCTTAATTAATGCTTGGGAATTAATCTTAGA 1680  
| | | | |  
Db 1621 AATGTACAAAGCAAAAGCGGCAACAAACCTTAATTAATGCTTGGGAATTAATCTTAGA 1680  
QY 1681 TCAGATGAGGCCATTAACAAATATGTGAACAGATGAAGGAAGAGTTCCTTAATAG 1740  
| | | | |  
Db 1681 TCAGATGAGGCCATTAACAAATATGTGAACAGATGAAGGAAGAGTTCCTTAATAG 1740  
QY 1741 TAAATTTGTGAAAAGTTCTGCTGATCTGTCAAGTTCAAGAGATTAAGAAATTAATCAACGGT 1800  
| | | | |  
Db 1741 TAAATTTGTGAAAAGTTCTGCTGATCTGTCAAGTTCAAGAGATTAAGAAATTAATCAACGGT 1800  
QY 1801 TGTATATGACCAAAAGACGATATACGGGTAGAAACGGTAAAGAGGCGGCTCAATTTGC 1860  
| | | | |  
Db 1801 TGTATATGACCAAAAGACGATATACGGGTAGAAACGGTAAAGAGGCGGCTCAATTTGC 1860  
QY 1861 GAGCCAGGCTTCAACAACTCCGTTCTACCGCTTCAACGGAACAGTCTCAATCAATGAGAC 1920  
| | | | |  
Db 1861 GAGCCAGGCTTCAACAACTCCGTTCTACCGCTTCAACGGAACAGTCTCAATCAATGAGAC 1920  
QY 1921 CGGCGCTTATGCAAGTGTGCTTATAGAAATGATGAAGAGGCAAAATTAACATGCGGC 1980  
| | | | |  
Db 1921 CGGCGCTTATGCAAGTGTGCTTATAGAAATGATGAAGAGGCAAAATTAACATGCGGC 1980  
QY 1981 TGTATATTCGGGATTTGCAATCTTATTTAAACAGTATGACCTTGGCTATATCTGTAGCC 2040  
| | | | |  
Db 1981 TGTATATTCGGGATTTGCAATCTTATTTAAACAGTATGACCTTGGCTATATCTGTAGCC 2040  
QY 2041 TCCCTTTTATATAGCATGCGGGGCTAGACACCTTAGAGATCTTGAAGCATACGACCTAGG 2100  
| | | | |  
Db 2041 TCCCTTTTATATAGCATGCGGGGCTAGACACCTTAGAGATCTTGAAGCATACGACCTAGG 2100  
QY 2101 ATTTCCAGGCGAAGAAAGATTTAACAATTGCACTTGTGCTTCAATCAAGATGTATGAT 2160  
| | | | |  
Db 2101 ATTTCCAGGCGAAGAAAGATTTAACAATTGCACTTGTGCTTCAATCAAGATGTATGAT 2160  
QY 2161 AGGATATATTAAGCAAGTGGCTTGTAGTCTCGGTGCACTTGTAAATTAATTAAGACCA 2220  
| | | | |  
Db 2161 AGGATATATTAAGCAAGTGGCTTGTAGTCTCGGTGCACTTGTAAATTAATTAAGACCA 2220  
QY 2221 ATTAATGAAGCAATTAACATCTCTCTGTATCAATTAATTAAGAGCTGCAACCAAGTGG 2280  
| | | | |  
Db 2221 ATTAATGAAGCAATTAACATCTCTCTGTATCAATTAATTAAGAGCTGCAACCAAGTGG 2280  
QY 2281 TGGGGGGCACTATCCATGACCCAGATTAATTAAGGGGGGATTAAGCAAGAACTCATTTGTA 2340  
| | | | |  
Db 2281 TGGGGGGCACTATCCATGACCCAGATTTAATGAGGGGGATTAAGCAAGAACTCATTTGTA 2340  
QY 2341 GATGATGCTATGATGTCAATCATTTCTATCCCTGTGCAATTTCAAGAACTATGAAATTTT 2400  
| | | | |  
Db 2341 GATGATGCTATGATGTCAATCATTTCTATCCCTGTGCAATTTCAAGAACTATGAAATTTT 2400  
QY 2401 ATCCCGGCGCTACTACAGATCAAGTTGCACTCGAATACCTCATTTTGAATGAGTGTCT 2460  
| | | | |



```
Db 2401 ATCCGCGCGCTACTACAGATCAGGTTCATTCGATACCTTACATTTGACATGAGTCT 2460
Qy 2461 ACCCATTAAGTCTACACCATATATGATATATTTGTCTGGATGACAGAGATCACTCAATTTCA 2520
Db 2461 ACCCATTAAGTCTACACCATATATGATATATTTGTCTGGATGACAGAGATCACTCAATTTCA 2520
Qy 2521 TATCAGATATTTAGACATTTGTGTCTCCGAGCATCTGCAACAGGAGGATTTCTTTTCT 2580
Db 2521 TATCAGATATTTAGACATTTGTGTCTCCGAGCATCTGCAACAGGAGGATTTCTTTTCT 2580
Qy 2581 ACTCTGGGTTCATCAACCTTGGAGACACCCCAAAATCGGAAGTCTTGGAGTGTAGTCA 2640
Db 2581 ACTCTGGGTTCATCAACCTTGGAGACACCCCAAAATCGGAAGTCTTGGAGTGTAGTCA 2640
Qy 2641 ACTCCCTGGGTGATGATGATGCTGTGCAAAAGTCAAGAGACAGAGAGAAGATTTAT 2700
Db 2641 ACTCCCTGGGTGATGATGATGCTGTGCAAAAGTCAAGAGACAGAGAGAAGATTTAT 2700
Qy 2701 AACTCAGCTGTCCCTACGCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
Db 2701 AACTCAGCTGTCCCTACGCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
Qy 2761 GAAAGAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820
Db 2761 GAAAGAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820
Qy 2821 GGGGGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
Db 2821 GGGGGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
Qy 2881 AATTCAACCAAGTGAACACTGTATCAGAGAGGAAATATGATATATCAAGCGATACATGAC 2940
Db 2881 AATTCAACCAAGTGAACACTGTATCAGAGAGGAAATATGATATATCAAGCGATACATGAC 2940
Qy 2941 ACATGCCAGATGAGCAAGACTACCAAGTGTGAATGCGCAAGTCTTGTATTAAGCTTGA 3000
Db 2941 ACATGCCAGATGAGCAAGACTACCAAGTGTGAATGCGCAAGTCTTGTATTAAGCTTGA 3000
Qy 3001 CGGTTTGTGGGAAAGCATACAGAGGCTATCTTATCTATCAAGGTGTCAACATCTCTTA 3060
Db 3001 CGGTTTGTGGGAAAGCATACAGAGGCTATCTTATCTATCAAGGTGTCAACATCTCTTA 3060
Qy 3061 GGGCAAGACCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
Db 3061 GGGCAAGACCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
Qy 3121 AGAATTTCTACAGATGAGGACATCTATTCTTGTATCAAGAGGCTATCAATCTTCTCT 3180
Db 3121 AGAATTTCTACAGATGAGGACATCTATTCTTGTATCAAGAGGCTATCAATCTTCTCT 3180
Qy 3181 CCGCGGTTATATATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
Db 3181 CCGCGGTTATATATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
Qy 3241 ACATTCATGCTTCACTCGGCGAGTATGATGATGATGATGATGATGATGATGATGATGAT 3300
Db 3241 ACATTCATGCTTCACTCGGCGAGTATGATGATGATGATGATGATGATGATGATGATGAT 3300
Qy 3301 AACTGTGTGTACTGAGTCTATACAGATCCATATCCCTATCTTATAGGAAC 3358
Db 3301 AACTGTGTGTACTGAGTCTATACAGATCCATATCCCTATCTTATAGGAAC 3358
```

```
RESULT 15
NDVFNH Newcastle disease virus gene for fusion glycoprotein precursor.
LOCUS 3825 bp RNA linear VRL 09-JAN-1998
DEFINITION haemagglutinin-neuraminidase glycoprotein precursor.
ACCESSION D00243
VERSION D00243.1 GI:222174
KEYWORDS haemagglutinin-neuraminidase glycoprotein precursor; fusion
SOURCE Newcastle disease virus
```

ORGANISM Newcastle disease virus  
Viruses; ssRNA negative-strand viruses; Mononegavirales;  
Paramyxoviridae; Paramyxovirinae; Avulavirus.  
REFERENCE 1 (bases 1 to 3825)  
AUTHORS Miller N.S., Chambers P. and Emerson P.T.  
TITLE Nucleotide sequence of the fusion and haemagglutinin-neuraminidase glycoprotein genes of Newcastle disease virus, strain Ulster: molecular basis for variations in pathogenicity between strains  
JOURNAL J. Gen. Virol. 69 (Pt 3), 613-620 (1988)  
PUBMED 3351479

FEATURES  
source

misc\_feature

CDS

1  
/note="start site of F mRNA (putative)"  
47..1708  
/note="F0"  
/codon\_start=1  
/product="fusion glycoprotein precursor"  
/protein\_id="BA00173.1"  
/db\_xref="GI:222175"  
/translation="MGRSSTRIPVPLMLTVRVALALSCVPSLSDRPLAAGIVTGDRAVITYTSQTSIIVKLPMPDPKCAKAPLEAVRRTITLLTPGDSIRITQESVYTSGGKQGLIGAILGALVATAQTALANANALILKESIAATNEAVEHTDGLSQLAVAGKMOQFVNDQPKTAQELDKITQOVELEMLYLETITVPEQITSPALROLTIQALYNLAGEMDYLTLEGGNNQSLISGLTGNPILYDSOTFLGIQVTLPSVGNLNNRATYLETLSVSTKGFASALVKVTVQVSGVEILDTSYCEITPDILCTRIYTPFPMSPGIVSGSACMYSTEGALTTPMYMLKGVIANCKRTTGRSDPPEIISQNYGASGLIDROSCHVLSIDGITRLSGSDATYKQNSIVTATGNLIDISTELGNVNSISNLDLRESNSKLDKVNKLTSTALITIVLTVISLVGILSLVYACLYMKOKAQKTLMLGNNTLDQMATTYK"  
1783..1792  
/note="putative"  
1824  
/note="start site of HN mRNA (putative)"  
1915..3765  
/note="HNO"  
/codon\_start=1  
/product="haemagglutinin-neuraminidase glycoprotein precursor"  
/protein\_id="BA00174.1"  
/db\_xref="GI:222176"  
/translation="MDRAVSQVALLENDERAKNTWLVFRIAILLTVTLTASNAALAYSEASTPBDLIGIPALISRAEKITSALGSNOVDVDRYKQVALSPALNTTESTIMAAITLSYOINMAANSGCCGAPIDHPDVIIGIKGLIYDDASDVSFVPSAFQEHLLNFIAPLTGSGCTRIKPSFDSATHYCTTHRVILSGCDHSHSHOYLAIGVLRISATGRVFSPTLHSLINDPTDNKSCSVSATPIGCMLOSKVLEBEDNNSAVPISVHGRIGFVQGYHEKDDLVTLTFEDMYANYPVGWGSFIDRWAFPYVGGIKPMSPTDAQEKKVYKRVNDCPEBDDYQIRMAKSYKRGSRVQQAIIISKVSTLGEPTVLTVPNTYTMGAERGVLTGSHFLYORGSYFSPALLIYPTMSKRTLLSPPEDFAETP GSVPQASACRNSCYGVYTDPIPLVFNHNLIRGVETGMDKQALNDVSAVPSISRRITRVSSSTKAAVYTSCTCKVKVINKTKYLSIAESNTLPFGFRIVPLVLEILKDDGVRARARGLSQLEKWKDIVSPIFDANKQTEYRRELSYAASWP"  
3816..3825

polyA\_signal  
ORIGIN

Query Match 84.2%; Score 2826.8; DB 13; Length 3825;  
Best Local Similarity 90.1%; Pred. No. 0;  
Matches 3026; Conservative 0; Mismatches 332; Indels 0; Gaps 0;  
Qy 1 ACGGGTGAAGATTCTGGATCCGGTTGGCGCCTCCAGGTGCAAGATGGCTCCAGACC 60  
Db 1 ACGGGTGAAGATTCTGGATCCGGTTGGCGCCTCCAGGTGCAAGATGGCTCCAGATC 60  
Qy 61 TTCTACAGAACCCAGACCTATGATGCTGACTATCCGGGTTCCGCTGCCTGAGTTG 120

Db	61	TTCTACCAAGATCCCAAGTACCTCTGATGCTGACCGTCCGGGTCGGCGCTGGACACTGAAGTTG	120
Oy	121	CATCTGTCGGGCAAACTCCATTGATGAGAGGCTCTTGACCTGCAGGAAATTTGGTTAC	180
Db	121	CGTGTGTCGACAAGCTCCCTTGATGGCAGGGCTCTTGACCTGCAGGGAATTTGGTTAC	180
Oy	181	AGGAGACAAAGCCGTCAACATATACCTCATCCGACAGGATCAATCATATGTTAACT	240
Db	181	AGGAGACAAAGCAGTCAACATATACCTCATCTCAGCAGGGTCAATCATATGTTAACTT	240
Oy	241	CCTCCGGAATCTGGCCCAAGAGTTAAAGAGCAGTGTGCGAAAGGCCCTTGATGTCATCAAA	300
Db	241	ACTCCCAATATTGCCCCAAGATTAAGAGGCGTGTGCAAAAAGCCCGTTGGAGGGGTACAA	300
Oy	301	CAGGACATTGACCACTTTGCTCACCCCCTTGTTGTACTCTATCCGTAGATTAACAAGCTC	360
Db	301	CAGGACATTGACTACTTTGCTCACCCCCTTGTTGTAATCTATGCTAGATTAACAAGCTC	360
Oy	361	TGTGACTATCATCTGGAGGGGGGAGACAGGGGGCGCTTATAGGGCCATATTATGGCGGTGT	420
Db	361	TGTGACTATCATCTGGAGGAGGGGAAACAGGGAGCGCTTATAGGGCCATATTATGGCGGTGC	420
Oy	421	GGCTCTTGGGGGTTGGACATGCGCGGCAAAATTAACAGGGCCGAGCTCATACAAGCCAA	480
Db	421	AGCTCTGGGGGTTGGACACCGCTGCACAAATTAACAGAGCTTTCGGCTCTGATATCTTGCCA	480
Oy	481	ACAAATATCTGCCAACATCTCTCCGACTTAAAGAGAGCATTCGCGCAACCAATGAGCGTGT	540
Db	481	CCAAATATCTGCCAACATCTCTCGGCTTAAAGAGAGCATTTGCTGCAACCAATGAGCGGTGT	540
Oy	541	GCATGAGGTCACATGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAAGATGCACAGTT	600
Db	541	GCACAGGATCACTGATGATTATCAACAATGACAGTGGCAGTTGGGAAAGATGCACAGATT	600
Oy	601	TGTTATATACCAATTTATATTAATAACGCTCAGGAATTTACATCGAATCAAAATTTGACAAGCA	660
Db	601	TGTTATATATACCAATTTATATTAATAACGCTCAGGAATTTGATGTAATAAATTTACCCAGCA	660
Oy	661	AGTTGGTGTAGAGCTCAACTGTATCTTAACCGAATTTGACTACAGTATTCGGAGCCACAAT	720
Db	661	GGTTGGTGTAGAACTCAACTGTATCTTAACCTGAATTTGACTACAGTATTCGGAGCCACAAT	720
Oy	721	CACTTGACCTGCTTTAAACAAGCTGACTATTTCAGGCACTTTACAACTTAGCTGTGGAAA	780
Db	721	CACTTGCCCTGCTTTAAACCAAGCTGACTATTCAGGCGCTTTACAACTTAGCTGTGGGAAA	780
Oy	781	TATGATATTAATTTATGACTAAAGTTAGGTAGGGAAACAACAACCTACAGCTATTTAATTTGG	840
Db	781	TATGATATTAATTTATGACTAAAGTTAGGTAGGGAAACAACAACCTACAGCTATTTAATTTGG	840
Oy	841	TAGCGGCTTAATCACCCGGTAACCTTAATCTATACAGACTCACAGACTCAACTCTTGGGTAT	900
Db	841	TAGCGGCTTAATCACCCGGCAACCTTAATCTGTAGCACTCACAGACTCAAGCTCTTGGGTAT	900
Oy	901	ACAGGTAACTCTACCTTCAGTCGGGAACCTAATTAATATGCGTGCACCTTCTGGAAC	960
Db	901	ACAGGTAACTCTACCTTCAGTCGGGAACCTGAATTAATGCGTGCACCTCTCTGGAAC	960
Oy	961	CTTATCCGTAAAGCACACAGGGGATTTGCTCGGCACTTGTGCCAAAAGTGTGACACA	1020
Db	961	CTTGTCTGTAAAGTACACCCAAAGATTGCTCAGACACTCGTCCCAAAGTGTGACACA	1020
Oy	1021	GGTCGGTCTGTGATAGAGAAGACTTGACACCTCACTAGTATTAAGAAACTGACTTAGATTTT	1080
Db	1021	GGTCGGTCTCGTATAGAGAAGCTTGACACCTCACTACTGTATTAAGAACCCGATTTGGATCT	1080
Oy	1081	ATATTGTACAAGAATAGTACGTTCCCTATGTCCCTGCTATTTATTCCTGCTTGAAGCGG	1140
Db	1081	ATATTGTACAAGAATAGTACATTCCTATGTCTCTGTAATTTATTCCTGTTTGAAGCGG	1140
Oy	1141	CAATACGTGGCTGTATATGTACTCAAAGACCGAAGGGCGCACTTACTACACATACATGAC	1200
Db	1141	CAATACATCGGCTTGCATGTACTCGAACACTGAAGGGCGCACTACATACGCGGTACATGAC	1200

QY	1201	TATCAAAAGGTTCAGTCAATCGCCAACTGCAGATGAACAATCTATGATGTGTAAACCCCCC	1250
Db	1201	TCTCAAAAGGCTCAGTTATTGCCAATCTATAGATACAACAATGTATGATCTGGAGCCCCC	1250
QY	1261	GGATATCAATATCGAAAACTATGAGAAAGCGGTCTCTAAATAGATAAACAATATGCAA	1320
Db	1261	GGATATCAATATCGAAAAATTATGAGAAAGCTGTCTCTTAATAGATATGGCAATATGCAA	1320
QY	1321	TGTTTATCTCTTAGGCGGGATATACCTTAAAGGCTCAGTGGGGAAATTCATGTAACTTATCA	1380
Db	1321	TGCTCTATCTTAAAGCGGAATATCTTTGAGGCTCAGTGGGGAAATTATATGCACTTATCA	1380
QY	1381	GAAGAAATCTCAATACAAAGATTCTCAAGTAAATATTAACAGGCAATCTTGATATCTCAAC	1440
Db	1381	AAAGAAATCTCAATACAAAGATTCTCAAGTAAATGTATACAGGCAATCTTGATATCTGCAC	1440
QY	1441	TGAGCTTGGGAATGTCAACAATCGATCAGTAATGCTTGAATTAAGTATGAGGAACAA	1500
Db	1441	TGAGCTTGGGAATGTCAACAATCGATTAAGTAATGCTTGAATTAAGTATGAGGAACAA	1500
QY	1501	CAGAAAATAGACAAAGTCAATGTCAAACTGACATGACACATCTGCTCTCAATTACATAAT	1560
Db	1501	CAGCAAACTAGACAAAGTCAATGTCAAACTGACACACATCCGCTCTCAATCACTATAT	1560
QY	1561	CGTTTGAATATCATATCTCTGTTTTTGTATACCTTAGCCCTGATTTAGCATCTACT	1620
Db	1561	CGTTTAACTGTCAATATCTCTGTTTTGTGATACCTTAGCCCTGTTACATGCTACT	1620
QY	1621	AATGTACAGAAAGGCGCAACAAACCTTATTTATGGCTTGGAAATTAATCTCAGA	1680
Db	1621	GATGTACAGAAAGGCGCAACGAAGACCTTGTATGGCTTGGAAATTAATCCTCGA	1680
QY	1681	TCAGATGAGACCACTACAAAATGTGAAACAGATAGGAAACGAAGTTTCCCTAATAG	1740
Db	1681	TCAGATGAGACCACTACAAAATGTGAAATGTATATAGATAGAGGCGGAGGCATCTCCAATAG	1740
QY	1741	TAAATTGTGTAAAGTTCTGTGATCTGTCAGTTCAAGAGATTAGAAAAAATCAACCGGT	1800
Db	1741	CAGTTTGTGTAAAGTGTGACAGCTTGTAAATTAGAAATTAAGAAAAAATGCGGGA	1800
QY	1801	TGTATATGACCAAAAGGACGATATACGGGTAGAACGGTAAAGAGAGCCGCCCTCAATTGC	1860
Db	1801	TGTATATGACCAAAAGGCGCAATACGGGTAGAAAGGTCAGAGAGCCGCCCTCAATTCG	1860
QY	1861	GAGCAGGCTTCAAAACCTCGGCTTACCGGTTACAGCAGCAACAACGCTCTCAATCATGAC	1920
Db	1861	GAGCAGGCTTCAACAACCTCGGCTTACCGCATCAACAATATGCACTTCAATGATGAC	1920
QY	1921	CGCGCCGTTAGCCAAAGTTGCGTTAGAGATGATGAAAGAGGCAAAAATATCAATGGCGC	1980
Db	1921	CGCGAGTTAGCCAAAGTTGGCGCTAGAGATGATGAAAGAGGCAAAAATATCAATGGCGC	1980
QY	1981	TTGATATTCGGATTCGAATTTTATCTTAAACAGTATGACCTTGGCTATATCTGTAGCC	2040
Db	1981	TTGGATATTCGGATTCGGATCTTATTTAAACAATATGACCTTTAGCCATCTTCGACGC	2040
QY	2041	TCCCTTATATATAGATGAGGGGCTTAGACACCTTAGGCATCTTGAAGGATTCGAGTAGG	2100
Db	2041	GCCCTTGATATATATAGAGGGCTTAGACACACTTAGGCATCTTATAGGATTCGAGTAGG	2100
QY	2101	ATTTCAGAGGCGAAGAAAGATTACATCTACACTTGTTGTTCCAAATCAAGATGTATGAT	2160
Db	2101	ATCTCTAGAGAGAGAAABATATTCATCTGCACTCGGTTCCAAACAAAGATGTATGAT	2160
QY	2161	AGGATATATTAAGCAATGGCCCTTGAAGTCTCGTTGCGATTTGTTAAATCTGAGACACA	2220
Db	2161	AGGATATATTAAGCAGTGGCCCTCGAATCTCCATTTGGCATTTGCTAAACACCGAATCTACA	2220
QY	2221	ATTATGAACGCAATTAATCTCTCTCTTATACAGTTAATGAGAGCTGCAACAAACAGTGG	2280
Db	2221	ATTATGAACGCAATTAATCTCTCTCTTATACAGTCAATGAGAGCTGCAACAAATGAGCGGG	2280

QY 2281 TGGGGGGGACCTATTCATGACCCAGATTATATAGGGGGGAAAGGCAAAAGCTCATTTGTA 2340  
 DB 2281 TGGCGGGGACCTATTCATGATCCAGATTATATCGGGGAAATAGGTAAGAACTTATGTA 2340  
 QY 2241 GATGATGCTAGTGAATGTCACATTCATTCCTCTGCAATTCAGAAACATCTGAAATTTT 2400  
 DB 2241 GATGATGCTAGTGAATGTCACATTCATTCCTCTGCAATTCAGAAACATCTGAACTTT 2400  
 QY 2401 ATCCCGGGCCCTACTACAGATCAGTTGCACTCGAATACCTCTCATTTGACATGAGTGCCT 2460  
 DB 2401 ATCCCGGGCCCTACTACAGATCAGTTGCACTCGAATACCTCTCATTTGACATGAGTGCCT 2460  
 QY 2461 ACCCATTACTGCTACACCCATTAATGTAATATTGCTGAGTGAAGATCACTCATTTCA 2520  
 DB 2461 ACCCATTACTGCTACACCCATTAATGTAATATTGCTGAGTGAAGATCACTCGCATCA 2520  
 QY 2521 TATGAGTATTTAAGCACTTGAGTGTGCTCGGACATCTGCAACAGGAGGGTATTCCTTTCT 2580  
 DB 2521 TATGAGTATTTAAGCACTTGAGTGTGCTCGGACATCTGCAACAGGAGGGTATTCCTTTCT 2580  
 QY 2581 ACTCTGCGTTCATCAACCTTGAACGACACCCAAATCGGAATCTTGCAGTGTGAGTGA 2640  
 DB 2581 ACTCTGCGTTCATCAACCTTGAATGACACCCAAATCGGAATCTTGCAGTGTGAGTGA 2640  
 QY 2641 ACTCCCTGGGTTGATATGCTGTCTGAAAGTCAAGACAGAGAAAGAAATTTAT 2700  
 DB 2641 ACTCCCTGGGTTGATATGCTGTCTGAAAGTCAAGACAGAGAAAGAAATTTAT 2700  
 QY 2701 AACTCAGCTGTCTTACCGCGGATGTAATGAGAGTTAGGGTTGAGAGGCCAGTACAC 2760  
 DB 2701 AACTCAGCTGTCTTACCGCGGATGTAATGAGAGTTAGGGTTGAGAGGCCAAATACAT 2760  
 QY 2761 GAAAGGACCTAGATGTGCAAACTTATTCGGGGGCTGGTGCCCACTAACCCAGAGTA 2820  
 DB 2761 GAGAGGACCTAGATGTGCAAACTTATTCAGAGACTGGTGCCCAATTAACCCAGAGTA 2820  
 QY 2821 GGGGGGTGATCTTTTATTTGACAGCGCGTATGTTCTCAGTCTACGAGGGTTAAACC 2880  
 DB 2821 GGGGGGTGATCTTTTATTTGACAGCGCGTATGTTCTCAGTCTACGAGGGCTAAACC 2880  
 QY 2881 AATTCAACCAGTGAACCTGTACAGAGAGGAAATATGATATACAGGATCAATGAC 2940  
 DB 2881 AACTCGCTAGTGAACCTGTACAGAGAGGAAATATGATATACAGGATCAATGAC 2940  
 QY 2941 ACATGCCAGATGACAAAGATCAAGATTCGAATGCGCAAGTCTTGATTAAGGCTGGA 3000  
 DB 2941 ACATGTCAGATGACAAAGATTCAGATTCGAATGCGTAAGTCTTGATTAAGGCTTGG 3000  
 QY 3001 CGGTTTGGTGGAAACGGCTACAGAGGCTATCTTATCTATCAAGTGTCAACATCTTGA 3060  
 DB 3001 CGGTTTGGTGGAAACGGCTACAGAGGCTATCTTATCTATCAAGTGTCAACATCTTGG 3060  
 QY 3061 GGGGAGAGCCGGTACTGACTGTACCGGCCAAACACATGACATTCATGAGGGGCGGAAGGC 3120  
 DB 3061 GGGGAGAGCCGGTACTGACTGTACCGGCCAAACACATGACATTCATGAGGGGCGGAAGGC 3120  
 QY 3121 AGAATTTCTACAGAGGACATCTCATTTCTTGATACAGAGGTCATCTACTCTCT 3180  
 DB 3121 AGAATTTCTACAGAGGACATCTCATTTCTTGATACAGAGGTCATCTACTCTCTCT 3180  
 QY 3181 CCCGCTTATATATCTCTATGACAGTCAAGCAAAACAGGCACTCTCATAGTCTTAT 3240  
 DB 3181 CTCGCTTATATATCTCTATGACAGTCAAGCAAAACAGGCACTCTCATAGTCTTAT 3240  
 QY 3241 ACATTTCAAATGCTTCACTCGGCGAGTATTCCTTGCGAGGCTTCAGCAAGATGCCCC 3300  
 DB 3241 ACATTTCAAATGCTTCACTCGGCGAGTATTCCTTGCGAGGCTTCAGCAAGATGCCCT 3300  
 QY 3301 AACTCGTGTATCTGAGTCTATACAGATCAATCCCTAATCTTCTATAGAAAC 3358  
 DB 3301 AACTCATGTGTATCCGAGTCTATATCTGATCAATCCCTTATCTTATAGAAAC 3358

Search completed: February 5, 2006, 02:40:31  
 Job time : 16571 secs

This Page Blank (uspio)

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: February 4, 2006, 20:45:18 ; Search time 1895 Seconds  
(without alignments)  
11810.046 Million cell updates/sec

Title: US-10-800-256-1  
Perfect score: 3358  
Sequence: 1 acggcgaagaagatctcgat.....cctaactctatagaacc 3358

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapect 1.0

Searched: 4996997 seqs, 3332346308 residues  
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3358	100.0	3358	8	ACC47077 Nucleotide
2	3353.2	99.9	15186	3	AAZ44617 Newcastl
3	3353.2	99.9	15186	10	ADH71088 Newcastl
4	3353.2	99.9	15186	10	ADH71088 Newcastl
5	3240.4	96.5	5292	12	ADM78414 Newcastl
6	3196.4	95.2	3825	1	AAW70261 Newcastl
7	2441.6	72.7	5291	12	ADM78418 Newcastl
8	1741.8	51.9	4177	2	AAO68943 Newcastl
9	1741.8	51.9	4177	2	AAO70570 Newcastl
10	1741.8	51.9	4177	2	AAO70570 Newcastl
11	1741.8	51.9	4177	2	AAO70570 Newcastl
12	1741.8	51.9	4177	2	AAO70570 Newcastl
13	1741.8	51.9	4177	2	AAO70570 Newcastl
14	1701.6	50.7	3570	6	ABK90556 Newcastl
15	1631.6	48.6	1662	2	AAO70570 Newcastl
16	1511	45.0	1907	2	AAO99633 Newcastl
17	1509.4	44.9	1907	2	AAO99633 Newcastl
18	1448	43.1	2176	2	AAQ13668 Newcastl

20	1434.4	42.7	1734	13	ADU69205 Newcastl
21	1427.2	42.5	1704	2	AAQ10060 F gene of
22	1421.6	42.3	1734	2	AAO18205 Newcastl
23	1414.6	42.1	1812	4	AAO31148 Newcastl
24	1414	42.1	1662	12	ADP64628 DNA encod
25	1374.6	40.9	1685	6	AAI39864 DNA of F
26	1374.6	40.9	1685	10	ACC83258 Nucleotid
27	1368.4	40.8	2521	2	AAV42534 DNA encod
28	1368.4	40.8	2521	12	ADM41154 Nucleotid
29	1365.2	40.7	2521	2	AAO35875 Newcastl
30	1365.2	40.7	2521	2	AAO35875 Newcastl
31	1365.2	40.7	2521	2	AAO35875 Newcastl
32	1365.2	40.7	2521	2	AAO35875 Newcastl
33	1364	40.6	1734	2	AAO35875 Newcastl
34	1362.8	40.3	1764	1	AAO35875 Newcastl
35	1354.8	40.3	1764	1	AAO35875 Newcastl
36	1353.2	40.3	1764	1	AAO35875 Newcastl
37	1325.2	39.5	1602	13	ADX00955 Infectio
38	1290	38.4	1999	2	AAO05549 Sequence
39	1290	38.4	2000	1	AAO05549 Sequence
40	1238.2	36.9	1867	6	ABA99929 NDV HN DN
41	1196.8	35.6	1584	11	ADO55921 Newcastl
42	1193.6	35.5	1584	11	ADO55921 Newcastl
43	1192	35.5	1584	11	ADO55920 Newcastl
44	1160.8	34.6	1716	2	AAV49335 Newcastl
45	1090.4	32.5	1805	1	AAO91032 Haemagglu

## ALIGNMENTS

RESULT 1	ACC47077	standard; DNA; 3358 BP.
ID	ACC47077	
AC	ACC47077	
AC	ACC47077	
DT	23-JUN-2003	(first entry)
XX		
DE	Nucleotide sequence of F and HN genes of NDV strain HUJ.	
XX		
KW	NDV, lentogenic; oncolytic; fusion glycoprotein; F gene; HN gene;	
KW	haemagglutinin-neuraminidase; cytosolic; gene therapy; cancer; gene; ds.	
XX		
OS	Newcastle disease virus.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	47..3358
FT		/*tag= a
FT		/note= "contains internal stop codons"
XX		
PN	WO2003022202-A2.	
PD	20-MAR-2003.	
XX		
PF	12-SEP-2002; 2002WO-IL000765.	
XX		
PR	12-SEP-2001; 2001IL-00145397.	
XX		
PA	(YISS) YISSUM RES & DEV CO.	
XX	(OVCUR-) OVCURE INC.	
PI	Zakay-Rones Z, Panet A, Irving C;	
XX	WPI; 2003-354496/33.	
DR	P-PSDB; ABR39678.	
XX		
PT	Clonal lentogenic oncolytic strain, particularly a HUJ strain, of Newcastle Disease Virus, useful for treating cancer, comprises a DNA encoding a fusion gene and/or a hemagglutinin-neuraminidase gene.	
XX		
PS	Claim 1; Page 18-21; 51pp; English.	

CC The invention relates to a clonal lentogenic oncolytic strain of  
CC Newcastle Disease Virus (NDV) comprising a DNA sequence encoding for the  
CC fusion glycoprotein (F) gene and a part of the haemagglutinin-  
CC neuraminidase (HN) gene. The lentogenic oncolytic strain of NDV or a  
CC viral glycoprotein having oncolytic activity, is useful in preparing a  
CC composition for the treatment of cancer. The present sequence represents  
CC a NDV strain HUJ nucleotide sequence containing all of the F gene, an  
CC intergene and most of the HN gene  
XX

Sequence 3358 BP; 984 A; 785 C; 746 G; 843 T; 0 U; 0 Other;

Query Match 100.0%; Score 3358; DB 8; Length 3358;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ACGGGTGAAGATTCTGGATCCGGTTGGCGCCCTCCAGTGCAGAGTGGGCTCAGACC 60
Db 1 ACGGGTGAAGATTCTGGATCCGGTTGGCGCCCTCCAGTGCAGAGTGGGCTCAGACC 60
QY 61 TTCTACCAAGAACCCAGCAGCTATGATGCTGACTATCCGGGTTGGGCTGCACTGAGTTG 120
Db 61 TTCTACCAAGAACCCAGCAGCTATGATGCTGACTATCCGGGTTGGGCTGCACTGAGTTG 120
QY 121 CATCTGTCCGCAAACTTCATTTGATGCGAGGCTCTTGACAGCTGCAGGAATTGGTTAC 180
Db 121 CATCTGTCCGCAAACTTCATTTGATGCGAGGCTCTTGACAGCTGCAGGAATTGGTTAC 180
QY 181 AGGAGCAAAAGCCGTCAACATATACACTGATCCAGACAGATCAATCATATGTTAACT 240
Db 181 AGGAGCAAAAGCCGTCAACATATACACTGATCCAGACAGATCAATCATATGTTAACT 240
QY 241 CCTCCGGAATCTGCCCAGAGTAAGAGGCAATGTCGCAAAAGCCCTTGGATGCATCA 300
Db 241 CCTCCGGAATCTGCCCAGAGTAAGAGGCAATGTCGCAAAAGCCCTTGGATGCATCA 300
QY 301 CAGGACATTTGACCACTTTGCTCACCCCTTGGTGACTCTATCCGTAGATACAAAGTTC 360
Db 301 CAGGACATTTGACCACTTTGCTCACCCCTTGGTGACTCTATCCGTAGATACAAAGTTC 360
QY 361 TGTGACATCACTTGGAGGGGGGAGACAGGGGGGCTTATAGGGGCACTTATTTGGGGTGT 420
Db 361 TGTGACATCACTTGGAGGGGGGAGACAGGGGGGCTTATAGGGGCACTTATTTGGGGTGT 420
QY 421 GGCTCTTGGGGTTGCAACTGCGCGACAAATTAACGCGGCGCAGCTCTGATACAAGCAA 480
Db 421 GGCTCTTGGGGTTGCAACTGCGCGACAAATTAACGCGGCGCAGCTCTGATACAAGCAA 480
QY 481 ACAAATGCTGCGCAACATCTCCGACTTAAAGAGACATTCGCCAACAATGAGGCTGT 540
Db 481 ACAAATGCTGCGCAACATCTCCGACTTAAAGAGACATTCGCCAACAATGAGGCTGT 540
QY 541 GCATGAGGTCACTGACGATTAATGCAACTGACGAGTGGCAATTTGGGAATGACGAGTT 600
Db 541 GCATGAGGTCACTGACGATTAATGCAACTGACGAGTGGCAATTTGGGAATGACGAGTT 600
QY 601 TGTAAATGACCAATTTAATAAAGAGCTCAGAGATTAAGTCACTCAAAATTTGACAGCA 660
Db 601 TGTAAATGACCAATTTAATAAAGAGCTCAGAGATTAAGTCACTCAAAATTTGACAGCA 660
QY 661 AGTTGTGTGAGAGCTCAACTGTGACCTTAACCGAATTTGACTACATATTCGGAACAAT 720
Db 661 AGTTGTGTGAGAGCTCAACTGTGACCTTAACCGAATTTGACTACATATTCGGAACAAT 720
QY 721 CACTTCACCTGCTTTAAACAAGCTGACTGATTCAGGCACTTAAATCTAGTGTGTGAAA 780
Db 721 CACTTCACCTGCTTTAAACAAGCTGACTGATTCAGGCACTTAAATCTAGTGTGTGAAA 780
QY 781 TATGATTAATCTATTTGACTAAGTGTAGGTGAGGAACATCACTCAGCTCATTAATCGG 840
Db 781 TATGATTAATCTATTTGACTAAGTGTAGGTGAGGAACATCACTCAGCTCATTAATCGG 840
QY 841 TAGCGGCTTAATCAACGGTAAACCTATTTCTATGACTCAGACACTGAACCTTTGGGTAT 900
Db 841 TAGCGGCTTAATCAACGGTAAACCTATTTCTATGACTCAGACACTGAACCTTTGGGTAT 900
```

```
Db 841 TAGCGGCTTAATCAACGGTAAACCTATTTCTATGACTCAGACACTGAACCTTTGGGTAT 900
QY 901 ACAAGTAATCTACCTTCAAGTCGGGAACCTTAATATATATGTCGCCACTTATTTGAAC 960
Db 901 ACAAGTAATCTACCTTCAAGTCGGGAACCTTAATATATATGTCGCCACTTATTTGAAC 960
QY 961 CTTATCCGTAGACCAACAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGGTACACA 1020
Db 961 CTTATCCGTAGACCAACAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGGTACACA 1020
QY 1021 GGTCGGTCTGTGATTAAGAACTTGACACCTCATCTGATATGAACTGACTAGATTT 1080
Db 1021 GGTCGGTCTGTGATTAAGAACTTGACACCTCATCTGATATGAACTGACTAGATTT 1080
QY 1081 ATATTGACAAAGATATGTAAGTTCCCTATGTCCTCGTATTTATTCCTGCTTGACGG 1140
Db 1081 ATATTGACAAAGATATGTAAGTTCCCTATGTCCTCGTATTTATTCCTGCTTGACGG 1140
QY 1141 CAATACGTGGCTGTATGTAATCTCAAAAGACCGAAGCGCACTTAACCAATACATGAC 1200
Db 1141 CAATACGTGGCTGTATGTAATCTCAAAAGACCGAAGCGCACTTAACCAATACATGAC 1200
QY 1201 TATCAAAAGTTCACTCATCCGCAACTGCAAGATGACAAATGTAAGTGTAAACCCGCC 1260
Db 1201 TATCAAAAGTTCACTCATCCGCAACTGCAAGATGACAAATGTAAGTGTAAACCCGCC 1260
QY 1261 GGGTATCATATCGCAAAACTATGAGAGCCGTGTCTTAATAGATTAACAATCATGCAA 1320
Db 1261 GGGTATCATATCGCAAAACTATGAGAGCCGTGTCTTAATAGATTAACAATCATGCAA 1320
QY 1321 TGTTTATCCTTAGCGGGATTAACCTTTAAGGCTCAGTGGGAAATTCGATGTAACTTCA 1380
Db 1321 TGTTTATCCTTAGCGGGATTAACCTTTAAGGCTCAGTGGGAAATTCGATGTAACTTCA 1380
QY 1381 GAAGAAATATCTCAATTAACAAGATTCTCAAGTAATTAACAAGGAATCTGATATCTCAAC 1440
Db 1381 GAAGAAATATCTCAATTAACAAGATTCTCAAGTAATTAACAAGGAATCTGATATCTCAAC 1440
QY 1441 TGAGCTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAATTAAGTAAAGGAACAA 1500
Db 1441 TGAGCTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAATTAAGTAAAGGAACAA 1500
QY 1501 CAGAAAATAGACAAAGTCAATGCTCAACTGACATGACATCTGCTCATTAATCTATAT 1560
Db 1501 CAGAAAATAGACAAAGTCAATGCTCAACTGACATGACATCTGCTCATTAATCTATAT 1560
QY 1561 CGTTTGAATCATATCTCTGTTTGGTATTACTTAAGCTGATTTACAGAGCTACCT 1620
Db 1561 CGTTTGAATCATATCTCTGTTTGGTATTACTTAAGCTGATTTACAGAGCTACCT 1620
QY 1621 AATGTAACAAGCAAAAGCGCAACAAAACCTTATTATGCTTGGGAATTAATCTTAGA 1680
Db 1621 AATGTAACAAGCAAAAGCGCAACAAAACCTTATTATGCTTGGGAATTAATCTTAGA 1680
QY 1681 TCAGATGAGGCACTACAAAATGTGAAACACAGATGAGGAAGAAAGTTTCCCTAATAG 1740
Db 1681 TCAGATGAGGCACTACAAAATGTGAAACACAGATGAGGAAGAAAGTTTCCCTAATAG 1740
QY 1741 TAAATTTGTGAAGATTTCTGTAGTCTGTCAAGTTCAAGAGTTTAAGAAAACCTACCGGT 1800
Db 1741 TAAATTTGTGAAGATTTCTGTAGTCTGTCAAGTTCAAGAGTTTAAGAAAACCTACCGGT 1800
QY 1801 TGTAGATGACCAAAAGGACATATACGGGTGAAACGGTAAAGAGAGCGCCCTCAATTTGC 1860
Db 1801 TGTAGATGACCAAAAGGACATATACGGGTGAAACGGTAAAGAGAGCGCCCTCAATTTGC 1860
QY 1861 GAGCCAGGCTTCAACAACCTCGTTTCAACCGCTTCAACGACCAACAGTCTCAATCATGAC 1920
Db 1861 GAGCCAGGCTTCAACAACCTCGTTTCAACCGCTTCAACGACCAACAGTCTCAATCATGAC 1920
QY 1921 CGGCGGCTTAGCCAAAGTTGCTTAAGAGATGATGAAGAGGCAAAAATTAATATGCGCG 1980
Db 1921 CGGCGGCTTAGCCAAAGTTGCTTAAGAGATGATGAAGAGGCAAAAATTAATATGCGCG 1980
```



```
Qy 1981 TTGATATTCGGATTCGATCTTATCTTAAACAGTAGTGAACCTTGGCTATATCTGTAACC 2040
Db 1981 TTGATATTCGGATTCGATCTTATCTTAAACAGTAGTGAACCTTGGCTATATCTGTAACC 2040
Qy 2041 TCCCTTTTATATAGCAATGGGGGCTAGCAACACTTGCCATCTTTAGGCAATCCGACTAGG 2100
Db 2041 TCCCTTTTATATAGCAATGGGGGCTAGCAACACTTGCCATCTTTAGGCAATCCGACTAGG 2100
Qy 2101 ATTTCCAGGGGAGAAAGAAATTACATCTACCTGGTTCATCAAGATGTAGAT 2160
Db 2101 ATTTCCAGGGGAGAAAGAAATTACATCTACCTGGTTCATCAAGATGTAGAT 2160
Qy 2161 AGGATATATAGCAATGGGCTTGAAGTCTCGTTGGCATTTGTTAAATCTAGAACACA 2220
Db 2161 AGGATATATAGCAATGGGCTTGAAGTCTCGTTGGCATTTGTTAAATCTAGAACACA 2220
Qy 2221 ATATAGAACGCAATTAACATCTCTCTTATCAAGATTAATGGAGCTGCACAAACAAGTGG 2280
Db 2221 ATATAGAACGCAATTAACATCTCTCTTATCAAGATTAATGGAGCTGCACAAACAAGTGG 2280
Qy 2281 TGGGGGGCACTATCCATGACCCAGATTATAGGGGGGATAGGCAAGAACTGATTGTA 2340
Db 2281 TGGGGGGCACTATCCATGACCCAGATTATAGGGGGGATAGGCAAGAACTGATTGTA 2340
Qy 2341 GATGATGCTAGTGAATGTCATCATCTATCCCTGCTGCAATTCAGAAACATCTGAATTTT 2400
Db 2341 GATGATGCTAGTGAATGTCATCATCTATCCCTGCTGCAATTCAGAAACATCTGAATTTT 2400
Qy 2401 ATCCCGGCGCTTACTACAGATCAGGTGACCTGCAATACCTCATTTGACATGAGTCT 2460
Db 2401 ATCCCGGCGCTTACTACAGATCAGGTGACCTGCAATACCTCATTTGACATGAGTCT 2460
Qy 2461 ACCCATACGCTACACCCCAATATGTAATATTTGCTGGAATGCAAGAGATCACTCAATTCA 2520
Db 2461 ACCCATACGCTACACCCCAATATGTAATATTTGCTGGAATGCAAGAGATCACTCAATTCA 2520
Qy 2521 TATCAGATTTTGAAGCACTTGTGTCTCCGACATCTGCAACAGGAGGATTTCTTTTCT 2580
Db 2521 TATCAGATTTTGAAGCACTTGTGTCTCCGACATCTGCAACAGGAGGATTTCTTTTCT 2580
Qy 2581 ACTCTGGGTTTCATCAACCTGGAAGCAACCAAAATCGGAAGTCTTGCAATGTGAGTGA 2640
Db 2581 ACTCTGGGTTTCATCAACCTGGAAGCAACCAAAATCGGAAGTCTTGCAATGTGAGTGA 2640
Qy 2641 ACTCCCTGGGTTGTGATATGCTGTGCTCGAAAGTCAAGGAGACAGAGAAAGATTTAT 2700
Db 2641 ACTCCCTGGGTTGTGATATGCTGTGCTCGAAAGTCAAGGAGACAGAGAAAGATTTAT 2700
Qy 2701 AACTCAGCTGTCCCTACGCGGATGGTATCATAGGAGGTTAGGGTTGACGCGCAGTACAC 2760
Db 2701 AACTCAGCTGTCCCTACGCGGATGGTATCATAGGAGGTTAGGGTTGACGCGCAGTACAC 2760
Qy 2761 GAAAAGACCTAGATGTCAACAATTAATTCGGGAGCTGGGTGCGCAACTACCGAGAGTA 2820
Db 2761 GAAAAGACCTAGATGTCAACAATTAATTCGGGAGCTGGGTGCGCAACTACCGAGAGTA 2820
Qy 2821 GGGGGTGGATCTTTTATTTGACAGCCGCTATGTTCTCAGTCTACGAGGGTTAAACC 2880
Db 2821 GGGGGTGGATCTTTTATTTGACAGCCGCTATGTTCTCAGTCTACGAGGGTTAAACC 2880
Qy 2881 AATTCAACCCGCTGACATGTACAGGAAGGAAATATGATATCAAGCGATTAACAATAC 2940
Db 2881 AATTCAACCCGCTGACATGTACAGGAAGGAAATATGATATCAAGCGATTAACAATAC 2940
Qy 2941 ACATGCCAGATGAGCAAGACTACAGATTCGAAATGSCCAAGTCTTCGTATAGGCTTGA 3000
Db 2941 ACATGCCAGATGAGCAAGACTACAGATTCGAAATGSCCAAGTCTTCGTATAGGCTTGA 3000
Qy 3001 CGGTTTGGTGGAAACGATACAGAGGCTATCTTATCTATCAAGGTCTCAACATCTTGA 3060
Db 3001 CGGTTTGGTGGAAACGATACAGAGGCTATCTTATCTATCAAGGTCTCAACATCTTGA 3060
```

```
Qy 3061 GCGGAGAACCCCGGATCTGATCTGTAACCGCCCAACAGCTCACTCATAGGGGCGGAAGGC 3120
Db 3061 GCGGAGAACCCCGGATCTGATCTGTAACCGCCCAACAGCTCACTCATAGGGGCGGAAGGC 3120
Qy 3121 AGAATTCACAGTAGGAGACATCTCATTTCTTGATACAGAGGGTCACTACTTCTCT 3180
Db 3121 AGAATTCACAGTAGGAGACATCTCATTTCTTGATACAGAGGGTCACTACTTCTCT 3180
Qy 3181 CCCGCTTATATATCTTATGACAGTACAGCAACAAACAGGCACTTTCATATGCTTAT 3240
Db 3181 CCCGCTTATATATCTTATGACAGTACAGCAACAAACAGGCACTTTCATATGCTTAT 3240
Qy 3241 ACATTCATGCTTCACTCGGCGCAGTAGTATCCCTTCCAGGGTTACAGCAAGATGCC 3300
Db 3241 ACATTCATGCTTCACTCGGCGCAGTAGTATCCCTTCCAGGGTTACAGCAAGATGCC 3300
Qy 3301 AACTCGTGTGTACTGAGTCTATACAGATCATATCCCTTATCTTATAGAAACC 3358
Db 3301 AACTCGTGTGTACTGAGTCTATACAGATCATATCCCTTATCTTATAGAAACC 3358

RESULT 2
AAZ44617
ID AAZ44617 standard; DNA, 15186 BP.
XX
AC AAZ44617;
XX
DT 07-Apr-2000 (first entry)
XX
DE Newcastle disease virus LaSota genomic DNA.
XX
KW Avian-paramyxovirus; infection; lentogenic; F protein; vaccine;
KW respiratory disease; gastrointestinal disease; poultry pathogen;
KW local immunity; ds.
XX
OS Newcastle disease virus.
XX
FH Key location/Qualifiers
FT CDS 122..1591
FT FT /*tag= a
FT CDS 1887..3074
FT FT /*tag= b
FT CDS 3290..4384
FT FT /*tag= c
FT CDS 4544..6205
FT FT /*tag= d
FT CDS 6412..8145
FT FT /*tag= e
FT CDS 8381..14995
FT FT /*tag= f
XX
PN MO9966045-A1.
XX
PD 23-DEC-1999.
XX
PF 17-JUN-1999; 99WO-NL000377.
XX
PR 19-JUN-1998; 98EP-00202054.
XX
PA (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
XX
PI Peeters BPH, De Leeuw OS, Koch G, Gielkens ALJ;
XX
DR WPI; 2000-106102/09.
XX
PT New avian paramyxovirus cDNA, useful for production of vaccine against
XX Newcastle disease virus.
XX
PS Disclosure; Fig 3; 115pp; English.
XX
CC This invention describes a novel avian-paramyxovirus cDNA (1) which
XX comprises a nucleic acid sequence corresponding to the 5' terminal end of
XX the genome of avian-paramyxovirus allowing the generation of an
```

CC infectious copy of avian paramyxovirus. The cell line is useful for the  
CC production of infectious lentogenic NDV (Newcastle Disease virus) without  
CC the addition of exogenous proteolytic activity. Also it is possible to  
CC generate a stable transfected cell line that expresses the wild-type F  
CC protein in the virus envelope therefore providing infectious particles,  
CC useful in the form of a vaccine, especially against respiratory and/or  
CC gastrointestinal diseases. NDV can be easily cultured to very high titers  
CC in embryonated eggs. Mass culture of embryonated eggs is relatively  
CC cheap. NDV vaccines are relatively stable and can be simply administered  
CC by mass application methods e.g. drinking water or by spraying or by  
CC aerosol formation. The natural route of infection is by the respiratory  
CC and/or gastrointestinal tract which are also the major routes of  
CC infection of many other poultry pathogens. NDV can induce local immunity  
CC despite the presence of circulating maternal antibody. This sequence  
CC represents the NDV strain laSota genome DNA  
CC  
XX  
SQ Sequence 15186 BP; 4431 A; 3544 C; 3462 G; 3749 T; 0 U; 0 Other;  
Query Match 99.9%; Score 3353.2; DB 3; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3353; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ACGGGTGAAGATCTGGATCCGGTTGGGGCCCTCCAGGTCGAAGATGGGCTCCAGACC 60  
DB 4498 ACGGGTGAAGATCTGGATCCGGTTGGGGCCCTCCAGGTCGAAGATGGGCTCCAGACC 4557  
QY 61 TTTCACCAAGAACCCAGACCTATGATGCTGATCTATCCGGGTTGCGGTGGCATGAGTTG 120  
DB 4558 TTTCACCAAGAACCCAGACCTATGATGCTGATCTATCCGGGTTGCGGTGGCATGAGTTG 4617  
QY 121 CATCTGTCGGGCAATCTTCATTTGATGGAGCCCTTTGGACGCTGCAGGAATTTGGTTAC 180  
DB 4618 CATCTGTCGGGCAATCTTCATTTGATGGAGCCCTTTGGACGCTGCAGGAATTTGGTTAC 4677  
QY 181 AGGAGCAAAAGCCGTCAACATATACCTCATCTCCAGACAGGATCAATCATGTTAAGCT 240  
DB 4678 AGGAGCAAAAGCCGTCAACATATACCTCATCTCCAGACAGGATCAATCATGTTAAGCT 4737  
QY 241 CCTCCCAATCTGCCCAAGATAGAGGCAATGTCGCAAAAGCCCTTGGATGTCATCAA 300  
DB 4738 CCTCCCAATCTGCCCAAGATAGAGGCAATGTCGCAAAAGCCCTTGGATGTCATCAA 4797  
QY 301 CAGGACATTTGACCTTTGCTCAACCCCTTGGTGAATCTTATCCGTAGATCAAGATC 360  
DB 4798 CAGGACATTTGACCTTTGCTCAACCCCTTGGTGAATCTTATCCGTAGATCAAGATC 4857  
QY 361 TGTGACATCAATCTGGAGGGGGGAGACAGGGGGCCCTTATAGGGGCCCTTATTTGGCGGTG 420  
DB 4858 TGTGACATCAATCTGGAGGGGGGAGACAGGGGGCCCTTATAGGGGCCCTTATTTGGCGGTG 4917  
QY 421 GGGCTTTGGGGTTGCACTGCGGCAAAATTAAGCGGCGCAGCTGATCAAGCCAA 480  
DB 4918 GGGCTTTGGGGTTGCACTGCGGCAAAATTAAGCGGCGCAGCTGATCAAGCCAA 4977  
QY 481 ACAAAATGCTGCCAATCTCTCGACTTTAAAGAGAGCATTTGCCGAACCAATGAGGCTGT 540  
DB 4978 ACAAAATGCTGCCAATCTCTCGACTTTAAAGAGAGCATTTGCCGAACCAATGAGGCTGT 5037  
QY 541 GCATGAGGTGACGAGGATTAATGCAACTAGCAGTGGCAGTTGGGAAGATGCGACGTT 600  
DB 5038 GCATGAGGTGACGAGGATTAATGCAACTAGCAGTGGCAGTTGGGAAGATGCGACGTT 5097  
QY 601 TGTTAATGACCAATTTAATAAAGAGCTCAGGAATTAAGCTGATCAAAATTTGCACGCA 660  
DB 5098 TGTTAATGACCAATTTAATAAAGAGCTCAGGAATTAAGCTGATCAAAATTTGCACGCA 5157  
QY 661 AGTTGTGTAAGCTCAACCTGTACCTAACCGAATTTGACTAAGTATTTCCGACCAAAAT 720  
DB 5158 AGTTGTGTAAGCTCAACCTGTACCTAACCGAATTTGACTAAGTATTTCCGACCAAAAT 5217  
QY 721 CACTTACCTGCTTTAAACAAGCTGATATTTCAAGGCACTTTACAATTTAGTGTGGAAA 780  
DB 5218 CACTTACCTGCTTTAAACAAGCTGATATTTCAAGGCACTTTACAATTTAGTGTGGAAA 5277

QY 781 TATGATTAATCTTATTTGATCTAAGTTAGTGAAGAAACATCACTCAAGCTCATTAATCGG 840  
DB 5278 TATGATTAATCTTATTTGATCTAAGTTAGTGAAGAAACATCACTCAAGCTCATTAATCGG 5337  
QY 841 TAGCGGTTTATACACCGGTAAACCTATTTATACGACTCAACAGCTCAACTCTTGGGTAT 900  
DB 5338 TAGCGGTTTATACACCGGTAAACCTATTTATACGACTCAACAGCTCAACTCTTGGGTAT 5397  
QY 901 ACAAGTAACTCTACCTTCAGTGGGAACCTAAATATATATGCTGCCACTTATTTGAAGAAC 960  
DB 5398 ACAAGTAACTCTACCTTCAGTGGGAACCTAAATATATGCTGCCACTTATTTGAAGAAC 5457  
QY 961 CTATTCGTAGACCAACACAGGGGATTTGCTTGGGCACTTGTCCCAAAAGTGTGACACA 1020  
DB 5458 CTATTCGTAGACCAACACAGGGGATTTGCTTGGGCACTTGTCCCAAAAGTGTGACACA 5517  
QY 1021 GGTCCGTTCTGTATTAAGAAACCTTGACACTCTCACTATGTAATGAACCTGATTAAGTTT 1080  
DB 5518 GGTCCGTTCTGTATTAAGAAACCTTGACACTCTCACTATGTAATGAACCTGATTAAGTTT 5577  
QY 1081 ATATTGTACAAGAAATAGTAAGTTCCCTATGTCCCTGATTTATTTCTGCTTGAACGG 1140  
DB 5578 ATATTGTACAAGAAATAGTAAGTTCCCTATGTCCCTGATTTATTTCTGCTTGAACGG 5637  
QY 1141 CAATACGTCGGCTGTATTTGATCTCAAAAGACCGAAGCGCACTTATCAACCATATCATGAC 1200  
DB 5638 CAATACGTCGGCTGTATTTGATCTCAAAAGACCGAAGCGCACTTATCAACCATATCATGAC 5697  
QY 1201 TATCAAAAGTTTCACTGCTATGCGCAACTGCAAGATGACAAACATGTATGTAAACCCGCC 1260  
DB 5698 TATCAAAAGTTTCACTGCTATGCGCAACTGCAAGATGACAAACATGTATGTAAACCCGCC 5757  
QY 1261 GGGTATCATATGCGCAAACTATGAGAAAGCGGTGCTCTATATAGATTAACATATGCAAA 1320  
DB 5758 GGGTATCATATGCGCAAACTATGAGAAAGCGGTGCTCTATATAGATTAACATATGCAAA 5817  
QY 1321 TGTTTATCTTATAGCGGGATTAACCTTAAAGCTCAGTGGGAAATTCGATGTAACCTATCA 1380  
DB 5818 TGTTTATCTTATAGCGGGATTAACCTTAAAGCTCAGTGGGAAATTCGATGTAACCTATCA 5877  
QY 1381 GAAGAAATATCTCAATTAACAATCTCAAGTAATTAACAAGGCAATTTGATATCTCAAC 1440  
DB 5878 GAAGAAATATCTCAATTAACAATCTCAAGTAATTAACAAGGCAATTTGATATCTCAAC 5937  
QY 1441 TGAGCTTGGGAATGTCAACAATCGATCAGTAATGCTTTGAATTAAGTGAAGAAAGCAA 1500  
DB 5938 TGAGCTTGGGAATGTCAACAATCGATCAGTAATGCTTTGAATTAAGTGAAGAAAGCAA 5997  
QY 1501 CAGAAAATAGACAAAGTCAATGTCAAACTGACTAGACATCTGCTCATTAATAT 1560  
DB 5998 CAGAAAATAGACAAAGTCAATGTCAAACTGACTAGACATCTGCTCATTAATAT 6057  
QY 1561 CGTTTGAATCATATATCTTGTGTTTGTATATCAATTAAGCTGATTTACAGATGCTACCT 1620  
DB 6058 CGTTTGAATCATATATCTTGTGTTTGTATATCAATTAAGCTGATTTACAGATGCTACCT 6117  
QY 1621 AATGTACAGCAAAAGCGGCAAAACCTTATTAATGCTTGGGAATATATCTTACA 1680  
DB 6118 AATGTACAGCAAAAGCGGCAAAACCTTATTAATGCTTGGGAATATATCTTACA 6177  
QY 1681 TCAGATGAGACCACTACAAAAAATGTGAACACAGATGAGGAAGAAAGTTTCCCTAATAG 1740  
DB 6178 TCAGATGAGACCACTACAAAAAATGTGAACACAGATGAGGAAGAAAGTTTCCCTAATAG 6237  
QY 1741 TAAATTTGTGAAGATTTCTGTGTCTGTAGTTCAGAGTTTAAGAAAAAATCAACCGGT 1800  
DB 6238 TAAATTTGTGAAGATTTCTGTGTCTGTAGTTCAGAGTTTAAGAAAAAATCAACCGGT 6297  
QY 1801 TGTAGATGACCAAAAGACGATATACGGGTTGAACGGGTAAGAGAGCGCCCTCAATTTGC 1860  
DB 6298 TGTAGATGACCAAAAGACGATATACGGGTTGAACGGGTAAGAGAGCGCCCTCAATTTGC 6357

QY 1861 GAGCGAGGCTTCACAACTCCGTTCTACCGCTTCACCGACAAGTCTCATCATGGAC 1920  
Db 6358 GAGCGAGGCTTCACAACTCCGTTCTACCGCTTCACCGACAAGTCTCATCATGGAC 6417  
QY 1921 CGCGCCCTTAGCCAAAGTTGCGTTAGAGATAGTAAAGAGAGGCAAAAATACATGGGC 1980  
Db 6418 CGCGCCCTTAGCCAAAGTTGCGTTAGAGATAGTAAAGAGAGGCAAAAATACATGGGC 6477  
QY 1981 TTGATATTCGGAGTTGCAATCTTATTTCTTAAACAGTAGTGACTTGGCTATCTGTAGCC 2040  
Db 6478 TTGATATTCGGAGTTGCAATCTTATTTCTTAAACAGTAGTGACTTGGCTATCTGTAGCC 6537  
QY 2041 TCCCTTTATATATAGCATGGGGGCTAGCACACTAGCCATCTTATAGGCAATACCACTAGG 2100  
Db 6538 TCCCTTTATATATAGCATGGGGGCTAGCACACTAGCCATCTTATAGGCAATACCACTAGG 6597  
QY 2101 ATTTCCAGGGCAAGAAAGAAATTAATCATCTACCTTGGTTCCATCAAGATGTAGTANT 2160  
Db 6598 ATTTCCAGGGCAAGAAAGAAATTAATCATCTACCTTGGTTCCATCAAGATGTAGTANT 6657  
QY 2161 AGGATATATAGCAAGTGGCCCTGAGTCTCGTTGGCAATGTTAAATACTGAGACACA 2220  
Db 6658 AGGATATATAGCAAGTGGCCCTGAGTCTCGTTGGCAATGTTAAATACTGAGACACA 6717  
QY 2221 ATTATGAACGCAATPAACATCTCTCTTATCAGATTATGAGCTCAACAAACAGTGGG 2280  
Db 6718 ATTATGAACGCAATPAACATCTCTCTTATCAGATTATGAGCTCAACAAACAGTGGG 6777  
QY 2281 TGGGGGGGCACTTATTCATGACCCAGATTATATAGGGGGGATAGGCAAACTCATTTGTA 2340  
Db 6778 TGGGGGGGCACTTATTCATGACCCAGATTATATAGGGGGGATAGGCAAACTCATTTGTA 6837  
QY 2341 GATGATGTAGTGAATGTGACATCTTATCCCTCTGCAATTCGAAGCACTGAATTTT 2400  
Db 6838 GATGATGTAGTGAATGTGACATCTTATCCCTCTGCAATTCGAAGCACTGAATTTT 6897  
QY 2401 ATCCCGGCGCTTACTACAGATCAGTTCGATCGAATACCTCATTTGACATGAGTCT 2460  
Db 6898 ATCCCGGCGCTTACTACAGATCAGTTCGATCGAATACCTCATTTGACATGAGTCT 6957  
QY 2461 ACCCATTACTGCTACACCCATATATGTATATTTGTGATGACAGATCATCTCATTTCA 2520  
Db 6958 ACCCATTACTGCTACACCCATATATGTATATTTGTGATGACAGATCATCTCATTTCA 7017  
QY 2521 TATCAGATTATAGCACTTGTGTGTCGGAATCTGCAACAGGGAGGGTATCTTTCT 2580  
Db 7018 TATCAGATTATAGCACTTGTGTGTCGGAATCTGCAACAGGGAGGGTATCTTTCT 7077  
QY 2581 ACTCTGCGTTCCATCAACCTGAGACACACCAAAATCGAAGTCTTGGCATGTGAGTCA 2640  
Db 7078 ACTCTGCGTTCCATCAACCTGAGACACACCAAAATCGAAGTCTTGGCATGTGAGTCA 7137  
QY 2641 ACTCCCTGGGTTGTGATATGCTGTGCTGAAAGTCAAGAGACAGAGAAAGAAATAT 2700  
Db 7138 ACTCCCTGGGTTGTGATATGCTGTGCTGAAAGTCAAGAGACAGAGAAAGAAATAT 7197  
QY 2701 AACTCAGCTGTCCCTACCGCGATGTATAGGAGTTAGAGTTGAGGCGCAGACAC 2760  
Db 7198 AACTCAGCTGTCCCTACCGCGATGTATAGGAGTTAGAGTTGAGGCGCAGACAC 7257  
QY 2761 GAAAAGGACCTAGATGTACAAATTTTGGGGGCTGGGTGGCCAACTACCGAGAGTA 2820  
Db 7258 GAAAAGGACCTAGATGTACAAATTTTGGGGGCTGGGTGGCCAACTACCGAGAGTA 7317  
QY 2821 GGGGGGTGATCTTTTATTTAGACAGCCGCTATGTTCTCAGTCTCAGAGGGTTAAACC 2880  
Db 7318 GGGGGGTGATCTTTTATTTAGACAGCCGCTATGTTCTCAGTCTCAGAGGGTTAAACC 7377  
QY 2881 AATTCAACCACTGACACTGTACAGAGAGGAAATTTGATATATCAACCGATACATATAC 2940  
Db 7378 AATTCAACCACTGACACTGTACAGAGAGGAAATTTGATATATCAACCGATACATATAC 7437  
QY 2941 ACATGCCAGATGAGCAAGACTACCAAGATTGCAATGGCCAAGTCTTCTATTAAGCTGGA 3000

Db 7438 ACATGCCAGATGAGCAAGACTACCAAGTTGCAATGGCCAAGTCTTCTATTAAGCTGGA 7497  
QY 3001 CGGTTTGGTGGAAACCATACAGACGCTATCTTATCTATCAAGTGTCAACATCTTTA 3060  
Db 7498 CGGTTTGGTGGAAACCATACAGACGCTATCTTATCTATCAAGTGTCAACATCTTTA 7557  
QY 3061 GGGCAAGCCGGTATGACTGTACCGCCCAACACACTGACACTCATAGGGGGCCGAAGGC 3120  
Db 7558 GGGCAAGCCGGTATGACTGTACCGCCCAACACACTGACACTCATAGGGGGCCGAAGGC 7617  
QY 3121 AGAATTCACAGTAGGGAACATCATTTCTGTATCAAGAGGGGTATCATCTTCT 3180  
Db 7618 AGAATTCACAGTAGGGAACATCATTTCTGTATCAAGAGGGGTATCATCTTCT 7677  
QY 3181 CCCCGTTATATATATCTTATGACAGTACAGCAACAAAACAGCACTTTCATATGCTTAT 3240  
Db 7678 CCCCGTTATATATATCTTATGACAGTACAGCAACAAAACAGCACTTTCATATGCTTAT 7737  
QY 3241 ACATTCATGCTTACTGAGTGTATATACATATCCCATATCCCTATATAGAAAC 3300  
Db 7738 ACATTCATGCTTACTGAGTGTATATACATATCCCATATCCCTATATAGAAAC 7797  
QY 3301 AACTCGTGTGTACTGAGTGTATATACATATCCCATATCCCTATATAGAAAC 3358  
Db 7798 AACTCGTGTGTACTGAGTGTATATACATATCCCATATCCCTATATAGAAAC 7855

RESULT 3  
ADH71088  
ID ADH71088 standard; DNA; 15186 BP.  
XX  
AC ADH71088;  
XX  
DT 25-MAR-2004 (first entry)  
XX  
DE Newcastle disease virus HN gene.  
XX  
XX Virulence; vaccine accelerator factor; VAF; immuno-stimulant;  
XX infectious bronchitis virus; IBV; Newcastle disease virus; NDV;  
XX infectious bursal disease virus; IBDV; Newcastle disease virus; NDV;  
XX infectious bronchitis virus; IBV; fowlpox virus; FPV;  
XX infectious laryngotracheitis virus; ILTV; avian encephalomyelitis virus;  
XX AEV; avian leukosis virus; ALV; avian parainfluenza virus; APV;  
XX duck hepatitis virus; DHV; hemorrhagic enteritis virus; HEV; HN; ds.  
OS Newcastle disease virus.  
XX  
XX US2003207836-A1.  
XX  
XX 06-NOV-2003.  
XX  
XX 06-MAY-2003; 2003US-00429735.  
XX  
XX 08-MAR-2002; 2002US-0362547P.  
XX  
XX 04-MAR-2003; 2003US-00377718.  
XX  
XX (KUDT/) KUD T Y.  
XX  
XX Kuo TY;  
XX  
XX WPI, 2003-875897/81.  
XX  
XX  
XX New vaccine accelerator factor (VAF) comprising one or more DNA  
XX constructs, each comprising a DNA molecule and a vector, useful as a  
XX vaccine for viruses that affect chicken.  
PS Claim 13; SEQ ID NO 3; 28bp; English.  
XX  
XX The present invention provides a vaccine accelerator factor (VAF) which  
XX is an in ovo nucleoclide immuno-stimulant. The VAF comprises one or more  
XX DNA constructs, each comprising a DNA molecule and a vector, where each  
XX of the DNA molecule contains one or more genes or gene fragments each

CC encoding an antigenic peptide of an avian virus. VAF accelerates and  
CC stimulates a protective immune response of a viral vaccine against the  
CC avian virus. VAF is useful as a vaccine against Marek's disease virus  
CC (MDV), infectious bursal disease virus (IBDV), Newcastle disease virus  
CC (NDV), infectious bronchitis virus (IBV), fowlpox virus (FPV), infectious  
CC laryngotracheitis virus (ILT), avian encephalomyelitis virus (AEV),  
CC avian leukosis virus (ALV), avian parainfluenza virus (APV), duck  
CC hepatitis virus (DHV) and hemorrhagic enteritis virus (HEV) in chicken.  
CC The present sequence is NDV HN gene.  
XX

Sequence 15186 BP; 4431 A; 3542 C; 3464 G; 3749 T; 0 U; 0 Other;

Query Match 99.9%; Score 3353.2; DB 10; Length 15186;

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACGGGTGAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTCAGAAATGGGCTCCAGACC 60  
DB 4498 ACGGGTGAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTCAGAAATGGGCTCCAGACC 4557  
QY 61 TTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTTGGCTGCACTGAGTTG 120  
DB 4558 TTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTTGGCTGCACTGAGTTG 4617  
QY 121 CATCTGTCGGCAAACTTCATTGATGCGAGCCCTCTTGCACTGAGGAATTTGGTTAC 180  
DB 4618 CATCTGTCGGCAAACTTCATTGATGCGAGCCCTCTTGCACTGAGGAATTTGGTTAC 4677  
QY 181 AGGAGCAAAAGCCGTCAACATATACCTCATCCCAAGAGATCAATAGTTAAAGCT 240  
DB 4678 AGGAGCAAAAGCCGTCAACATATACCTCATCCCAAGAGATCAATAGTTAAAGCT 4737  
QY 241 CCTCCCAATCTGCGCAAGATAGAGGATGTCGCAAGAGCCCTTGATGATCAAA 300  
DB 4738 CCTCCCAATCTGCGCAAGATAGAGGATGTCGCAAGAGCCCTTGATGATCAAA 4797  
QY 4738 CCTCCCAATCTGCGCAAGATAGAGGATGTCGCAAGAGCCCTTGATGATCAAA 4797  
DB 4738 CCTCCCAATCTGCGCAAGATAGAGGATGTCGCAAGAGCCCTTGATGATCAAA 4797  
QY 301 CAGGACATTGACCACTTGTCTCAACCCCTTGTTGACTCTATCCGTAGAGATCAAGATC 360  
DB 4798 CAGGACATTGACCACTTGTCTCAACCCCTTGTTGACTCTATCCGTAGAGATCAAGATC 4857  
QY 361 TGTGACATCATCTGAGAGGGGGAGACAGGGGGGCTTATAGGCGCATTTATTTGGCGGT 420  
DB 4858 TGTGACATCATCTGAGAGGGGGAGACAGGGGGGCTTATAGGCGCATTTATTTGGCGGT 4917  
QY 421 GGCTCTTGGGGTTGCAACTGCGGCAAAATTAACAGCGGCGCACTGTGATACAAAGCAA 480  
DB 4918 GGCTCTTGGGGTTGCAACTGCGGCAAAATTAACAGCGGCGCACTGTGATACAAAGCAA 4977  
QY 481 ACAAATGCTGCGCAACATCTCCGACTTTAAAGAGACATTTGCGCAACCAATGAGCGCT 540  
DB 4978 ACAAATGCTGCGCAACATCTCCGACTTTAAAGAGACATTTGCGCAACCAATGAGCGCT 5037  
QY 541 GCATGAGGTGACATGACGATTAATGCGCACTGACAGTGGCAAGTGGGAAGATGACGAGTT 600  
DB 5038 GCATGAGGTGACATGACGATTAATGCGCACTGACAGTGGCAAGTGGGAAGATGACGAGTT 5097  
QY 601 TGTATATGACCAATTTATATAAAACAGCTCAGGAATTAAGCTGATCAAAATTTGACAGCA 660  
DB 5098 TGTATATGACCAATTTATATAAAACAGCTCAGGAATTAAGCTGATCAAAATTTGACAGCA 5157  
QY 661 AGTTGTGTAGAGCTCAACCTGTACCTTAACCGAAATTAAGCTAAGATTTGCGACCAAAAT 720  
DB 5158 AGTTGTGTAGAGCTCAACCTGTACCTTAACCGAAATTAAGCTAAGATTTGCGACCAAAAT 5217  
QY 721 CACTTCACTGCTTTAAACAAAGCTGACTATTCAGGCACTTTAACAATCTAGCTGTGAGAAA 780  
DB 5218 CACTTCACTGCTTTAAACAAAGCTGACTATTCAGGCACTTTAACAATCTAGCTGTGAGAAA 5277  
QY 781 TATGATTAATCTTATTTGACTAAGTTAGGTGAGGAAACAATCAATCACTGATCAATTAATCG 840  
DB 5278 TATGATTAATCTTATTTGACTAAGTTAGGTGAGGAAACAATCAATCACTGATCAATTAATCG 5337  
QY 841 TAGCGGCTTAATCAACCGGTAAACCTATTTATTAAGACTCAAGACTCAATCTTTGGGTAT 900

DB 5338 TAGCGGCTTAATCAACCGGTAAACCTATTTATTAAGACTCAAGACTCAATCTTTGGGTAT 5397  
QY 901 ACAGTAATCTTACTACTTCACTGCGGAAACCTAAATATATGCTGCGCACTTATTTGAAGAC 960  
DB 5398 ACAGTAATCTTACTACTTCACTGCGGAAACCTAAATATATGCTGCGCACTTATTTGAAGAC 5457  
QY 961 CTATTCGCTAAGCAACAACAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
DB 5458 CTATTCGCTAAGCAACAACAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 5517  
QY 1021 GGTGCTTCTGTGTAGAAAGAACTTGACACCTCATAGTATGAACTGACTAGATTT 1080  
DB 5518 GGTGCTTCTGTGTAGAAAGAACTTGACACCTCATAGTATGAACTGACTAGATTT 5577  
QY 1081 ATATTGACAAAGAAATAGTAAAGTTCCCTAATGTCCTGATATTTATCTGCTGAGCGG 1140  
DB 5578 ATATTGACAAAGAAATAGTAAAGTTCCCTAATGTCCTGATATTTATCTGCTGAGCGG 5637  
QY 1141 CAATACGTGGCCCTGATATGATTAAGCAAGGCGCACTTAACACATACATGAC 1200  
DB 5638 CAATACGTGGCCCTGATATGATTAAGCAAGGCGCACTTAACACATACATGAC 5697  
QY 1201 TATCAAAAGTTCACTCATTCGCAACTGCAAGATGACAAACATGATGATGTTAAACCCGCC 1260  
DB 5698 TATCAAAAGTTCACTCATTCGCAACTGCAAGATGACAAACATGATGATGTTAAACCCGCC 5757  
QY 1261 GGGTATCATATCCGCAAACTATGAGAGCCGCTCTCTAATAGATTAACATCATGACAA 1320  
DB 5758 GGGTATCATATCCGCAAACTATGAGAGCCGCTCTCTAATAGATTAACATCATGACAA 5817  
QY 1321 TGTATTATCTTATAGCGGGAATTAACCTTAAGGCTCATAGTGGGAAATTCGATTAACCTATCA 1380  
DB 5818 TGTATTATCTTATAGCGGGAATTAACCTTAAGGCTCATAGTGGGAAATTCGATTAACCTATCA 5877  
QY 1381 GAAGAAATATCTCAATTAACAATTTCTCAAGTAATTAACAAGGAAATTTGATATCTCAAC 1440  
DB 5878 GAAGAAATATCTCAATTAACAATTTCTCAAGTAATTAACAAGGAAATTTGATATCTCAAC 5937  
QY 1441 TGAGCTTGGGAAATGTCAAACAACCTGATCAATATGCTTTGAATTAAGGAAAGCAA 1500  
DB 5938 TGAGCTTGGGAAATGTCAAACAACCTGATCAATATGCTTTGAATTAAGGAAAGCAA 5997  
QY 1501 CAGAAAATAGACAAAGTCAATGTCAAATCTGACTAGACATCTGCTCATTAACCTATAT 1560  
DB 5998 CAGAAAATAGACAAAGTCAATGTCAAATCTGACTAGACATCTGCTCATTAACCTATAT 6057  
QY 1561 CGTTTGAATCATATCTCTGTTTGTGATATCTTAAGCTGATTTCTAGATGCTATCCT 1620  
DB 6058 CGTTTGAATCATATCTCTGTTTGTGATATCTTAAGCTGATTTCTAGATGCTATCCT 6117  
QY 1621 AATGTACAAAGCAAAAGCGGCAAAACCTTATTATGCTTGGGAAATTAATCTTACA 1680  
DB 6118 AATGTACAAAGCAAAAGCGGCAAAACCTTATTATGCTTGGGAAATTAATCTTACA 6177  
QY 1681 TCAGATGAGGCACTACAAAAAATGTGAACAAGATGAGGAAAGGTTTCCCTAATAG 1740  
DB 6178 TCAGATGAGGCACTACAAAAAATGTGAACAAGATGAGGAAAGGTTTCCCTAATAG 6237  
QY 1741 TAAATTTGTGAAAGTTCTGCTAGTCTGTCAAGTTCAAGAGTTTAAGAAAAATCAACGGGT 1800  
DB 6238 TAAATTTGTGAAAGTTCTGCTAGTCTGTCAAGTTCAAGAGTTTAAGAAAAATCAACGGGT 6297  
QY 1801 TGTATGATGACAAAGGCGATATACGGGTTGAACGGGTAAGAGAGGCGCGCCCTCAATTTGC 1860  
DB 6298 TGTATGATGACAAAGGCGATATACGGGTTGAACGGGTAAGAGAGGCGCGCCCTCAATTTGC 6357  
QY 1861 GAGCGAGGCTTCAACAACCTCCGTTCTACCGCTTCAACCGACCAACAGTCTCTCAATCATGAC 1920  
DB 6358 GAGCGAGGCTTCAACAACCTCCGTTCTACCGCTTCAACCGACCAACAGTCTCTCAATCATGAC 6417  
QY 1921 CGCGCGCTTAAGCAAGTTGCGTTAAGAAATGATGAAGAGGCAAAAATACATGGCGC 1980

```
Db 6418 GCGCCGTTAGCCAAAGTTCCGTTAGAGATGATGAAAGAGCGCAAAAATACATGGCC 6477
Qy 1981 TTGATATTCGGATTCGATCTTATTTCTTAAACAGTAGTACCTTGCTATATCTGAGCC 2040
Db 6478 TTGATATTCGGATTCGATCTTATTTCTTAAACAGTAGTACCTTGCTATATCTGAGCC 6537
Qy 2041 TCCCTTTTATATAGCATGGGGCTAGACACCTAGCCGATCTTGTAGGCACTACCTAGG 2100
Db 6538 TCCCTTTTATATAGCATGGGGCTAGACACCTAGCCGATCTTGTAGGCACTACCTAGG 6597
Qy 2101 ATTTCCAGGGAGAGAAAGAAATTAACATCACTAGTTCGATCAATCAAGATGTAGAT 2160
Db 6598 ATTTCCAGGGAGAGAAAGAAATTAACATCACTAGTTCGATCAATCAAGATGTAGAT 6657
Qy 2161 AGATATATATAGCAAGTGGCCCTTGAAGTCCGTTGGCAATTTAAATAGTACACCA 2220
Db 6658 AGATATATATAGCAAGTGGCCCTTGAAGTCCGTTGGCAATTTAAATAGTACACCA 6717
Qy 2221 ATATGAAACGCAATPAACATCTCTCTTATGAGATTAATGAGCTGCAACCAAGTGG 2280
Db 6718 ATATGAAACGCAATPAACATCTCTCTTATGAGATTAATGAGCTGCAACCAAGTGG 6777
Qy 2281 TGGGGGGCACTATCCATGACCCGATTAATAGGGGGATAGGCAAAAGTCAATTTGTA 2340
Db 6778 TGGGGGGCACTATCCATGACCCGATTAATAGGGGGATAGGCAAAAGTCAATTTGTA 6837
Qy 2341 GATGATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
Db 6838 GATGATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6897
Qy 2401 ATCCCGGCGCTTACTACAGATCAGTTGCACTGCAATACCTCATTTGACATGAGTCT 2460
Db 6898 ATCCCGGCGCTTACTACAGATCAGTTGCACTGCAATACCTCATTTGACATGAGTCT 6957
Qy 2461 ACCCATTAATGCTACACCCATTAATGTAATTTGTCTGATGCAAGATCACTCATTTCA 2520
Db 6958 ACCCATTAATGCTACACCCATTAATGTAATTTGTCTGATGCAAGATCACTCATTTCA 7017
Qy 2521 TATGATATTTAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
Db 7018 TATGATATTTAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7077
Qy 2581 ACTGCGGTTCCATCAACCTGAGACACACCCAAATCGAAGTCTTGGCATGTGAGTCA 2640
Db 7078 ACTGCGGTTCCATCAACCTGAGACACACCCAAATCGAAGTCTTGGCATGTGAGTCA 7137
Qy 2641 ACTCCCTGGTGTGATATGCTGTCTGAAAGTCAAGATGCAAGAGAAAGATTAAT 2700
Db 7138 ACTCCCTGGTGTGATATGCTGTCTGAAAGTCAAGATGCAAGAGAAAGATTAAT 7197
Qy 2701 AACTGACTGCTCCCTAGCGGAGTGGTACATGGAGGTTAGGCTTCAGCGGCAATACAC 2760
Db 7198 AACTGACTGCTCCCTAGCGGAGTGGTACATGGAGGTTAGGCTTCAGCGGCAATACAC 7257
Qy 2761 GAAAGGACCTAGATGATCAACATTAATCGGGGATGCTGGCCAACTACCCAGAGTA 2820
Db 7258 GAAAGGACCTAGATGATCAACATTAATCGGGGATGCTGGCCAACTACCCAGAGTA 7317
Qy 2821 GGGGGTGGATCTTTTATTTGACAGCGCGGTATGTTCTCAGTCTACGAGGGTTAAACC 2880
Db 7318 GGGGGTGGATCTTTTATTTGACAGCGCGGTATGTTCTCAGTCTACGAGGGTTAAACC 7377
Qy 2881 AATTCAACCACTGATCACTGTACAGAAAGGAAATATGATATCAAGCGATACCAATAC 2940
Db 7378 AATTCAACCACTGATCACTGTACAGAAAGGAAATATGATATCAAGCGATACCAATAC 7437
Qy 2941 ACATGCCAGATGAGCAAGATCAACAGATGCAATGCGCAAGTCTTCTATAGGCTGGA 3000
Db 7438 ACATGCCAGATGAGCAAGATCAACAGATGCAATGCGCAAGTCTTCTATAGGCTGGA 7497
Qy 3001 CGGTTTGGTGGAAACGATACAGAGGCTATCTTATCTATCAAGTGTCAACATCCTTA 3060
Db 7498 CGGTTTGGTGGAAACGATACAGAGGCTATCTTATCTATCAAGTGTCAACATCCTTA 7557
```

```
Qy 3061 GCGAAGACCCGTAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
Db 7558 GCGAAGACCCGTAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7617
Qy 3121 AGAATTTCTACAGAGGAGCAATCTCTTCTGATGATGATGATGATGATGATGATGATGAT 3180
Db 7618 AGAATTTCTACAGAGGAGCAATCTCTTCTGATGATGATGATGATGATGATGATGATGAT 7677
Qy 3181 CCCCGTTATATATATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
Db 7678 CCCCGTTATATATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7737
Qy 3241 ACATTCATGCTTCACTCGGCGAGTATGATGATGATGATGATGATGATGATGATGATGAT 3300
Db 7738 ACATTCATGCTTCACTCGGCGAGTATGATGATGATGATGATGATGATGATGATGATGAT 7797
Qy 3301 AACTCGTGTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3358
Db 7798 AACTCGTGTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7855

RESULT 4
ADH62844
ID ADH62844 standard; DNA; 15186 BP.
XX
XX ADH62844;
XX
XX 25-MAR-2004 (first entry)
XX
XX Newcastle disease virus (NDV) HN gene.
DE Newcastle disease virus (NDV) HN gene.
XX
XX Multivalent DNA vaccine; ovo injection; avian viral disease; fowl;
KW immune response; gene; Newcastle disease virus; NDV;
KW haemagglutinin neuraminidase; ds; HN.
XX
XX Newcastle disease virus.
OS Newcastle disease virus.
XX
XX US2003175291-A1.
XX
XX 18-SEP-2003.
XX
XX 04-MAR-2003; 2003US-00377718.
XX
XX 08-MAR-2002; 2002US-0362547P.
XX
XX (KUOT/) KUO T Y.
XX
XX KUO TY;
XX
XX WPI; 2003-898502/82.
XX
XX Multiple DNA vaccine for in ovo injection, useful for inducing protective
PT immune response against the avian viral diseases in fowl, comprises two
PT or more DNA constructs.
XX
XX Claim 10; SEQ ID NO 3; 26pp; English.
XX
XX The invention relates to multiple and multivalent DNA vaccine for in ovo
CC injection which comprises two or more DNA constructs, where each DNA
CC construct expresses an antigenic protein of an avian virus causing avian
CC viral disease in fowl. The antigenic protein of the avian virus is
CC capable of inducing a protective immune response against the avian viral
CC disease in the fowl. The vaccine is useful for inducing protective immune
CC response against the avian viral diseases in fowl. The present sequence
CC is Newcastle disease virus (NDV) haemagglutinin neuraminidase (HN) gene
CC used in multiple and multivalent DNA vaccine.
XX
XX Sequence 15186 BP; 4431 A; 3542 C; 3464 G; 3749 T; 0 U; 0 Other;
SQ
Query Match 99.9%; Score 3353.2; DB 10; Length 15186;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```



Qy 1 ACGGGTAGAAGATTCTGGATTCGCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60  
Db 4498 ACGGGTAGAAGATTCTGGATTCGCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 4557  
Qy 61 TTCTACCAAGAACCCAGACACTTATGATGCTGACTATACCGGGTTGGCTGGCACTGAGATTG 120  
Db 4558 TTCTACCAAGAACCCAGACACTTATGATGCTGACTATACCGGGTTGGCTGGCACTGAGATTG 4617  
Qy 121 CATCTGCCGGCAAACTCCATTGATGGCAGGCTCTTGAGCTGCAGGAAATTGTTGTTAC 180  
Db 4618 CATCTGCCGGCAAACTCCATTGATGGCAGGCTCTTGAGCTGCAGGAAATTGTTGTTAC 4677  
Qy 181 AGGAGCAAAAGCCGTCACAATATACCTCATCCAGACAGGATCAATCATAGTTAAAGT 240  
Db 4678 AGGAGCAAAAGCCGTCACAATATACCTCATCCAGACAGGATCAATCATAGTTAAAGT 4737  
Qy 241 CTTCCGCAATCTGCGCAAGATTAAGAGGCAATGTCGCAAAAGCCCTTGGATGATCA 300  
Db 4738 CTTCCGCAATCTGCGCAAGATTAAGAGGCAATGTCGCAAAAGCCCTTGGATGATCA 4797  
Qy 301 CAGGACATTGACCACTTTGCTCACCCCTTGGTGACTTATCGGTAGATTAACAAGATC 360  
Db 4798 CAGGACATTGACCACTTTGCTCACCCCTTGGTGACTTATCGGTAGATTAACAAGATC 4857  
Qy 361 TGTGACTACACTGTGAGAGGGGGAGACAGGGGCGCTTATAGGCGCAATTATGGCGGTGT 420  
Db 4858 TGTGACTACACTGTGAGAGGGGGAGACAGGGGCGCTTATAGGCGCAATTATGGCGGTGT 4917  
Qy 421 GGGCTTTGGGGTTCACAATGCGCAAAATTAACGCGCGCGAGCTCTGATTAACAAGCA 480  
Db 4918 GGGCTTTGGGGTTCACAATGCGCAAAATTAACGCGCGCGAGCTCTGATTAACAAGCA 4977  
Qy 481 ACAAATAGTCCCAACATCTCCGCACTTAAAGAGAGATGGCGCAACAATGAGGCTGT 540  
Db 4978 ACAAATAGTCCCAACATCTCCGCACTTAAAGAGAGATGGCGCAACAATGAGGCTGT 5037  
Qy 541 GCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGATT 600  
Db 5038 GCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGATT 5097  
Qy 601 TGTATATGACCAATTTATATAAACAGCTCAGGAATTAAGCTGCATCAAAATTGCAACGA 660  
Db 5098 TGTATATGACCAATTTATATAAACAGCTCAGGAATTAAGCTGCATCAAAATTGCAACGA 5157  
Qy 661 AGTTGGTGAAGTCAACCTGTACCTTAACCGAATTGACTACATTTGGGACCAAAAT 720  
Db 5158 AGTTGGTGAAGTCAACCTGTACCTTAACCGAATTGACTACATTTGGGACCAAAAT 5217  
Qy 721 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGA 780  
Db 5218 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGA 5277  
Qy 781 TATGATTAATCTTATTTGACTTAAGTTAGGTGAAGCAATCACTCAGCTCATTAATCGG 840  
Db 5278 TATGATTAATCTTATTTGACTTAAGTTAGGTGAAGCAATCACTCAGCTCATTAATCGG 5337  
Qy 841 TAGCGGTTTAAATCAACGGTAAACCTATTTCTATAGACTCAAGACTCAACTCTTGGGAT 900  
Db 5338 TAGCGGTTTAAATCAACGGTAAACCTATTTCTATAGACTCAAGACTCAACTCTTGGGAT 5397  
Qy 901 ACAGGTACTCTACTCTCAGTCGGAACCTTAATATATGCGTGCACCTACTTGGAAAC 960  
Db 5398 ACAGGTACTCTACTCTCAGTCGGAACCTTAATATATGCGTGCACCTACTTGGAAAC 5457  
Qy 961 CTTATCCGTAGACCAACAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGGTGAACA 1020  
Db 5458 CTTATCCGTAGACCAACAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGGTGAACA 5517  
Qy 1021 GGTTCGGTTCTGTATAGAAGAACTTGAACCTCATCTGTTATGAACCTGACTTAAGTTT 1080  
Db 5518 GGTTCGGTTCTGTATAGAAGAACTTGAACCTCATCTGTTATGAACCTGACTTAAGTTT 5577

Qy 1081 ATATTGTACAGAATAGTAACTTCCCTATGTCCTCCCTGGATTTATTTCTGCTTGAAGCG 1140  
Db 5578 ATATTGTACAGAATAGTAACTTCCCTATGTCCTCCCTGGATTTATTTCTGCTTGAAGCG 5637  
Qy 1141 CAATAGCTGGCGCTGTATGTAATCAAGACCGAAGGCGCACTTACTACACCATATGAC 1200  
Db 5638 CAATAGCTGGCGCTGTATGTAATCAAGACCGAAGGCGCACTTACTACACCATATGAC 5697  
Qy 1201 TATCAAGGTTCACTGATCGCAACTGCAAGATGACAACTGTAGTGTAAACCCGCC 1260  
Db 5698 TATCAAGGTTCACTGATCGCAACTGCAAGATGACAACTGTAGTGTAAACCCGCC 5757  
Qy 1261 GGGTATCATATCGCAAAACTATGAGAGCGGTGTCTTATATGATTAACATCAAGCA 1320  
Db 5758 GGGTATCATATCGCAAAACTATGAGAGCGGTGTCTTATATGATTAACATCAAGCA 5817  
Qy 1321 TGTATTATCTTATAGGGGGATTACTTTAAGGCTCAGTGGGGAATGATGTAACTTATCA 1380  
Db 5818 TGTATTATCTTATAGGGGGATTACTTTAAGGCTCAGTGGGGAATGATGTAACTTATCA 5877  
Qy 1381 GAAGAAATCTCAATCAAGATTTCTAAGTAATATTAACAGGCAATCTTGATATCTCAAC 1440  
Db 5878 GAAGAAATCTCAATCAAGATTTCTAAGTAATATTAACAGGCAATCTTGATATCTCAAC 5937  
Qy 1441 TGAAGTTGGGAATGTCAACAATCGATCAGTAATGCTTTGAATATAGTAAAGCA 1500  
Db 5938 TGAAGTTGGGAATGTCAACAATCGATCAGTAATGCTTTGAATATAGTAAAGCA 5997  
Qy 1501 CAGAAACTGACAAAGTCAATGTCAAACTGATGACATCTGCTCAATTACTTAT 1560  
Db 5998 CAGAAACTGACAAAGTCAATGTCAAACTGATGACATCTGCTCAATTACTTAT 6057  
Qy 1561 CGTTTGACTATCATATCTCTGTTTTTGGTATATTAATAGCTGATTTAGCATGTCACT 1620  
Db 6058 CGTTTGACTATCATATCTCTGTTTTTGGTATATTAATAGCTGATTTAGCATGTCACT 6117  
Qy 1621 AATGTACAGCAAAAGGCGCAACAACCTTATTAAGCTTGGGAATTAATCTTGA 1680  
Db 6118 AATGTACAGCAAAAGGCGCAACAACCTTATTAAGCTTGGGAATTAATCTTGA 6177  
Qy 1681 TCAAGTAGAGCCACTACAAATAATGTGAACAGATGAGGAAGAAAGTTCCCTATAG 1740  
Db 6178 TCAAGTAGAGCCACTACAAATAATGTGAACAGATGAGGAAGAAAGTTCCCTATAG 6237  
Qy 1741 TAAATTTGTGAAGATTTCTGTAGTCTGTCAATTCAGAGATTAAAGAAAACTACCGGT 1800  
Db 6238 TAAATTTGTGAAGATTTCTGTAGTCTGTCAATTCAGAGATTAAAGAAAACTACCGGT 6297  
Qy 1801 TGTATGATGACCAAGACGATATACGGGTGAACGGTAAAGAGGCGCCCTCAATTGC 1860  
Db 6298 TGTATGATGACCAAGACGATATACGGGTGAACGGTAAAGAGGCGCCCTCAATTGC 6357  
Qy 1861 GAGCCAGGCTTCAACACCTCCGTTCAACGCTTCAACGACAGCTCAATCATAGGAC 1920  
Db 6358 GAGCCAGGCTTCAACACCTCCGTTCAACGCTTCAACGACAGCTCAATCATAGGAC 6417  
Qy 1921 CGCGCGTTTACCAAGTTGCGTTAGAGAAATGATGAAGGCAAAAAATACATGGCGC 1980  
Db 6418 CGCGCGTTTACCAAGTTGCGTTAGAGAAATGATGAAGGCAAAAAATACATGGCGC 6477  
Qy 1981 TTGATATTCGGATTGCAATCTTATTTCTTAACAGTATGACTTTGGCTATATCTGAGCC 2040  
Db 6478 TTGATATTCGGATTGCAATCTTATTTCTTAACAGTATGACTTTGGCTATATCTGAGCC 6537  
Qy 2041 TCCCTTTATATATGATGAGGCGCTAGCAACCTAGGCACTTGTATAGGCAATACGACTAGG 2100  
Db 6538 TCCCTTTATATATGATGAGGCGCTAGCAACCTAGGCACTTGTATAGGCAATACGACTAGG 6597  
Qy 2101 ATTTCCAGGCGAGAAAGATTAATCATCTACACTTGGTTCCAATCAAGATGATAGAT 2160  
Db 6598 ATTTCCAGGCGAGAAAGATTAATCATCTACACTTGGTTCCAATCAAGATGATAGAT 6657  
Qy 2161 AGGATATATAGCAAGTGGCCCTTGAATCTCCGTTGGCATTTGTTAAATACAGAACCA 2220



```
Db 6658 AGATATATAAGCAAGTGGCCCTTGAGTCTCGTTGGCATTTGTAATAATCGAAGCCCA 6717
Qy 2221 ATATAGAACGGAATAACATCTCTCTTATGAGTTATGAGGCGCAACACAGTGGG 2280
Db 6718 ATATAGAACGGAATAACATCTCTCTTATGAGTTATGAGGCGCAACACAGTGGG 6777
Qy 2281 TGGGGGACCTATCATGACCCAGATTATAGGGGGATAGGCMAAGAACTCATTTGTA 2340
Db 6778 TGGGGGACCTATCATGACCCAGATTATAGGGGGATAGGCMAAGAACTCATTTGTA 6837
Qy 2341 GATGATGCTAGTGAATGTCACATCTCTATTCCTCTGCAATTTCAAGAACATCTGAATTTT 2400
Db 6838 GATGATGCTAGTGAATGTCACATCTCTATTCCTCTGCAATTTCAAGAACATCTGAATTTT 6897
Qy 2401 ATCCGGGCGCTACTACAGATCAGTGGTGCATCGAAATACCTCATTTGACATGAGTCT 2460
Db 6898 ATCCGGGCGCTACTACAGATCAGTGGTGCATCGAAATACCTCATTTGACATGAGTCT 6957
Qy 2461 ACCCATTAATGCTACACCCATATATGATATTTGTCTGGATCAGAGATCACTCATTTCA 2520
Db 6558 ACCCATTAATGCTACACCCATATATGATATTTGTCTGGATCAGAGATCACTCATTTCA 7017
Qy 2521 TATCAGTATTTAGACATTTGTGTGCTCCGACATCTGCAACAGGAGGATTTCTTTTCT 2580
Db 7018 TATCAGTATTTAGACATTTGTGTGCTCCGACATCTGCAACAGGAGGATTTCTTTTCT 7077
Qy 2581 ACTCTGGGTTCCATCAACCTGGAAGACACCCAAAATCGGAAGTCTTGACAGTGTAGTGA 2640
Db 7078 ACTCTGGGTTCCATCAACCTGGAAGACACCCAAAATCGGAAGTCTTGACAGTGTAGTGA 7137
Qy 2641 ACTCCCGTGGTGTGATATGATCTGTGCTGAAAGTCACGAGACAGAGAGAAAGATTAT 2700
Db 7138 ACTCCCGTGGTGTGATATGATCTGTGCTGAAAGTCACGAGACAGAGAGAAAGATTAT 7197
Qy 2701 AACTCAGCTGTCCCTACGCGGATGATGATGAGAGGTTAGGTTTGAAGGCACTGACAC 2760
Db 7198 AACTCAGCTGTCCCTACGCGGATGATGATGAGAGGTTAGGTTTGAAGGCACTGACAC 7257
Qy 2761 GAAAAGACCTAGATGTCACAACTATTCGGGGACCTGGGTCGCACTACCCAGAGTA 2820
Db 7258 GAAAAGACCTAGATGTCACAACTATTCGGGGACCTGGGTCGCACTACCCAGAGTA 7317
Qy 2821 GGGGGTGGATCTTTTATTTGACAGCGCGATAGTGTCTCAGTCTACGAGGGTTAAACC 2880
Db 7318 GGGGGTGGATCTTTTATTTGACAGCGCGATAGTGTCTCAGTCTACGAGGGTTAAACC 7377
Qy 2881 AATTCAACCAAGTGAACCTGTAACAGAAAGGAAATATGATATACAGCGATACATGAC 2940
Db 7378 AATTCAACCAAGTGAACCTGTAACAGAAAGGAAATATGATATACAGCGATACATGAC 7437
Qy 2941 ACATGCCCAAGTGAAGCAAGATCTACCAATTTGAAATGCGCAAGTCTTCTATAGCTTGA 3000
Db 7438 ACATGCCCAAGTGAAGCAAGATCTACCAATTTGAAATGCGCAAGTCTTCTATAGCTTGA 7497
Qy 3001 CGGTTGTGGGAAACGATACAGAGGCTATCTTATCTACAGAGTGTCAACATCTCTTA 3060
Db 7498 CGGTTGTGGGAAACGATACAGAGGCTATCTTATCTACAGAGTGTCAACATCTCTTA 7557
Qy 3061 GGGCAGAACCCGATAGTGAACCTGTAACCGCCCAACAGTCACTCATGAGGGGCGAAGGC 3120
Db 7558 GGGCAGAACCCGATAGTGAACCTGTAACCGCCCAACAGTCACTCATGAGGGGCGAAGGC 7617
Qy 3121 AGAATTTCTACAGTAGGACATCTCATTTCTTTGTATCAAGAGGTCATCACTTCTCT 3180
Db 7618 AGAATTTCTACAGTAGGACATCTCATTTCTTTGTATCAAGAGGTCATCACTTCTCT 7677
Qy 3181 CCGCGGTATATATCCATAGACAGTCAAGCAAAAAGCACTCTTCAATGCTTAT 3240
Db 7678 CCGCGGTATATATCCATAGACAGTCAAGCAAAAAGCACTCTTCAATGCTTAT 7737
Qy 3241 ACATTCATAGCTTCACTGCGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCC 3300
```

```
Db 7738 ACATTCATAGCTTCACTGCGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCC 7797
Qy 3301 AACTCGTGTGTACTGAGATCTATACAGATCCATATCCCTATCTTATAGAAACC 3358
Db 7798 AACTCGTGTGTACTGAGATCTATACAGATCCATATCCCTATCTTATAGAAACC 7855

RESULT 5
ADM78414
ID ADM78414 standard; cDNA; 5292 BP.
XX
AC ADM78414;
XX
DT 03-JUN-2004 (first entry)
XX
DE Newcastle disease virus recombinant cDNA #10.
XX
KW Newcastle disease virus; T7 RNA polymerase; Hep-2 cell; influenza virus;
KW infectious bursal disease virus; rotavirus; infectious bronchitis virus;
KW chicken anaemia virus; Marek's disease virus; avian leukosis virus;
KW avian adenovirus; avian pneumovirus;
KW severe acute respiratory syndrome-causing virus; SARS;
KW human respiratory syncytial virus; human immunodeficiency virus;
KW hepatitis virus; measles virus; mumps virus; antiviral; ss.
XX
OS Newcastle disease virus.
XX
PN US2003224017-A1.
XX
PD 04-DEC-2003.
XX
PF 19-MAY-2003; 2003US-00440419.
XX
PR 05-MAY-2000; 2000WO-US006700.
PR 06-MAR-2002; 2002US-00926431.
PR 17-MAY-2002; 2002US-0381462P.
XX
PA (SAMA/) SAMAL S K.
PA (HUAN/) HUANG Z.
XX
PI Samal SK, Huang Z;
XX
DR WPI; 2004-051891/05.
XX
PT Novel antigenomic RNA of Newcastle disease virus having NP, P, M, F, HN,
PT L gene and foreign nucleotide complex inserted before NP gene, between
PT P, M genes and/or between HN, L gene, useful for producing vaccine
PT vector.
XX
PS Example 3; Page 12-14; 41pp; English.
XX
CC The invention relates to an antigenomic RNA of Newcastle disease virus
CC having NP, P, M, F, HN and L genes in the 5'-3' direction, with foreign
CC nucleotide complexes inserted between genes. The invention also relates
CC to cDNA related to the RNA, a plasmid comprising the cDNA, a cell
CC comprising the RNA, cDNA or plasmid, a method of preparing the RNA and a
CC recombinant Newcastle disease virus comprising the RNA. The RNA is useful
CC for producing a recombinant Newcastle disease virus by providing cells
CC capable of synthesizing T7 RNA polymerase, transfecting the cells with a
CC plasmid comprising cDNA or a protein of interest to obtain transfected
CC cells in a medium and isolating Newcastle disease virus from a
CC supernatant of the medium, where the cells capable synthesizing T7 RNA
CC polymerase are from a cell line expressing T7 RNA polymerase or plant
CC cells, mammalian cells, avian cells or Hep-2 cells infected with a
CC vaccinia virus that can synthesize T7 RNA polymerase. The recombinant
CC virus is useful for vaccinating an avian animal against Newcastle disease
CC or an avian pathogen chosen from influenza virus, infectious bursal
CC disease virus, rotavirus, infectious bronchitis virus, chicken anaemia
CC virus, Marek's disease virus, avian leukosis virus, avian adenovirus and
CC avian pneumovirus, where the avian animal is in need of the immunisation,
CC which involves administering the recombinant virus to the avian animal,
CC where the open reading frame of the foreign gene encodes an immunogenic
CC protein of the avian pathogen against which the avian animal is
```

CC Immunized. The recombinant virus is also useful for immunising a mammal  
CC against a non-avian pathogen such as severe acute respiratory syndrome-  
CC causing virus (SARS virus), human respiratory syncytial virus, human  
CC immunodeficiency virus, hepatitis virus, measles virus or mumps virus.  
CC This sequence represents Newcastle disease virus recombinant cDNA of the  
CC invention.

XX Sequence 5292 BP; 1574 A; 1207 C; 1186 G; 1324 T; 0 U; 1 Other;

Query Match 96.5%; Score 3240.4; DB 12; Length 5292;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 3267; Conservative 1; Mismatches 8; Indels 2; Gaps 2;

QY 82 TATGATGCTGATATCCGGGTGGCTGGCATGAGTTGATCTGTCCGGCAATCTCCAT 141  
DB 1 TATGATGCTGATATCCGGGTGGCTGGCTGATGATGATCTGTCCGGCAATCTCCAT 60  
QY 142 TGATGGCAGGCTTTTGCAAGTCGAGAAATTTGGTTACAGAGAACAAAGCCGTCAACAT 201  
DB 61 TGATGGCAGGCTTTTGCAAGTCGAGAAATTTGGTTACAGAGAACAAAGCCGTCAACAT 120  
QY 202 ATACACCTCATCCAGACAGGATCAATCATAGTTAGCTCTCCGAATCGCCCAAGGA 261  
DB 121 ATACACCTCATCCAGACAGGATCAATCATAGTTAGCTCTCTCCGAATCTGCCCAAGGA 180  
QY 262 TAAAGAGCATGTGCGAAAGCCCTTGATGATGATGATGATGATGATGATGATGATGAT 321  
DB 181 TAAAGAGCATGTGCGAAAGCCCTTGATGATGATGATGATGATGATGATGATGATGAT 240  
QY 322 CACCCCTTTGGTGAATCTATCCGTAGATACAAAGATCTGTGATCTGATCTGAGAGGG 381  
DB 241 CACCCCTTTGGTGAATCTATCCGTAGATACAAAGATCTGTGATCTGATCTGAGAGGG 300  
QY 382 GAGACAGAGGCGCTTATAGCGGCGCATTTATGGCGGTGGCTTTGAGGTTGCAATGC 441  
DB 301 GAGACAGAGGCGCTTATAGCGGCGCATTTATGGCGGTGGCTTTGAGGTTGCAATGC 360  
QY 442 CGCAACAATTAACAGCGCGCGAGCTGTGATACAAAGCAAAATCTGCAACATCT 501  
DB 361 CGCAACAATTAACAGCGCGCGAGCTGTGATACAAAGCAAAATCTGCAACATCT 420  
QY 502 CGCACTTAAAGAGCATTTGCCGCAACCAATGAGGCTGTGATGAGTCACTGACGAT 561  
DB 421 CGCACTTAAAGAGCATTTGCCGCAACCAATGAGGCTGTGATGAGTCACTGACGAT 480  
QY 562 ATGCAACTAGAGTGGAGTGGGAAAGATGACAGCTTTGTATGACCAATTAATTA 621  
DB 481 ATGCAACTAGAGTGGAGTGGGAAAGATGACAGCTTTGTATGACCAATTAATTA 540  
QY 622 AACAGCTCAGGAATTAGATGATCAAAATTTGACAGCAAGTTGGTGTAGAGCTCA 681  
DB 541 AACAGCTCAGGAATTAGATGATCAAAATTTGACAGCAAGTTGGTGTAGAGCTCA 600  
QY 682 GTACCTTAACCGAATTGATCAAGTATTCGACCAAAATCACTTCACTGTTTAAACAA 741  
DB 601 GTACCTTAACCGAATTGATCAAGTATTCGACCAAAATCACTTCACTGTTTAAACAA 660  
QY 742 GGTGACATTCAGGCACTTTACATCTAGCTGTGGAAATATGGAATTAATTAATGA 801  
DB 661 GGTGACATTCAGGCACTTTACATCTAGCTGTGGAAATATGGAATTAATTAATGA 720  
QY 802 GTTAGGTGAGGAAACAATCAATCACTCAGCTCAATTAATGAGCGCTTAATCAACGG 861  
DB 721 GTTAGGTGAGGAAACAATCAATCACTCAGCTCAATTAATGAGCGCTTAATCAACGG 780  
QY 862 CCTTATTTATACGATCTACAGATCTCAACTCTTGGGTATACAGGTAACTCTTCACT 921  
DB 781 CCTTATTTATACGATCTACAGATCTCAACTCTTGGGTATACAGGTAACTCTTCACT 840  
QY 922 CGGGAACCTAATTAATGAGTGGCACTACTTGGAAACCTTATCGGTAAGCAACAG 981  
DB 841 CGGGAACCTAATTAATGAGTGGCACTACTTGGAAACCTTATCGGTAAGCAACAG 900

QY 982 GGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACAGGTGCTGTGTATGAGA 1041  
DB 901 GGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACAGGTGCTGTGTATGAGA 960  
QY 1042 ACTGACACCTCATCTGATGATGAGAACTGACTTATATGATGATGATGATGATGAT 1101  
DB 961 ACTGACACCTCATCTGATGATGAGAACTGACTTATATGATGATGATGATGATGAT 1020  
QY 1102 GTTCCCTATGTCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1161  
DB 1021 GTTCCCTATGTCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
QY 1162 CTCAAAAGCCGAGGCGCACTTACTACACATATATATATATATATATATATATAT 1221  
DB 1081 CTCAAAAGCCGAGGCGCACTTACTACACATATATATATATATATATATATATAT 1140  
QY 1222 CAATGCAAGATGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1281  
DB 1141 CAATGCAAGATGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200  
QY 1282 TGGAGAAAGCGGTGCTCTAAATAGATTAACAATCATGCAATGTTTATCTTAAAGCGGAT 1341  
DB 1201 TGGAGAAAGCGGTGCTCTAAATAGATTAACAATCATGCAATGTTTATCTTAAAGCGGAT 1260  
QY 1342 AACTTTAAGGCTCAGTGGGGAATTCAGATGATCTTATCAGAAATATCTCAATACAGA 1401  
DB 1261 AACTTTAAGGCTCAGTGGGGAATTCAGATGATCTTATCAGAAATATCTCAATACAGA 1320  
QY 1402 TTCTCAAGTATATATATACAGCAATCTGATATCTCAACTGAGCTTGGAGATGCAACA 1461  
DB 1321 TTCTCAAGTATATATATACAGCAATCTGATATCTCAACTGAGCTTGGAGATGCAACA 1380  
QY 1462 CTCGATCAGTATGCTTTGATTAAGATTAAGAGAAAGCAAGAAACTGACCAAGTCAA 1521  
DB 1381 CTCGATCAGTATGCTTTGATTAAGATTAAGAGAAAGCAAGAAACTGACCAAGTCAA 1440  
QY 1522 TGTCAAACCTGACATGACATCTGCTCATTAATATATGTTTGAATCTATATCTCT 1581  
DB 1441 TGTCAAACCTGACATGACATCTGCTCATTAATATGTTTGAATCTATATCTCT 1500  
QY 1582 TGTTTTGGTATCTTACGCTGATTTACAGATGCTACCTAATGATGACAAAGAGGCA 1641  
DB 1501 TGTTTTGGTATCTTACGCTGATTTACAGATGCTACCTAATGATGATGACAAAGAGGCA 1560  
QY 1642 ACAAACCTTATATGAGCTTGGGAAATATATCTGATGATGATGATGATGATGAT 1701  
DB 1561 ACAAACCTTATATGAGCTTGGGAAATATATCTGATGATGATGATGATGATGAT 1620  
QY 1702 AATGTGAACACAGATGAGAACGAGGTTTCCCTAATATGATATTTGTGTGAAGTCTGG 1761  
DB 1621 AATGTGAACACAGATGAGAACGAGGTTTCCCTAATATGATATTTGTGTGAAGTCTGG 1680  
QY 1762 TAGTCTGTCAGTTCAGAGATTTAAGAAACCTACCGTGTGATGATGACAAAGAGAT 1821  
DB 1681 TAGTCTGTCAGTTCAGAGATTTAAGAAACCTACCGTGTGATGATGATGACAAAGAGAT 1740  
QY 1822 ATAGCGGTAGAAAGGTGAGAGAGGCGCCCTCAATTCGAGCGAGCTTACAACTCC 1881  
DB 1741 ATAGCGGTAGAAAGGTGAGAGAGGCGCCCTCAATTCGAGCGAGCTTACAACTCC 1800  
QY 1882 GTTTCACCGCTTCAACGACACAGTCTCAATCATGAGACCGCGCTTACCAAGTTGG 1941  
DB 1801 GTTTCACCGCTTCAACGACACAGTCTCAATCATGAGACCGCGCTTACCAAGTTGG 1860  
QY 1942 TTAGAGAAATGATGAAGAGGCAAAATATATATGAGGCTGATATTCGGATTTGCAATC 2001  
DB 1861 TTAGAGAAATGATGAAGAGGCAAAATATATATGAGGCTGATATTCGGATTTGCAATC 1920  
QY 2002 TTATTTCTTAACAGATGACCTTGGCTATATCTGTAGCTCTCCCTTTATATAGATGGG 2061  
DB 1921 TTATTTCTTAACAGATGACCTTGGCTATATCTGTAGCTCTCCCTTTATATAGATGGG 1980  
QY 2062 GCTAGCACACCTAGCATCTTGTAGGCATACGACTAGATTTTTCAGGGCAGAAAG 2121

```
Db 1981 GCTAGCACCTTAGGATCTTGTAGCATACCGATAGGATTTCCAGGCGAAGAAAG 2040
Qy 2122 ATTAACATCTAGACTGTGTTCCAAATGAATAGATAGATATATATAGCAATGCGC 2181
Db 2041 ATTACATCTACCTTGGTTCCAAATGAGATGATAGATATATATAGCAATGCGC 2100
Qy 2182 CTGAGTCTCGGTGGGCAATGTTAAATACTGAGACCAATTTATGACGCAATACATCT 2241
Db 2101 CTGAGTCTCGGTGGGCAATGTTAAATACTGAGACCAATTTATGACGCAATACATCT 2160
Qy 2242 CTCTCTTATCAGATTTAATGAGCTGCAAAACAATGGGTGGGGGCACTATCCATGAC 2301
Db 2161 CTCTCTTATCAGATTTAATGAGCTGCAAAACAATGGGTGGGGGCACTATCCATGAC 2220
Qy 2302 CCAGATTTATAGGGGGGATAGGCAAAAGACTCATTTGATAGATGCTAGTATGATCA 2361
Db 2221 CCAGATTTATAGGGGGGATAGGCAAAAGACTCATTTGATAGATGCTAGTATGATCA 2280
Qy 2362 TCATTTCTATCCCTCTGCAATTTCAAGAACATCTGAATTTTATCCCGCGCTTACTACAGGA 2421
Db 2281 TCATTTCTATCCCTCTGCAATTTCAAGAACATCTGAATTTTATCCCGCGCTTACTACAGGA 2340
Qy 2422 TCAGGTTGCACTCCGAATACCTCATTTGACATGAGTCTACCCATTACTGCTACACCAT 2481
Db 2341 TCAGGTTGCACTCCGAATACCTCATTTGACATGAGTCTACCCATTACTGCTACACCAT 2400
Qy 2482 AATGTAATATTTGTGCGATGAGAGATACATCACTCATATCAATATTTAGCATTTGAT 2541
Db 2401 AATGTAATATTTGTGCGATGAGAGATACATCACTCATATCAATATTTAGCATTTGAT 2460
Qy 2542 GTGCTCCGAGACATCTGCAACAGGAGGGTATTTCTTCTACTGCTGCTTCCATCAACCTG 2601
Db 2461 GTGCTCCGAGACATCTGCAACAGGAGGGTATTTCTTCTACTGCTGCTTCCATCAACCTG 2520
Qy 2602 GACGACACCCAAATTCGGAAGTCTTGCACTGCTGAGTCACTCCCTGCGGTGATATG 2661
Db 2521 GACGACACCCAAATTCGGAAGTCTTGCACTGCTGAGTCACTCCCTGCGGTGATATG 2580
Qy 2662 CTGCTGCGAAGTCAAGGAGCAAGAGAGAAAGTTTAACTCACTGCTGCTTCCATCAACCTG 2721
Db 2581 CTGCTGCGAAGTCAAGGAGCAAGAGAGAAAGTTTAACTCACTGCTGCTTCCATCAACCTG 2640
Qy 2722 ATGCTACATGGAGGTTAGGTTGCAAGGAGGTTTCAACG-AAAAGACTAGATGTCAC 2780
Db 2641 ATGCTACATGGAGGTTAGGTTGCAAGGAGGTTTCAACG-AAAAGACTAGATGTCAC 2699
Qy 2781 AACATTAATCGGGGACTGGGTGGCCCACTACCCAGAGATAGGGGTGATCTTTATTGA 2840
Db 2700 AACATTAATCGGGGACTGGGTGGCCCACTACCCAGAGATAGGGGTGATCTTTATTGA 2759
Qy 2841 CAGCGCGGTATGTTCTCAAGTCTACGAGGGTTAAACCCTTATCAACCACTGACATGCT 2900
Db 2760 CAGCGCGGTATGTTCTCAAGTCTACGAGGGTTAAACCCTTATCAACCACTGACATGCT 2819
Qy 2901 ACAGAAAGGAAATATGATGATATCAAGCGATACAAATGACATGCCCCAGATGAGCAAGA 2960
Db 2820 ACAGAAAGGAAATATGATGATATCAAGCGATACAAATGACATGCCCCAGATGAGCAAGA 2879
Qy 2961 CTACCAAGTTGAAATGCGCAAGTCTTCTGATATAGCTTGAACGTTTGGTGGAAAACGAT 3020
Db 2880 CTACCAAGTTGAAATGCGCAAGTCTTCTGATATAGCTTGAACGTTTGGTGGAAAACGAT 2939
Qy 3021 ACAGAGGCTATCTTATCTATCAAGGTGTCAACATCTTTAGCGAAGCCCGGTACTGAC 3080
Db 2940 ACAGAGGCTATCTTATCTATCAAGGTGTCAACATCTTTAGCGAAGCCCGGTACTGAC 2999
Qy 3081 TGTAACGGCCAAACAGTCACTCATATGGGGGCGAAGAGAAATTTCAACAGTAGGAGAC 3140
Db 3000 TGTAACGGCCAAACAGTCACTCATATGGGGGCGAAGAGAAATTTCTCAACAGTAGGAGAC 3059
Qy 3141 ATCTCATTTCTTGTATCAACAGGAGGTATCATCTTCTCCCGGTATTTATATCCAT 3200
```

```
Db 3060 ATCTCATTTCTTGTATCAACAGGAGGTATCATCTTCTCTCCCGGTATTATATCTAT 3119
Qy 3201 GACAGTCAACAACAACAGGCACTTCTATAGTCTTATACATTCAAATGCTTCACTG 3260
Db 3120 GACAGTCAACAACAACAGGCACTTCTATAGTCTTATACATTCAAATGCTTCACTG 3179
Qy 3261 GCCAGTGTATCCCTTCCGAGGCTTACGCAAGATGCCCAACTGTGTGTTACTGAGCT 3320
Db 3180 GCCAGTGTATCCCTTCCGAGGCTTACGCAAGATGCCCAACTGTGTGTTACTGAGCT 3239
Qy 3321 CTATACAGATCCATATCCCTAATCTTATATGAAGC 3358
Db 3240 CTATACAGATCCATATCCCTAATCTTATATGAAGC 3277

RESULT 6
AAN70261
ID AAN70261 standard; cDNA, 3825 BP.
XX
AC AAN70261;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 03-APR-1991 (first entry)
XX
DE Sequence of Newcastle Disease Virus (NDV) F gene and HN gene.
XX
KW Epitope; probe; diagnosis; ss.
XX
OS Newcastle disease virus.
XX
FH Key Location/Qualifiers
FT 1..1792 misc_feature
FT /*tag= a
FT /label= F gene
FT 47..1708
FT /*tag= c
FT /product= "F"
FT /note= "AAP70176"
FT 1795..3825
FT /*tag= b
FT /label= HN gene
FT 1915..3648
FT /*tag= d
FT /product= "HN"
FT /note= "AAP70843"
XX
EP227414-A.
FN
XX
PD 01-JUL-1987.
XX
PF 16-DEC-1986; 86EP-00309804.
XX
PR 18-DEC-1985; 85GB-00031147.
PR 14-APR-1986; 86GB-00009037.
PR 15-JUL-1986; 86US-00885765.
XX
PA (NATR ) NAT RES DEV CORP.
XX
PI Bingham RW, Chambers P, Emmerson PT, Millar NS;
XX
DR WPI; 1987-179630/26.
DR P-PSDB; AAP70176, AAP70843.
XX
PT Newcastle disease virus gene clones - comprise polynucleotide(s) encoding
PT the HN and/or F protein of Newcastle disease virus RNA.
XX
PS Example; Page 11-16; 22pp; English.
XX
CC An artificial polynucleotide encoding an HN and/or F polypeptide of
CC Newcastle Disease Virus (NDV) DNA, a bioprecursor of the polypeptide, or
CC an epitopic portion of the polypeptide or an artificial nucleotide
CC complementary to the polynucleotide are claimed. The polynucleotides are
```

CC useful for preparing a probe for extracting similar genes from a gene  
CC library or for identifying the presence of NDV virions in a sample obd.  
CC from poultry. (Updated on 25-MAR-2003 to correct PA field.) (Updated on  
CC 27-AUG-2003 to correct OS field.)  
XX

SO Sequence 3825 BP; 1122 A; 898 C; 856 G; 949 T; 0 U; 0 Other;

Query Match 95.2%; Score 3196.4; DB 1; Length 3825;  
Best Local Similarity 97.0%; Pred. No. 0;  
Matches 3257; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1 ACGGGTGAAGATTCTGGATCCGGTTGGCGCCCTCCAGGNGCAAGTGGGCTCCAGACC 60  
DB 1 ACGGGTGAAGATTCTGGATCCGGTTGGCGCCCTCTAGTGCAAGATGGGCCCCAGACC 60  
QY TTTCACCAAGAACCCAGACCTTATGATGCTACTATCCGGTTGGCGCTGAGCACTGATTG 120  
DB TTTCACCAAGAACCCAGACCTTATGATGCTACTATCCGGTTGGCGCTGAGCACTGATTG 120  
QY 121 CATCTGTCGGCAAACTTCATTTGATGCGAGGCTCTTTCGACCTGCAAGAAATTGTGTAC 180  
DB 121 CATCTGTCGGCAAACTTCATTTGATGCGAGGCTCTTTCGAGCTGCAAGAAATTGTGTAC 180  
QY 181 AGGAGCAAAAGCCCTCAACATATACCTCATCCCAAGAGATCAATCATAGTTAAGCT 240  
DB 181 AGGAGCAAAAGCAATCAATATACCTCATCCCAAGAGATCAATCATAGTTAAGCT 240  
QY 241 CCTCCCAATCTGCGCAAGATAGAGAGCATGTGCGAAACCCCTTGGATGATCAAA 300  
DB 241 CCTCCCAATCTGCGCAAGATAGAGAGCATGTGCGAAACCCCTTGGATGATCAAA 300  
QY 301 CAGGACATTTGACCACTTTGCTCACCCCTTGTGATCTTATCCGTAGATACAAAGATC 360  
DB 301 CAGGACATTTGACCACTTTGCTCACCCCTTGTGATCTTATCCGTAGATACAAAGATC 360  
QY 361 TGTGACTATCATCTGAGAGGGGAGACAGGGGCGCTTATAGCGCCATTTATGGCGGT 420  
DB 361 TGTGACTATCATCTGAGAGGGGAGACAGGGGCGCTTATAGCGCCATTTATGGCGGT 420  
QY 421 GGCTCTGGGGTTGCAACTGCGCGCAAAATTAACAGCGGCGCACTCTGATACAAAGCAA 480  
DB 421 GGCTCTGGGGTTGCAACTGCGCGCAAAATTAACAGCGGCGCACTCTGATACAAAGCAA 480  
QY 481 ACAAAATGCTGCCAACAATCTCCGACTTTAAAGAGAGCATTTGCCCAACCAATGAAGCT 540  
DB 481 ACAAAATGCTGCCAACAATCTCCGACTTTAAAGAGAGCATTTGCCCAACCAATGAAGCT 540  
QY 541 GCATGAGTCACTGACGGAATTAATGCAACTGAGCTGAGCTTGGGAAGATGACAGCTT 600  
DB 541 GCATGAGTCACTGACGGAATTAATGCAACTGAGCTGAGCTTGGGAAGATGACAGCTT 600  
QY 601 TGTTAATGACCAATTTAATAAAACAGCTCAGGAATTAAGCTGATCAAAATTTGACAGCA 660  
DB 601 TGTTAATGACCAATTTAATAAAACAGCTCAGGAATTAAGCTGATCAAAATTTGACAGCA 660  
QY 661 AGTTGATGAGAGCTCAACCTGTACCTTAACCGAATTTAGCTACATATTCGAGCACAAT 720  
DB 661 AGTTGATGAGAGCTCAACCTGTGTACCTTAACCGAATTTAGCTACATATTCGAGCACAAT 720  
QY 721 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTAACAATTTAGCTGTGGAAA 780  
DB 721 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTAACAATTTAGCTGTGGAAA 780  
QY 781 TATGATTAATCTTATTTGATGATAGTTAGGTTAGGGAACAATCACTCAGCTATTAATCG 840  
DB 781 TATGATTAATCTTATTTGATGATAGTTAGGTTAGGGAACAATCACTCAGCTATTAATCG 840  
QY 841 TAGCGGCTTATCAACCGTAACCTTATTTATAGACTCAAGACTCAACTCTTGGGAT 900  
DB 841 TAGCGGCTTATCAACCGTAACCTTATTTATAGACTCAAGACTCAACTCTTGGGAT 900  
QY 901 ACAGGTAACTTACCTTCACTGCGGAAACCTAATTAATGCGTGCACCTTACTTGAAC 960  
DB 901 ACAGGTAACTTACCTTCACTGCGGAAACCTAATTAATGCGTGCACCTTACTTGAAC 960

DB 901 ACAGGTAACTTACCTTCACTGCGGAAACCTAATTAATGCGTGCACCTTACTTGAAC 960  
QY 961 CTATTCGGTAAGCAACAACGAGGATTTGCTCGGCACTTGTCCTCAAAAGTGAGACACA 1020  
DB 961 CTATTCGGTAAGCAACAACGAGGATTTGCTCGGCACTTGTCCTCAAAAGTGAGACACA 1020  
QY 1021 GGTGCGTTCTGTGATTAAGAAACCTTGACCTGATCTGTATGAAACCTGACTAGATT 1080  
DB 1021 GGTGCGTTCTGTGATTAAGAAACCTTGACCTGATCTGTATGAAACCTGACTAGATT 1080  
QY 1081 ATATTGTACAAAGATTAAGTAAAGTTCCCTATGTCCTGATTTATTTCTGCTTGAGCGG 1140  
DB 1081 ATATTGTACAAAGATTAAGTAAAGTTCCCTATGTCCTGATTTATTTCTGCTTGAGCGG 1140  
QY 1141 CAATACGCGGCTGTATGTATCTCAAAAGACGAAAGGCGCACTTATCAACCAATCATGAC 1200  
DB 1141 CAATACGCGGCTGTATGTATCTCAAAAGACGAAAGGCGCACTTATCAACCAATCATGAC 1200  
QY 1201 TATCAAAAGTTCACTATTCGCAACCTGCAAGATGACAAACATGATGTGTAAACCCGCC 1260  
DB 1201 TATCAAAAGTTCACTATTCGCAACCTGCAAGATGACAAACATGATGTGTAAACCCGCC 1260  
QY 1261 GGGTATCATATTCGCAAAACTATGGAAGACCGTGTCTATATAGATTAACATCATGCAA 1320  
DB 1261 GGGTATCATATTCGCAAAACTATGGAAGACCGTGTCTATATAGATTAACATCATGCAA 1320  
QY 1321 TGTTTATCTTATAGCGGGAATACTTTAAGCTCAAGGGGAATTCGATGTAACTTATCA 1380  
DB 1321 TGTTTATCTTATAGCGGGAATACTTTAAGCTCAAGGGGAATTCGATGTAACTTATCA 1380  
QY 1381 GAAGATATCTCAATTAAGATTTCTCAAGTATTAATTAACAGGCAATCTTGTATCTCAAC 1440  
DB 1381 GAAGATATCTCAATTAAGATTTCTCAAGTATTAATTAACAGGCAATCTTGTATCTCAAC 1440  
QY 1441 TGAAGTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAATTAAGTTAGGAAAGCAA 1500  
DB 1441 TGAAGTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAATTAAGTTAGGAAAGCAA 1500  
QY 1501 CAGAAAATAGACAAAGTCAATGTCAAACTGACTAGACATCTGCTCTCATTTACTATAT 1560  
DB 1501 CAGAAAATAGACAAAGTCAATGTCAAACTGACTAGACATCTGCTCTCATTTACTATAT 1560  
QY 1561 CGTTTGTACTATCATATCTCTGTTTGTGTATCTTAAGCTGATTTCTAGATGCTACT 1620  
DB 1561 CGTTTGTACTATCATATCTCTGTTTGTGTATCTTAAGCTGATTTCTAGATGCTACT 1620  
QY 1621 AATGTACAAAGAAAGGCGCAACAAAACCTTATTAAGCTTGGGAAATATATCTTAGA 1680  
DB 1621 AATGTATAGCAAAAGGCGCAACAAAACCTTATTAAGCTTGGGAAATATATCTTAGA 1680  
QY 1681 TCAGATGAGGCACTTACAAAATTTGTGAACAAGATGAGGACGAAGGTTTCCCTAATAG 1740  
DB 1681 TCAGATGAGGCACTTACAAAATTTGTGAACAAGATGAGGACGAAGGTTTCCCTAATAG 1740  
QY 1741 TAATTTGTGAAAGTTCTGTGATCTGTCAAGTTCAAGAGTTTAAGAAAAATCAACGGGT 1800  
DB 1741 TAATTTGTGAAAGTTCTGTGATCTGTCAAGTTCTGTCAAGAGTTTAAGAAAAATCAACGGGT 1800  
QY 1801 TGTAGATGACCAAGAGCAATATACGGGGTGAAGCGGTAAAGAGAGCGCCCTCAATTGC 1860  
DB 1801 TGTAGATGACCAAGAGCAATATACGGGGTGAAGCGGTAAAGAGAGCGCCCTCAATTGC 1860  
QY 1861 GAGCGAGGCTTCAACAACCTCGTTTCAACCGTTCAACCGCAAGAGTCTCAATCATAGAC 1920  
DB 1861 GAGCGAGGCTTCAACAACCTCGTTTCAACCGTTCAACCGCAAGAGTCTCAATCATAGAC 1920  
QY 1921 CGGCGGTTAGCAAGTTGCGTTTGAAGATGATGAAAAGAGGCAAAAAATCAATGCGCG 1980  
DB 1921 CGGCGGTTAGCAAGTTGCGTTTGAAGATGATGAAAAGAGGCAAAAAATCAATGCGCG 1980  
QY 1981 TTGATATTCGGGATTCGAATCTTATCTTAAACGTATGTGACCTTGGCTATATCTGTAGCC 2040  
DB 1981 TTGATATTCGGGATTCGAATCTTATCTTAAACGTATGTGACCTTGGCTATATCTGTAGCC 2040

```
Qy 2041 TCCCTTTATATAGCATGGGGGCTAGACAACCTAGCGATCTTGAGGATACCGACTAGG 2100
Db 2041 TCCCTTTATATAGCATGGGGGCTAGACAACCTAGCGACTTGAGGATACCGACGAG 2100
Qy 2101 ATTTCCAGGGGAGAAAGAAAGATTATCATCTACCTTGTTCCATCAAGATGATAGAT 2160
Db 2101 ATTTCTAGGGGAGAAAGAAAGATTATCATCTGCTTCCATTCAAGATGATAGAT 2160
Qy 2161 AGGATATATAGCAAGTGGCCCTTGAGTCTCGGTTGGCATTTGTAATCTGAGACACA 2220
Db 2161 AGGATATATAGCAAGTGGCCCTTGAGTCTCGGTTGGCATTTGTAATCTGAGACACA 2220
Qy 2221 ATTATGAAACGCAATAACTCTCTCTTATGAGATTAATGAGCTGCAACAACAGTGGG 2280
Db 2221 ATTATGAAACGCAATAACTCTCTCTTATGAGATTAATGAGCTGCAACAACAGGCGG 2280
Qy 2281 TGGGGGCACTTATCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA 2340
Db 2281 TGGGGGCACTTATCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA 2340
Qy 2341 GATGATGCTAGTGAATGTCACATCTCATCTCTGATTTCAAGAACATCTGAATTTT 2400
Db 2341 GATGATGCTAGTGAATGTCACATCTCATCTCTGATTTCAAGAACATCTGAATTTT 2400
Qy 2401 ATCCGGGCGCTTACTACAGATCAGGTTGCACTGGAATACCTTATTTGACATGAGTCT 2460
Db 2401 ATCCGGGCGCTTACTACAGATCAGGTTGCACTGGAATACCTTATTTGACATGAGTCT 2460
Qy 2461 ACCGATTACTGCTACACCCATATGTAATATTTGTTGAGTCAAGATCACTCACTTCA 2520
Db 2461 ACCGATTACTGCTACACCTATATGTAATATTTGTTGAGTCAAGATCACTCACTTCA 2520
Qy 2521 TATGATATTTAGACATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2580
Db 2521 TATGATATTTAGACATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2580
Qy 2581 ACTCTGGGTTTCATCAACCTGAGACACCCAAATCGGAAGTCTTGAGTGTAGTGA 2640
Db 2581 ACTCTGGGTTTCATCAACCTGAGTGAACCCAAATCGGAAGTCTTGAGTGTAGTGA 2640
Qy 2641 ACTCTCTTAGGTTGATGATGCTGTGCTCGAAGTCAAGAGACAGAGAAAGATTAT 2700
Db 2641 ACTCTCTTAGGTTGATGATGCTGTGCTCGAAGTCAAGAGACAGAGAAAGATTAT 2700
Qy 2701 AACTCAGCTTCCCTACGCGGATGATGAGAGGTTAGGTTGACGCGCAAGTACAC 2760
Db 2701 AACTCAGCTTCCCTACGCGGATGATGAGAGGTTAGGTTGACGCGCAAGTACAC 2760
Qy 2761 GAAAAGACCTAGATGTCACAACTTATTCGGGGGCTGGGTCGCACTACCCAGAGTA 2820
Db 2761 GAAAAGACCTAGATGTCACAACTTATTCGGGGGCTGGGTCGCACTACCCAGAGTA 2820
Qy 2821 GGGGGTGGATTTTATTTGACAGCGCGGATGATGATGATGATGATGATGATGATGAT 2880
Db 2821 GGGGGTGGATTTTATTTGACAGCGCGGATGATGATGATGATGATGATGATGATGAT 2880
Qy 2881 AATTCAACCCAGTGAACCTGTAACAGAGAGAAATATGATATATACAGGATACATAC 2940
Db 2881 AATTCAACCCAGTGAACCTGTAACAGAGAGAAATATGATATATACAGGATACATAC 2940
Qy 2941 ACATGCCCAAGTGAAGCAAGTACCAATGGAATGAGCAAGTCTGATAGCTGGA 3000
Db 2941 ACATGCCCAAGTGAAGCAAGTACCAATGGAATGAGCAAGTCTGATAGCTGGA 3000
Qy 3001 CGGTTTGGTGGAAACGATACAGAGGCTATCTTATCTATCAAGGTCAACATCTCTTA 3060
Db 3001 CGGTTTGGTGGAAACGATACAGAGGCTATCTTATCTATCAAGGTCAACATCTCTTA 3060
Qy 3061 GGGCAAGACCGGTAATGATGTAACGCGCAACAGTCACTCATGAGGGGCGAGAGGC 3120
Db 3061 GGGCAAGACCGGTAATGATGTAACGCGCAACAGTCACTCATGAGGGGCGAGAGGC 3120
```

```
Qy 3121 AGAATTCTCAGAGTGGGACATCTCATTTCTTGTATACAGAGGTCATCATCTTCT 3180
Db 3121 AGAATTCTCAGAGTGGGACATCTCATTTCTTGTATACAGAGGTCATCATCTTCT 3180
Qy 3181 CCGCGTTATATATATCCATGACAGTACAGCAAGAAACAGGCACTCTTATAGTCCCTAT 3240
Db 3181 CCGCGTTATATATATCCATGACAGTACAGCAAGAAACAGGCACTCTTATAGTCCCTAT 3240
Qy 3241 ACATTCAATGCTTCACTCGGCGCAGTAGTATCCCTTCCAGGCTTACAGAAATGCC 3300
Db 3241 ACATTCAATGCTTCACTCGGCGCAGTAGTATCCCTTCCAGGCTTACAGAAATGCC 3300
Qy 3301 AACTCGTGTGTACTGAGTCTATACAGATTCATATCCCTATCTTATAGAAAC 3358
Db 3301 AACTCGTGTGTACTGAGTCTATACAGATTCATATCCCTATCTTATAGAAAC 3358

RESULT 7
ADM78418
ID ADM78418 standard; cDNA; 5291 BP.
XX
AC ADM78418;
XX
DT 03-JUN-2004 (first entry)
XX
DE Newcastle disease virus recombinant cDNA #14.
XX
KW Newcastle disease virus; T7 RNA polymerase; HEP-2 cell; influenza virus;
infectious bursal disease virus; rotavirus; infectious bronchitis virus;
chicken anaemia virus; Marek's disease virus; avian leukosis virus;
avian adenovirus; avian pneumovirus;
severe acute respiratory syndrome-causing virus; SARS;
human respiratory syncytial virus; human immunodeficiency virus;
hepatitis virus; measles virus; mumps virus; antiviral; ss.
XX
OS Newcastle disease virus.
XX
FN US2003224017-A1.
XX
PD 04-DEC-2003.
XX
PF 19-MAY-2003; 2003US-00440419.
XX
PR 05-MAY-2000; 2000WO-US006700.
PR 06-MAR-2002; 2002US-00926431.
PR 17-MAY-2002; 2002US-0381462P.
XX
PA (SAMA/) SAMAL S K.
PA (HUAN/) HUANG Z.
XX
PI Samal SK, Huang Z;
XX
WP1; 2004-051891/05.
XX
DR Novel antigenomic RNA of Newcastle disease virus having NP, P, M, F, HN,
PT L gene and foreign nucleotide complex inserted before NP gene, between
PT P, M genes and/or between HN, L genes, useful for producing vaccine
vector.
XX
XX Example 3; Page 18-19; 41pp; English.
XX
CC The invention relates to an antigenomic RNA of Newcastle disease virus
CC having NP, P, M, F, HN and L genes in the 5'-3' direction, with foreign
CC nucleotide complexes inserted between genes. The invention also relates
CC to cDNA related to the RNA, a plasmid comprising the cDNA, a cell
CC comprising the RNA, cDNA or plasmid, a method of preparing the RNA and a
CC recombinant Newcastle disease virus comprising the RNA. The RNA is useful
CC for producing a recombinant Newcastle disease virus by providing cells
CC capable of synthesizing T7 RNA polymerase, transfecting the cells with a
CC plasmid comprising cDNA or a protein of interest to obtain transfected
CC cells in a medium and isolating Newcastle disease virus from a
CC supernatant of the medium, where the cells capable synthesizing T7 RNA
CC polymerase are from a cell line expressing T7 RNA polymerase or plant
```



CC cells, mammalian cells, avian cells or HEP-2 cells infected with a  
CC vecchia virus that can synthesize 17 RNA polymerase. The recombinant  
CC virus is useful for vaccinating an avian animal against Newcastle disease  
CC or an avian pathogen chosen from influenza virus, infectious bursal  
CC disease virus, rotavirus, infectious bronchitis virus, chicken anemia  
CC virus, Marek's disease virus, avian leukosis virus, avian adenovirus and  
CC avian pneumovirus, where the avian animal is in need of the immunisation,  
CC which involves administering the recombinant virus to the avian animal,  
CC where the open reading frame of the foreign gene encodes an immunogenic  
CC protein of the avian pathogen against which the avian animal is  
CC immunized. The recombinant virus is also useful for immunizing a mammal  
CC against a non-avian pathogen such as severe acute respiratory syndrome-  
CC causing virus (SARS virus), human respiratory syncytial virus, human  
CC immunodeficiency virus, hepatitis virus, measles virus or mumps virus.  
CC This sequence represents Newcastle disease virus recombinant cDNA of the  
CC invention.  
XX  
SQ Sequence 5291 BP; 1565 A; 1202 C; 1186 G; 1332 T; 0 U; 6 Other;  
Query Match 72.7%; Score 2441.6; DB 12; Length 5291;  
Best Local Similarity 97.0%; Pred. No. 0;  
Matches 2486; Conservative 0; Mismatches 77; Indels 0; Gaps 0;  
QY 796 GACTAAGTTGGTGTAGGAAACATCACTCAGCTCATTTATCGGTAGCGGCTTAATCAC 855  
DB 1 GACTAAATTGGGTGTAGGAAACATCACTCAGCTCATTTATCGGTAGCGGCTTAATCAC 60  
QY 856 CGGTAAACCTTATTTATACGACTCAGAGACTCACTCTGGGGTAAAGGTAACCTCAAC 915  
DB 61 CGGCAACCTTATTTCTGACACTCAGAGACTCACTCTGGGGTAAAGGTAACCTCAAC 120  
QY 916 TTCACTCGGAAACCTAATAATATATGCGTCCACTACTTGGAAACCTTATCGTAAGAC 975  
DB 121 TTCACTCGGAAACCTAATAATATATGCGTCCACTACTTGGAAACCTTATCGTAAGAC 180  
QY 976 AACCAAGGGATTTGGCCCTCGGACCTTGCCCAAAGGTGACAGAGGTGGTCTGTGAT 1035  
DB 181 AACCAAGGGATTTGGCCCTCGGACCTTGCCCAAAGGTGACAGAGGTGGTCTGTGAT 240  
QY 1036 AGAAGAACTTGACACCTCATCTGTATAGAAAGTACTTATTTATTTATGACAAAGAT 1095  
DB 241 AGAAGAACTTGACACCTCATCTGTATAGAAAGTACTTATTTATTTATGACAAAGAT 300  
QY 1096 AGTAACTTCCTATGTGCTCCGTGGATTTATCTGTCTTGAAGGCGCAATAGTGGCCTG 1155  
DB 301 AGTAACTTCCTATGTGCTCCGTGGATTTATCTGTCTTGAAGGCGCAATAGTGGCCTG 360  
QY 1156 TATGTACTCAAAAGCCGAAGCGGACTTACTACACCATATGACTATCAAAAGTTGAGT 1215  
DB 361 TATGTACTCAAAAGCCGAAGCGGACTTACTACACCATATGACTATCAAAAGGCTAGT 420  
QY 1216 CATCGCAACTGCAAGATGACAAATGATGTGTAAACCCCGGGGGTATCATATGCA 1275  
DB 421 CATCGCAACTGCAAGATGACAAATGATGTGTAAACCCCGGGGGTATCATATGCA 480  
QY 1276 AAACATAGAGAAAGCCGTGTCTTAATAGATTAACAATCATGCAATGTTTATCTTAGG 1335  
DB 481 AAACATAGAGAAAGCCGTGTCTTAATAGATTAACAATCATGCAATGTTTATCTTAGG 540  
QY 1336 CGGGATTAACCTTTAAGGCTCAGTGGGGAATTGAGTAACTTATCAGAAAGATATCTCAAT 1395  
DB 541 CGGGATTAACCTTTAAGGCTCAGTGGGGAATTGAGTAACTTATCAGAAAGATATCTCAAT 600  
QY 1396 ACAAGATTTCAAGTAAATTAACAGGCAATCTGATATCTCACTGAGCTTGGGAAATG 1455  
DB 601 ACAAGATTTCAAGTAAATTAACAGGCAATCTGATATCTCACTGAGCTTGGGAAATG 660  
QY 1456 CAACAACTCGATCAGTAATGCTTGAATTAAGTAAAGAGAAAGCAAGAAACCTAGCAA 1515  
DB 661 CAACAACTCGATCAGTAATGCTTGAATTAAGTAAAGAGAAAGCAAGAAACCTAGCAA 720  
QY 1516 AGTCATGTCAAACTGACATCTGCTCTATTAACCTATATCGTTTGAATATCAT 1575

DB 721 AGTCATGTCAAACTGACAGACATCTGCTCTCATTAACCTATATCGTTTGAATATCAT 780  
QY 1576 ATCTCTGTTTTGGTATTAAGTACTGATCTGATTTAGCATGCTACTTAATGTAACAGCAA 1635  
DB 781 ATCTCTGTTTTGGTATTAAGTACTGATCTGATTTAGCATGCTACTTAATGTAACAGCAA 840  
QY 1636 GGGGCAACAAAAACCTTATTAAGGCTTGGGAATTAATCTAGATAGAGAGCAC 1695  
DB 841 GGGGCAACAAAAACCTTATTAAGGCTTGGGAATTAATCTAGATAGAGAGCAC 900  
QY 1696 TACAAAATGTGAACAGATGAGAAAGCAAGGTTTCCCTAATATAGTAAATTTGTGTGAAG 1755  
DB 901 TACAAAATGTGAACAGATGAGAAAGCAAGGTTTCCCTAATATAGTAAATTTGTGTGAAG 960  
QY 1756 TTCTGTAGTCTGTCACTGATGAGAGTTAAAGAAAACTACCGGTTGATGACCAAG 1815  
DB 961 TTCTGTAGTCTGTCACTGATGAGAGTTAAAGAAAACTACCGGTTGATGACCAAG 1020  
QY 1816 GAGCATTAACGGGTAAAGACGTAAAGAGAGGCCCCCTCAATTGCCAGCCAGCTTACA 1875  
DB 1021 GAGCATTAACGGGTAAAGACGTAAAGAGAGGCCCCCTCAATTGCCAGCCAGCTTACA 1080  
QY 1876 ACCTCGTTCTACCGCTTCAACCGACCAACAGTCTCAATCATGACCGCGCTTACGCCAA 1935  
DB 1081 ACCTCGTTCTACCGCTTCAACCGACCAACAGTCTCAATCATGACCGCGCTTACGCCAA 1140  
QY 1936 GTTCCGTTAGAGATGAATGAAGAGAGCAAAAAATACATGGCGCTTGAATTTCCGAT 1995  
DB 1141 GTTCCGTTAGAGATGAATGAAGAGAGCAAAAAATACATGGCGCTTGAATTTCCGAT 1200  
QY 1996 GCATCTTATTTCTTAAGATGATGACCTTGGCTATATCTGATGCTCCCTTATATAGC 2055  
DB 1201 GCATCTTATTTCTTAAGATGATGACCTTGGCTATATCTGATGCTCCCTTATATAGC 1260  
QY 2056 ATGGGGGCTAGACACACTTACGATCTTTGAGGATACCGATAGGATTTCCAGGGCAGAA 2115  
DB 1261 ATGGGGGCTAGACACACTTACGATCTTTGAGGATACCGATAGGATTTCCAGGGCAGAA 1320  
QY 2116 GAAAGATTAATCATCTACCTTGCTTCCAAATCAAGATGATAGATAGATATATAGCAA 2175  
DB 1321 GAAAGATTAATCATCTACCTTGCTTCCAAATCAAGATGATAGATAGATATATAGCAA 1380  
QY 2176 GTGGCCCTTGAAGTCTCCGTGGGCAATTTAAATCTGAGACCAATTAATGAACGCAATA 2235  
DB 1381 GTGGCCCTTGAAGTCTCCGTGGGCAATTTAAATCTGAGACCAATTAATGAACGCAATA 1440  
QY 2236 ACATCTCTCTTATGATTAATGAGCTGCAAAACAAGTGGGGGGGCACTATC 2295  
DB 1441 ACATCTCTCTTATGATTAATGAGCTGCAAAACAAGTGGGGGGGCACTATC 1580  
QY 2296 CATGACCCAGATTAATATAGGGGGGATAGGCAAAAGACTCATTTGATATGATGTAT 2355  
DB 1501 CATGACCCAGATTAATATAGGGGGGATAGGCAAAAGACTCATTTGATATGATGTAT 1560  
QY 2356 GTCAATCATTTCTATCCCTCTGCAATTTCAAGAACTTGAAATTTATCCCGGGGCTTACT 2415  
DB 1561 GTCAATCATTTCTATCCCTCTGCAATTTCAAGAACTTGAAATTTATCCCGGGGCTTACT 1620  
QY 2416 ACGAGATCAGTTGCACTCGAATACCCCTCAATTTGACATGAGTGTAACCTACTGTAC 2475  
DB 1621 ACGAGATCAGTTGCACTCGAATACCCCTCAATTTGACATGAGTGTAACCTACTGTAC 1680  
QY 2476 ACCCATTAATTAATATTTGCTGATGAGAGATCACTCATTCATATCAATGATTAAGCA 2535  
DB 1681 ACCCATTAATTAATATTTGCTGATGAGAGATCACTCATTCATATCAATGATTAAGCA 1740  
QY 2536 CTGTGTGTCTCGGACATCTGCAACAGGAGGATTTCTTTTCTACTCTGCGTTCCATC 2595  
DB 1741 CTGTGTGTCTCGGACATCTGCAACAGGAGGATTTCTTTTCTACTCTGCGTTCCATC 1800  
QY 2596 AACCTGAGACACCCCAAAATCGGAAGCTTTGAGGTGAGTGAACCTCCCGGCTTGT 2655  
DB 1801 AGCTGATGACACCCCAAAATCGGAAGCTTTGAGGTGAGTGAACCTCCCGGCTTGT 1860



```
QY 2656 GATATGCTGTGCTGAAAGTCAAGAGACAGAGAGAAAGATTATTAAGTCACTGCTGCTCT 2715
DB 1861 GATATGCTGTGCTGAAAGTCAAGAGACAGAGAGAAAGATTATTAAGTCACTGCTGCTCT 1920
QY 2716 ACCGGGATGATGATGATGAGGTTAGGCTTCCAGCCGCTGATCCAGAAAGACCTTAAT 2775
DB 1921 ACCGTGATGATGATGAGGTTAGGCTTCCAGCCGCTGATCCAGAAAGACCTTAAT 1980
QY 2776 GTCAACAATTATTCGGGGAATGGGTGGCAACTACCAAGAGATAGGGGGTGGATCTTTT 2835
DB 1981 GTCAACAATTATTCGGGGAATGGGTGGCAACTACCAAGAGATAGGGGGTGGATCTTTT 2040
QY 2836 ATTGACAGCCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 2895
DB 2041 ATTGACAGCCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 2100
QY 2896 ACTGTAACGAAAGGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2955
DB 2101 ACTGTAACGAAAGGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2160
QY 2956 CAAGACTACCGATTCGAATGGCCAAAGTCTGATTAAGCTGACGGTTTGGTGGAAA 3015
DB 2161 CAAGACTACCGATTCGAATGGCCAAAGTCTGATTAAGCTGACGGTTTGGTGGAAA 2220
QY 3016 CGCATACAGCAGGCTATCTTATCTATCAAGGCTGCAACATCTTAAAGCGAAACCCGGTA 3075
DB 2221 CGCATACAGCAGGCTATCTTATCTATCAAGGCTGCAACATCTTAAAGCGAAACCCGGTA 2280
QY 3076 CTGACTGTACCGCCCAACACAGTCACTCATGCGGGCCGAAAGCGAATTTCTACAGTA 3135
DB 2281 CTGACTGTACCGCCCAACACAGTCACTCATGCGGGCCGAAAGCGAATTTCTACAGTA 2340
QY 3136 GGGGATCTCACTTCTGATCAAGAGGGGATCATCTCTCCCGGCTTATTAAT 3195
DB 2341 GGGGATCTCACTTCTGATCAAGAGGGGATCATCTCTCCCGGCTTATTAAT 2400
QY 3196 CCTATGACAGTCAAGCAAAACAGCACTCTTATGATGCTTATTAATGATGCTTTC 3255
DB 2401 CCTATGACAGTCAAGCAAAACAGCACTCTTATGATGCTTATTAATGATGCTTTC 2460
QY 3256 ACTCGGCAAGTATATCTCTTCCGCAAGCTTCAAGCAAGTCCCAACTCGTGTGTTACT 3315
DB 2461 ACTCGGCAAGTATATCTCTTCCGCAAGCTTCAAGCAAGTCCCAACTCGTGTGTTACT 2520
QY 3316 GAGTCTATACAGTTCATATCCCTTAATCTTCTATTAAGAAC 3358
DB 2521 GAGTCTATACAGTTCATATCCCTTAATCTTCTATTAAGAAC 2563
```

```
RESULT 8
AA068943
ID AA068943 standard; DNA; 4177 BP.
XX
AC AA068943;
XX
AC 25-MAR-2003 (revised)
DT 13-APR-1995 (first entry)
XX
DE SfiI fragment contg. Newcastle Disease Virus HN and F genes.
XX
KM SfiI fragment; Newcastle Disease Virus; HN gene; F gene; ss.
XX
OS Synthetic.
XX
FH Key location/Qualifiers
FT 115..1860 /*tag= a
FT CDS /label= AAR58859
FT 2095..3756 /*tag= b
FT /label= AAR58858
XX
```

```
PN W09419014-A1.
XX
XX 01-SEP-1994.
PD
XX
XX 28-FEB-1994; 94W0-US001826.
PF
XX
XX 26-FEB-1993; 93US-00024156.
PR
XX
XX (SYTR ) SYNPRO CORP.
PA (JAPR ) NIPPON ZEON KK.
PI Cochran MD;
XX
XX WPI; 1994-294007/36.
DR P-PSDB; AAR58858, AAR58859.
XX
XX New recombinant fowl pox virus for use in vaccines - contains genes
PT expressing antigens of Newcastle disease virus and opt. infectious
PT bronchitis virus.
XX
XX Disclosure; Page 63-68; 85pp; English.
PS
XX Newcastle Disease Virus (NDV) HN and F genes were inserted as a SfiI
CC fragment into the homology vector 443-88.8 at the unique SfiI site. The
CC NDV HN and F genes were inserted in the same transcriptional orientation
CC as the ORF in the parental homology vector. The sequence of SfiI fragment
CC is in AA068943/R58858/AAR58859. The inserted SfiI fragment has the
CC following structure: Junction A - Fragment 1 (HN, AAR 2-577) - Junction B
CC - Fragment 2 (F, AAR 1-553) - Junction C - Fragment 3 (PBR322) - Junction
CC D. Fragment 1 is approx. 1811 bp Availi to NaeI fragment of the NDV HN
CC cDNA clone (BI strain). Fragment 2 is an approx 1812 bp BamHI to PciI
CC fragment of the full length NDV F cDNA (BI Strain). Fragment 3 is an
CC approx 235 bp PciI and ScaI fragment of the plasmid pBR322. The sequences
CC of the junctions are in AA068945, AA068946, AA068947 and AA068948.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 4177 BP; 1199 A; 980 C; 910 G; 1068 T; 0 U; 0 Other;
Query Match 51.9%; Score 1741.8; DB 2; Length 4177;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 16 TGAATCCCGGTTGGCGCCCTTCAGAGTGCAGAGATGGGCTCCAGACCTTCTACCAAGAAC 75
DB 2064 TGAATCCCGGTTGGCGCCCTTCAGAGTGCAGAGATGGGCTCCAGACCTTCTACCAAGAAC 2123
QY 76 AGCACCTATGATGCTGATCTATCCGGGTTGGCTGGCACTGATGATCTCTCCGGCAAA 135
DB 2124 AGCACCTATGATGCTGATCTATCCGGGTTGGCTGGCACTGATGATCTCTCCGGCAAA 2183
QY 136 CTCCATTGATGGAGGCGCTCTTGACGCTGCAGAAATTGGTTACAGAGACAAAGCCGT 195
DB 2184 CTCCATTGATGGAGGCGCTCTTGACGCTGCAGAAATTGGTTACAGAGACAAAGCAGT 2243
QY 196 CAACATATTAACCTCATCTCCAGACAGATCAATATGATTAAGTCTCTCCGAACTTGGC 255
DB 2244 CAACATATTAACCTCATCTCCAGACAGATCAATATGATTAAGTCTCTCCGAACTTGGC 2303
QY 256 CAAGGATTAAGAGGATGCTGGGAAAGCCCTTGGATGATCAACAGACATTTAGCCAC 315
DB 2304 CAAGGATTAAGAGGATGCTGGGAAAGCCCTTGGATGATCAACAGACATTTAGCCAC 2363
QY 316 TTGGCTACCCCTCTTGGTGAATCTATCCGTAAGATCAAGAGCTGTGACTATCATCTGG 375
DB 2364 TTGGCTACCCCTCTTGGTGAATCTATCCGTAAGATCAAGAGCTGTGACTATCATCTGG 2423
QY 376 AGGGGGAGACAGGGGCGCTTATAGCGGCATTAATGGCGGTGGCTTGGGGTTGC 435
DB 2424 AGGGGGAGACAGGGGCGCTTATAGCGGCATTAATGGCGGTGGCTTGGGGTTGC 2483
QY 436 AACTGCGGCACAAATTAACAGCGCGCGAGCTGTGATCAAGCCAAACAAATGCTGCCAA 495
DB 2484 AACTGCGGCACAAATTAACAGCGCGCGAGCTGTGATCAAGCCAAACAAATGCTGCCAA 2543
```

QY 496 CATCTCCGACTTAAGAGACATTGCCGCAACCAATGAGGCTGTGCATGAGTCACTGA 555  
 DB 2544 CATCTCCGACTTAAGAGACATTGCCGCAACCAATGAGGCTGTGCATGAGTCACTGA 2603  
 QY 556 CGGATTTCCCACTACGAGGCACTGGGAAAGATGACAGAGTTTGTATGACCAATT 615  
 DB 2604 CGGATTTCCCACTACGAGGCACTGGGAAAGATGACAGAGTTTGTATGACCAATT 2663  
 QY 616 TAAATAAACAGCTCAGGAATTAGACTGCATCAAAATTGACAGAGTTGTGTAGAGCT 675  
 DB 2664 TAAATAAACAGCTCAGGAATTAGACTGCATCAAAATTGACAGAGTTGTGTAGAGCT 2723  
 QY 676 CAACCTGTACCTAACCGAATTGACTACAGATTTGGACCAAAATCACTTCAGCTGCTTT 735  
 DB 2724 CAACCTGTACCTAACCGAATTGACTACAGATTTGGACCAAAATCACTTCAGCTGCTTT 2783  
 QY 736 AAACAGAGCTGACTTTTACGAGCACTTTTCAATCTGCTGGGAAATATGATTTACTATT 795  
 DB 2784 AAACAGAGCTGACTTTTACGAGCACTTTTCAATCTGCTGGGAAATATGATTTACTATT 2843  
 QY 796 GACTTAAGTATGATGAGGAAACAATCACTGAGCTCAATTAACGGTAGCGCTTAATCAC 855  
 DB 2844 GACTTAAGTATGATGAGGAAACAATCACTGAGCTCAATTAACGGTAGCGCTTAATCAC 2903  
 QY 856 CGGTAACCTTATTTCTATACGACTCAGACTCAACTCTTGGGATACAGGTAACCTTACC 915  
 DB 2904 CGGTAACCTTATTTCTATACGACTCAGACTCAACTCTTGGGATACAGGTAACCTTACC 2963  
 QY 916 TTCACTGTTGGGAACTTAATTAATATGCTGCGCACTTACTTGGAACTTTATCCGTAACAC 975  
 DB 2964 TTCACTGTTGGGAACTTAATTAATATGCTGCGCACTTACTTGGAACTTTATCCGTAACAC 3023  
 QY 976 AACGAGGGAATTTGCTCGGCACTTGTCCCAAAAGTGATGACAGAGTGGTCTGTGAT 1035  
 DB 3024 AACGAGGGAATTTGCTCGGCACTTGTGTCCCAAAAGTGATGACAGAGTGGTCTGTGAT 3083  
 QY 1036 AGAAGAACTTGACACTCATATGATAGAAAGTACTAGATTATATGTGTACAAAGAT 1095  
 DB 3084 AGAAGAACTTGACACTCATATGATAGAAAGTACTAGATTATATGTGTACAAAGAT 3143  
 QY 1096 AGTAACTTCCCTATGTCCTGCTGATTTTATCTGCTTGAAGCGGCAATAGTGGGCTG 1155  
 DB 3144 AGTAACTTCCCTATGTCCTGCTGATTTTATCTGCTTGAAGCGGCAATAGTGGGCTG 3203  
 QY 1156 TATGTACTGAAAAGACGAGGCGCACTTACTACCAATATATGCTATCAAAAGGCTAGT 1215  
 DB 3204 TATGTACTGAAAAGACGAGGCGCACTTACTACCAATATATGCTATCAAAAGGCTAGT 3263  
 QY 1216 CATCGCAACTGCAAGATGACAAATGTGTAAACCCCGGGGTATCATATGCA 1275  
 DB 3264 CATCGCAACTGCAAGATGACAAATGTGTAAACCCCGGGGTATCATATGCA 3323  
 QY 1276 AAATCTATGAGAAAGCCGTGTCTTAATAGATAAACATCATGCAATGTTTATCTTAAAG 1335  
 DB 3324 AAATCTATGAGAAAGCCGTGTCTTAATAGATAAACATCATGCAATGTTTATCTTAAAG 3383  
 QY 1336 CGGGATTAACCTTAAGGCTCAGTGGGAAATTGATGTAACCTTATCAGAAATATCTCAAT 1395  
 DB 3384 CGGGATTAACCTTAAGGCTCAGTGGGAAATTGATGTAACCTTATCAGAAATATCTCAAT 3443  
 QY 1396 ACAAGATTTCAAGTAATTAATTAACGCAATCTTGATATCTCACTGAGCTTGGGAAATG 1455  
 DB 3444 ACAAGATTTCAAGTAATTAATTAACGCAATCTTGATATCTCACTGAGCTTGGGAAATG 3503  
 QY 1456 CAACAACTGATCAGTATGCTTGAATTAAGTATGAGAAAGCAACGAAAACTAGACAA 1515  
 DB 3504 CAACAACTGATCAGTATGCTTGAATTAAGTATGAGAAAGCAACGAAAACTAGACAA 3563  
 QY 1516 AGTCAATGTCAAACTGATGAGCAATCTGCTCATTAACCTATATCTTTTGAATATCAT 1575  
 DB 3564 AGTCAATGTCAAACTGATGAGCAATCTGCTCATTAACCTATATCTTTTGAATATCAT 3623

QY 1576 ATCTCTGTTTTTGTATACTAGCTGATTTCTAGACATGCTACTTAATGTACAGCAAAA 1635  
 DB 3624 ATCTCTGTTTTTGTATACTAGCTGATTTCTAGACATGCTACTTAATGTACAGCAAAA 3683  
 QY 1636 GGGCAACAAAAAAGCTTTATTTATGCTTGGGAAATTAATCTCTAGATCAGATGAGAGCCAC 1695  
 DB 3684 GGGCAACAAAAAAGCTTTATTTATGCTTGGGAAATTAATCTCTAGATCAGATGAGAGCCAC 3743  
 QY 1696 TACAAAAATGTGAACACAGATGAGAAAGCAAGGTTTCCCTPATATGTAATTTGTGTAAAG 1755  
 DB 3744 TACAAAAATGTGAACACAGATGAGAAAGCAAGGTTTCCCTPATATGTAATTTGTGTAAAG 3803  
 QY 1756 TTCTGTAGTCTGTCACTTACGAGAGCTTAAGAAAAAA 1792  
 DB 3804 TTCTGTAGTCTGTCACTTACGAGAGCTTAAGAAAAAA 3840

RESULT 9  
 AAQ70570 standard; DNA; 4177 BP.  
 ID AAQ70570 standard; DNA; 4177 BP.  
 AC AAQ70570;  
 XX  
 AC 25-MAR-2003 (revised)  
 DT 14-APR-1995 (first entry)  
 DT  
 XX SfiI fragment contg. Newcastle disease virus HN and F genes.  
 DE  
 XX Newcastle disease virus; HN gene; F gene; SfiI; vector 502-26.22; ss.  
 KM  
 XX Synthetic.  
 OS  
 XX  
 FH Key Location/Qualifier  
 FT CDS 115..1860  
 FT /\*tag= a  
 FT /\*label= AAR58598, HN  
 FT CDS 2095..3756  
 FT /\*tag= b  
 FT /\*label= AAR49141, F  
 FT  
 PN W09419015-A1.  
 XX  
 XX 01-SEP-1994.  
 PD  
 XX 28-FEB-1994; 94MO-US002252.  
 PF  
 XX 26-FEB-1993; 93US-00024156.  
 PR  
 XX (SYTR ) SYNTRO CORP.  
 PA  
 XX Cochran MD;  
 PI  
 XX WPI: 1994-294008/36.  
 XX P-PSDB; AAR58598, AAR49141.  
 DR  
 XX  
 PT New recombinant fowl pox viruses - useful as vaccines against fowl pox  
 PT virus; Newcastle Disease Virus and infectious laryngotracheitis virus.  
 PS  
 XX Disclosure; Page 72-77; 97pp; English.  
 XX  
 XX AAQ70570 is the SfiI fragment insert in Homology Vector 502-26.22 contg.  
 CC Newcastle disease virus (NDV) HN and F genes. The structure of the  
 CC fragment is: 5'- Junction A - Fragment 1 (NDV HN AAs 2-577) - Junction B  
 CC - Fragment 2 (NDV F AAs 1-553) - Junction C - Fragment 3 (pBR322) -  
 CC Junction D - 3'. Fragment 1 is Avail to NaeI fragment of the full length  
 CC NDV HN cDNA clone (BI strain). Fragment 2 is BamHI to PstI fragment of  
 CC the full length NDV F cDNA (BI strain). Fragment 3 is a PstI and ScaI  
 CC fragment of pBR322. The structures of the junctions A, B, C and D are  
 CC given in AAQ70552, AAQ70553, AAQ70554 and AAQ70555 respectively. (Updated  
 CC on 25-MAR-2003 to correct PN field.)  
 CC  
 XX Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;

Query Match 51.9%; Score 1741.8; DB 2; Length 4177;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 16 TGAATCCGGTGGCGCCCTCCAGATGCAAGATGGGCTCCAGACCTTCTACCAAGACC 75  
DB 2064 TCGATCCCGGTGGCGCCCTCCAGATGCAAGATGGGCTCCAGACCTTCTACCAAGACC 2123

QY 76 AGCACTATGATGCTGATCTATCCGGGTTGCGCTGGCACTGAGTTGATCTGCGGCAAA 135  
DB 2124 AGCACTATGATGCTGATCTATCCGGGTTGCGCTGGCACTGAGTTGATCTGCGGCAAA 2183

QY 136 CTCATTGATGAGCAGGCTCTTTCAGCTGCAAGAAATGCTTACAGAGAACAAAGCCGT 195  
DB 2184 CTCATTGATGAGCAGGCTCTTTCAGCTGCAAGAAATGCTTACAGAGAACAAAGCAGT 2243

QY 196 CAACATATACCTCATCTCCAGACAGAGTCAATCATAGTTAAAGTCTCCCGGAATCTGCC 255  
DB 2244 CAACATATACCTCATCTCCAGACAGAGTCAATCATAGTTAAAGTCTCCCGGAATCTGCC 2303

QY 256 CAAGATTAAGGAGGATGTCGAAAGCCCTTGGATGATACAAAGAGTTCGACAC 315  
DB 2304 CAAGATTAAGGAGGATGTCGAAAGCCCTTGGATGATACAAAGAGTTCGACAC 2363

QY 316 TTGCTCACCCCTTGGTGACTCTATCCGATGATCAAGAGTCTGATCTACATCTGG 375  
DB 2364 TTGCTCACCCCTTGGTGACTCTATCCGATGATCAAGAGTCTGATCTACATCTGG 2423

QY 376 AGGGGGAGACAGGGCGCTTATAGCGCCATTAATGCGGTGCTCTTGGGTTGC 435  
DB 2424 AGGGGGAGACAGGGCGCTTATAGCGCCATTAATGCGGTGCTCTTGGGTTGC 2483

QY 436 AACTGCGGCAAAATTAACAGGCGCGAGCTCTGATCAAGCAAAAGAAATGCGCCAA 495  
DB 2484 AACTGCGGCAAAATTAACAGGCGCGAGCTCTGATCAAGCAAAAGAAATGCGCCAA 2543

QY 496 CATCTCCGACTTAAAGAGACATTCGCGCAACCAATGAGGCTGTGATGAGTCACTGA 555  
DB 2544 CATCTCCGACTTAAAGAGACATTCGCGCAACCAATGAGGCTGTGATGAGTCACTGA 2603

QY 556 CGGATTAACGAACTAGACAGTGGAGTTGGGAAGATGCAAGTTGTTAATGACAAAT 615  
DB 2604 CGGATTAACGAACTAGACAGTGGAGTTGGGAAGATGCAAGTTGTTAATGACAAAT 2663

QY 616 TAAATAAACAGCTAGAGAAATTAAGCTGATCAAAATGCAAGAGTTGGTGAAGACT 675  
DB 2664 TAAATAAACAGCTAGAGAAATTAAGCTGATCAAAATGCAAGAGTTGGTGAAGACT 2723

QY 676 CAACCTGATCAACGAAATGATCAAGTATGCGAACCAAAATCACTTCACTGCTTT 735  
DB 2724 CAACCTGATCAACGAAATGATCAAGTATGCGAACCAAAATCACTTCACTGCTTT 2783

QY 736 AAACAACTGATCAATTCAGGCACTTAAATCTAGCTGGTGAATATGATTAATTT 795  
DB 2784 AAACAACTGATCAATTCAGGCACTTAAATCTAGCTGGTGAATATGATTAATTT 2843

QY 796 GACTTAAGTTAGGTAGGAAACAATCAATCACTGATTAATCGGTAGCGGCTTAATAC 855  
DB 2844 GACTTAAGTTAGGTAGGAAACAATCAATCACTGATTAATCGGTAGCGGCTTAATAC 2903

QY 856 CGGTAACCTTATCTATACGACTCAAGACTCACTCTGGGTATACAGTAACTTAC 915  
DB 2904 CGGTAACCTTATCTATACGACTCAAGACTCACTCTGGGTATACAGTAACTTAC 2963

QY 916 TTCAGTCGGGAACCTAAATTAATATGCGTGCACACTTATGGAACCTTATCGTAAGCAC 975  
DB 2964 TTCAGTCGGGAACCTAAATTAATATGCGTGCACACTTATGGAACCTTATCGTAAGCAC 3023

QY 976 AACCAAGGAGATTGCTCGGCACTTGTCCAAAGGTGTGACACAGTGGTCTGTAT 1035  
DB 3024 AACCAAGGAGATTGCTCGGCACTTGTGTCCAAAGGTGTGACACAGTGGTCTGTAT 3083

QY 1036 AGAAGAACTTGACACCTCATCTGTATGAAAGACGACTTAATTAATTTGTAACAAGAT 1095

DB 3084 AGAAGAACTTGACACCTCATCTGTATGAAAGACTGACTTAATTTATTTGTACAAGAT 3143

QY 1096 AGTAACGTTCCCTATATGTCCTCCGTGATTTATTCCTGTGAGCGGCAATAGTCGGCTG 1155

DB 3144 AGTAACGTTCCCTATATGTCCTCCGTGATTTATTCCTGTGAGCGGCAATAGTCGGCTG 3203

QY 1156 TATGTACTCAAAAGCCGAAGGCGCACTTATACACCATATGACTATCAAAAGTTCACT 1215

DB 3204 TATGTACTCAAAAGCCGAAGGCGCACTTATACACCATATGACTATCAAAAGCTCAGT 3263

QY 1216 CATGCCAACCTGCAAGATGACACATGTAGATGTAAACCCCGGGGTATCATATGCA 1275

DB 3264 CATGCCAACCTGCAAGATGACACATGTAGATGTAAACCCCGGGGTATCATATGCA 3323

QY 1276 AAACATGAGAGAACCCGTGCTCTAATAGATAAACAATCATGCAATGTTTATCTTATAG 1335

DB 3324 AAACATGAGAGAACCCGTGCTCTAATAGATAAACAATCATGCAATGTTTATCTTATAG 3383

QY 1336 CGGATTAACCTTAAAGGCTCAGTGGGAAATTCATGTAACTTATCAAGAAATATCTCAAT 1395

DB 3384 CGGATTAACCTTAAAGGCTCAGTGGGAAATTCATGTAACTTATCAAGAAATATCTCAAT 3443

QY 1396 ACAAGATTTCTCAATTAATTAACAAGCAATCTTGATATCTCACTGAGCTTGGGAATGT 1455

DB 3444 ACAAGATTTCTCAATTAATTAACAAGCAATCTTGATATCTCACTGAGCTTGGGAATGT 3503

QY 1456 CAACAACCTGATCACTGATATGTTGAATTAAGTTAGAGAAAGCAAGAAACTAGACAA 1515

DB 3504 CAACAACCTGATCACTGATATGTTGAATTAAGTTAGAGAAAGCAAGAAACTAGACAA 3563

QY 1516 AGTCAATGTCAAACTGATAGACATCTGCTCTGATTAACCTATATCGTTTGACTATCAT 1575

DB 3564 AGTCAATGTCAAACTGATAGACATCTGCTCTGATTAACCTATATCGTTTGACTATCAT 3623

QY 1576 ATCTCTGTTTTGGTATCTTACCTGATTCATGACATGCTAATGTTGACAGCAAAA 1635

DB 3624 ATCTCTGTTTTGGTATCTTACCTGATTCATGACATGCTAATGTTGACAGCAAAA 3683

QY 1636 GGGCCAAACAAAACCTTATATGCTTGGGAATTAATCTAGATCAGATGAGAGCCAC 1695

DB 3684 GGGCCAAACAAAACCTTATATGCTTGGGAATTAATCTAGATCAGATGAGAGCCAC 3743

QY 1696 TACAAAAATGGAACACAGATGAGAAAGAAAGTTCCCTAATATGATTTGTGTGAAG 1755

DB 3744 TACAAAAATGGAACACAGATGAGAAAGAAAGTTCCCTAATATGATTTGTGTGAAG 3803

QY 1756 TTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAAA 1792

DB 3804 TTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAAA 3840

RESULT 10  
AAT48510  
ID AAT48510 standard; DNA; 4177 BP.  
XX  
AC AAT48510;  
XX  
DT 05-MAY-1997 (first entry)  
XX  
DE Sfil fragment encoding Newcastle disease virus HN and F genes.  
XX  
XX Fowlpox virus; FPV, recombinant virus; vector: vaccine; immunisation;  
KM Newcastle disease virus; NDV; haemagglutinin; fusion protein; poultry;  
KM ds.  
XX  
OS Newcastle disease virus.  
XX  
FH Key Location/Qualifiers  
FT CDS 115..1860  
FT /tag= a  
FT /product= "NDV haemagglutinin"  
FT 2095..3756  
CDS

```
FT      /*tag= b
FT      /product= "NDV fusion protein"
PN      MO640880-A1.
XX      19-DEC-1996.
PD      04-JUN-1996; 96WO-US011187.
XX      07-JUN-1995; 95US-00484790.
XX      (SYTR ) SYNTHRO CORP.
XX      Cochran MD, Junker DE, Singer PA;
XX      WPI; 1997-087060/08.
DR      P-PSDB; AAM10690, AAM10691.
XX      New recombinant fowlpox virus - contg. a foreign DNA sequence inserted
PT      into the fowlpox virus genome, used for the produ. of vaccines.
XX      Disclosure; Page 102-107; 134pp; English.
XX      An Sfil fragment (AAT48510), contg. coding sequences for Newcastle
CC      disease virus (NDV) haemagglutinin (HN) (AAM10690) and fusion protein (F)
CC      (AAM10691), was inserted into homology vector 443-88.8 (see also
CC      AAT48511) at the unique Sfil site, yielding homology vector 502-26.22
CC      (see also AAT48502-05). The NDV HN and F genes were inserted in the same
CC      transcriptional orientation as the parental homology vector. 502-26.22
CC      was used to insert the NDV HN and F genes into fowlpox virus. The
CC      resulting recombinant virus can be used to deliver the vaccine antigens
CC      to poultry.
XX      Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;
XX      Query Match 51.9%; Score 1741.8; DB 2; Length 4177;
XX      Best Local Similarity 98.8%; Pred. No. 0;
XX      Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY      16 TGGATCCCGGTTGGCGGCTTCAGAGTGCAGAGATGGGCTCCAGACCTTCTACCAAGAACCC 75
DB      2064 TCGATCCCGGTTGGCGGCTTCAGAGTGCAGAGATGGGCTCCAGACCTTCTACCAAGAACCC 2123
QY      76 AGCACTATGATGCTGACTATCCGGGTTGGCGCTGSCACTGAGTGCATCTGTCGGGCAAA 135
DB      2124 AGCACTATGATGCTGACTATCCGGGTTGGCGCTGSCACTGAGTGCATCTGTCGGGCAAA 2183
QY      136 CTCATTGATGAGCGAGGCTCTTGCAGCTGCAGGAATTGTGTTACAGAGACCAAGCCGT 195
DB      2184 CTCATTGATGAGCGAGGCTCTTGCAGCTGCAGGAATTGTGTTACAGAGACCAAGCCGT 2243
QY      196 CAACATATACACCTCATCCAGACAGAGATCAATCATGTTAAGCTCCGCCGAATCTGCC 255
DB      2244 CAACATATACACCTCATCCAGACAGAGATCAATCATGTTAAGCTCCGCCGAATCTGCC 2303
QY      256 CAAGATTAAGAGGCGATGTGGAAGGCCCTTGGATGATACATCAAGACGATTTGACAC 315
DB      2304 AAAGGATTAAGAGGCGATGTGGAAGGCCCTTGGATGATACATCAAGACGATTTGACAC 2363
QY      316 TTTGCTCACCCCCCTTGGTGACTCTATCCGTAGATACAAAGTCTGTGACTACATCTGG 375
DB      2364 TTTGCTCACCCCCCTTGGTGACTCTATCCGTAGATACAAAGTCTGTGACTACATCTGG 2423
QY      376 AGGGGGGAGACAGGGGGGCTTTAAGGGCGCATTAATTGGGGTGTGCTCTTGGGGTTGC 435
DB      2424 AGGGGGGAGACAGGGGGGCTTTAAGGGCGCATTAATTGGGGTGTGCTCTTGGGGTTGC 2483
QY      436 AACTGCGCAACAATAACAGCGCGCGAGCTGTGATCAAGCCAAACAAATGCTGCCAA 495
DB      2484 AACTGCGCGCAACAATAACAGCGCGCGAGCTGTGATCAAGCCAAACAAATGCTGCCAA 2543
QY      496 CATCTTCGACTTAAAGAGCATTTGCCGCAACCAATGAGGCTGTGATGAGTCACTGA 555
DB      CATCTTCGACTTAAAGAGCATTTGCCGCAACCAATGAGGCTGTGATGAGTCACTGA 555
```

```
DB      2544 CATCTTCGACTTAAAGAGCATTTGCCGCAACCAATGAGGCTGTGATGAGTCACTGA 2603
QY      556 CGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAGAGTTTGTAAATGCAAAAT 615
DB      2604 CGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAGAGTTTGTAAATGCAAAAT 2663
QY      616 TAATTAACAGCTCAGGAATTTAGCTGCATCAAAATTTGCAACAGCAATTTGGTGAAGCT 675
DB      2664 TAATTAACAGCTCAGGAATTTAGCTGCATCAAAATTTGCAACAGCAATTTGGTGAAGCT 2723
QY      676 CAACCTGTACTTAAACGAATTGACTACAGTATTCGAGCACAATCACTTCACTGCTTT 735
DB      2724 CAACCTGTACTTAAACGAATTGACTACAGTATTCGAGCACAATCACTTCACTGCTTT 2783
QY      736 AAACAAGCTGACTATTACGAGCACTTTAACAATGACTGTGGAATAATGGAATTAATTAAT 795
DB      2784 AAACAAGCTGACTATTACGAGCACTTTAACAATGACTGTGGAATAATGGAATTAATTAAT 2843
QY      796 GACTAATTAGGTGATGGAACAATCAATCACTGACTCTTAATCGGTAGCGGCTTAATCAC 855
DB      2844 GACTAATTAGGTGATGGAACAATCAATCACTGACTCTTAATCGGTAGCGGCTTAATCAC 2903
QY      856 CGGTAACCTTATCTATAGACTCAGAGCTCAACCTGTTGGGTATACAGGTAACCTTACC 915
DB      2904 CGGTAACCTTATCTATAGACTCAGAGCTCAACCTGTTGGGTATACAGGTAACCTTACC 2963
QY      916 TTCACTGCGGAACTTAATTAATATGCTGCGCACCTACTTGGAAACCTTATCCGTAGCAC 975
DB      2964 TTCACTGCGGAACTTAATTAATATGCTGCGCACCTACTTGGAAACCTTATCCGTAGCAC 3023
QY      976 AACCAAGGATTTGGCTTCGGCACTTGTCCCAAAAGTGTACACAGGTCCGTTCTGTGAT 1035
DB      3024 AACCAAGGATTTGGCTTCGGCACTTGTCCCAAAAGTGTACACAGGTCCGTTCTGTGAT 3083
QY      1036 AGAAGAACTTGAACACCTCATCTGATATAGAAATGACTTGAATTTATTTATGTAACAAGAT 1095
DB      3084 AGAAGAACTTGAACACCTCATCTGATATAGAAATGACTTGAATTTATTTATGTAACAAGAT 3143
QY      1096 AGTAACGTTCCCTATGTCCCTGCTGATTTATTCCTGCTAGGCGGCAATAAGTCGGCTG 1155
DB      3144 AGTAACGTTCCCTATGTCCCTGCTGATTTATTCCTGCTAGGCGGCAATAAGTCGGCTG 3203
QY      1156 TATGTACTCAAGAAGCGAAGCGGCACTTACTACCATATGATCTATCAAAAGTTCAAGT 1215
DB      3204 TATGTACTCAAGAAGCGAAGCGGCACTTACTACCATATGATCTATCAAAAGTTCAAGT 3263
QY      1216 CATGCGCAATGCAAGATGACCAATGATGATGTAAACCCCGGGGTATCATATGCA 1275
DB      3264 CATGCGCAATGCAAGATGACCAATGATGATGTAAACCCCGGGGTATCATATGCA 3323
QY      1276 AAACATGAGAAAGCGGTCTCTTAATAGATAAACAATCATGCAATGTTTATCTTAAAG 1335
DB      3324 AAACATGAGAAAGCGGTCTCTTAATAGATAAACAATCATGCAATGTTTATCTTAAAG 3383
QY      1336 CGGGATTACTTTAAGGCTCAGTGGGGAATTCGATGTAATCTTATCAGAAATATCTCAAT 1395
DB      3384 CGGGATTACTTTAAGGCTCAGTGGGGAATTCGATGTAATCTTATCAGAAATATCTCAAT 3443
QY      1396 ACAAGATTCCTCAAGTAAATAAACAAGCAATCTTGATATCTCAACGAGCTTGGGAATGT 1455
DB      3444 ACAAGATTCCTCAAGTAAATAAACAAGCAATCTTGATATCTCAACGAGCTTGGGAATGT 3503
QY      1456 CAACAATCGATCAGTAATGCTTTGAATAAGTTAGAGAAAGCAACAGAAAATAGACAA 1515
DB      3504 CAACAATCGATCAGTAATGCTTTGAATAAGTTAGAGAAAGCAACAGAAAATAGACAA 3563
QY      1516 AGTCAATGTCAAACTGAATGACATCTGCTCATTAATCTATATGTTTGAATCAT 1575
DB      3564 AGTCAATGTCAAACTGAATGACATCTGCTCATTAATCTATATGTTTGAATCAT 3623
QY      1576 ATCTCTGTTTTTGGTAACTTGAAGCTGATTTAGAGATGCTACTAATGTAACAAGCAAA 1635
DB      3624 ATCTCTGTTTTTGGTAACTTGAAGCTGATTTAGAGATGCTACTAATGTAACAAGCAAA 3683
```

```
QY 1636 GGGCGCAACAAAACTTATTATGGCTTGGGAATTAATCTTAGATCAGATGAGCCAC 1695
DB 3684 GGGCGCAACAAAACTTATTATGGCTTGGGAATTAATCTTAGATCAGATGAGCCAC 3743
QY 1696 TACAAAAATGTGAACACAGATGAGGAAAGGTTTCCCTTAATAGTAATTTGTGGAAG 1755
DB 3744 TACAAAAATGTGAACACAGATGAGGAAAGGTTTCCCTTAATAGTAATTTGTGGAAG 3803
QY 1756 TTCTGGTAGTCTGTCACTTCCAGAGATTAAAGAAAAA 1792
DB 3804 TTCTGGTAGTCTGTCACTTCCAGAGATTAAAGAAAAA 3840

RESULT 11
AAK81147
ID AAK81147 standard; DNA; 4177 BP.
XX
AC AAK81147;
XX
DT 07-SEP-1999 (first entry)
XX
DE Seq ID No: 12 of US5925358.
XX
KM Fowlpox virus; FPV; recombinant; vaccine; immunisation; chicken; NDV;
XX Newcastle disease virus; NDV; Fowlpox; Infectious Laryngotracheitis; ds.
XX
OS Fowlpox virus.
XX
FH Key Location/Qualifiers
FT CDS 115..1860
FT FT /*tag= a
FT FT 2095..3756
FT FT /*tag= b

XX
XX US5925358-A.
XX
XX 20-JUL-1999.
XX
XX 07-JUN-1995; 95US-00484575.
XX
XX 26-FEB-1993; 93US-00024156.
XX 28-FEB-1994; 94WO-US002252.
XX
XX (SYTR ) SYNPRO CORP.
XX
XX Junker DE, Cochran MD;
XX
XX WPI; 1999-418249/35.
XX P-PSDB; AAY21982, AAY21983.
XX
XX Fowlpox viruses, useful as vaccines for immunization of chickens/turkeys
XX against Fowlpox and Newcastle disease virus.
XX
XX PS Disclosure; Col 61-70; 108pp; English.
XX
XX The invention relates to a recombinant fowlpox virus (FPV) comprising a
XX foreign DNA inserted into a region of the fowlpox virus genome
XX corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a
XX host cell. The virus is used as a vaccine for immunising chickens against
XX Newcastle disease virus (NDV), Fowlpox, and infectious laryngotracheitis
XX
SQ Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;
Query Match 51.9%; Score 1741.8; DB 2; Length 4177;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 16 TGAATCCCGGTGGCGCCCTCCAGATGCAAGATGGCTCCAGACCTTACCAAGAACCC 75
DB 2064 TCGATCCCGGTGGCGCCCTCCAGATGCAAGATGGCTCCAGACCTTACCAAGAACCC 2123
QY 76 AGACCTATGATGCTGACTATCCGGGTTGCGCTGGCACTGAGTTGCACTCTGTCGGCAAA 135
```

```
DB 2124 AGACCTATGATGCTGACTATCCGGGTTGCGCTGGCACTGAGTTGCACTCTGTCGGCAAA 2183
QY 136 CTCATTTGATGCAAGGCTCTTTCAGCTGCAAGAAATTTGTGTTACAGAGACAAAGCCGT 195
DB 2184 CTCATTTGATGCAAGGCTCTTTCAGCTGCAAGAAATTTGTGTTACAGAGACAAAGCAGT 2243
QY 196 CAACATTTACACTCTATCCAGACAGATCAATATATGTTAAGTCTCTCCGGAATCTGCC 255
DB 2244 CAACATTTACACTCTATCCAGACAGATCAATATATGTTAAGTCTCTCCGGAATCTGCC 2303
QY 256 CAAGATTAAGAGGCAATGCGGAAGGCCCTTGATGATACAAAGACATTTAGCCAC 315
DB 2304 AAAGATTAAGAGGCAATGCGGAAGGCCCTTGATGATACAAAGACATTTAGCCAC 2363
QY 316 TTTCCTACCCCTTGGTGTGATCTCTATCCGATGATACAAAGTCTGTGACTACATCTGG 375
DB 2364 TTTCCTACCCCTTGGTGTGATCTCTATCCGATGATACAAAGTCTGTGACTACATCTGG 2423
QY 376 AGGGGGAGACAGGGGCGCTTATAGCGCCATTTATGGCGGTGGCTCTGGGGTTGC 435
DB 2424 AGGGGGAGACAGGGGCGCTTATAGCGCCATTTATGGCGGTGGCTCTGGGGTTGC 2483
QY 436 AACTGCCGCAAAATAACAGGGCGCGAGCTGTGATCAAGCCAAACAAATGCTGCCAA 495
DB 2484 AACTGCCGCAAAATAACAGGGCGCGAGCTGTGATCAAGCCAAACAAATGCTGCCAA 2543
QY 496 CATCTCCGACTTAAAGAGACATTTGCGCAACCAATGAGCTGTGATGAGTCACTGA 555
DB 2544 CATCTCCGACTTAAAGAGACATTTGCGCAACCAATGAGCTGTGATGAGTCACTGA 2603
QY 556 CGGATTAATCGCACTAGCAGTGGCGATTTGGAGATGACAGATTTGTTATGACCAATT 615
DB 2604 CGGATTAATCGCACTAGCAGTGGCGATTTGGAGATGACAGATTTGTTATGACCAATT 2663
QY 616 TAAATAAAACGCTCAGGAATTTAGCTGCATCAAAATTGCAAGCAAGTTGGTAGAGCT 675
DB 2664 TAAATAAAACGCTCAGGAATTTAGCTGCATCAAAATTGCAAGCAAGTTGGTAGAGCT 2723
QY 676 CAACCTGACCTAACCGAATTTGACTACAGTATTCGACCAACAAATCACTTGACCTGCTTT 735
DB 2724 CAACCTGACCTAACCGAATTTGACTACAGTATTCGACCAACAAATCACTTGACCTGCTTT 2783
QY 736 AAACAACTGACTATTCAGGACCTTTTCAATCTAGCTGTGGTGAATAATGATTAATT 795
DB 2784 AAACAACTGACTATTCAGGACCTTTTCAATCTAGCTGTGGTGAATAATGATTAATT 2843
QY 796 GACTAAGTTAGGTAGGGAACAAATCAATCACTGCTCATTAATCGGTAGCGGCTTAATCAG 855
DB 2844 GACTAAGTTAGGTAGGGAACAAATCAATCACTGCTCATTAATCGGTAGCGGCTTAATCAG 2903
QY 856 CGGTAACCTTATTCATACGCTCAGACACTCACTCTGGGGTTATACAGTAATCTTACC 915
DB 2904 CGGTAACCTTATTCATACGCTCAGACACTCACTCTGGGGTTATACAGTAATCTTACC 2963
QY 916 TTCAGTCGGGAACCTTAATATATATATGCTGCCACTTCTTGAAACCTTATCCGTAAGCAG 975
DB 2964 TTCAGTCGGGAACCTTAATATATATATGCTGCCACTTCTTGAAACCTTATCCGTAAGCAG 3023
QY 976 AACCAAGGATTTCCCTCGGCACTTTCGCCAAAGTGTGACACAGTCCGTTCTGTAT 1035
DB 3024 AACCAAGGATTTCCCTCGGCACTTTCGCCAAAGTGTGACACAGTCCGTTCTGTAT 3083
QY 1036 AGAAGACTTGACACTCATCTGATATAGAAAGTACTTAGATTTATTTATCAAGAAAT 1095
DB 3084 AGAAGACTTGACACTCATCTGATATAGAAAGTACTTAGATTTATTTATCAAGAAAT 3143
QY 1096 AGTAACGTTCCCTATGTCCTCGTGTATTTATTCCTGCTTGAAGCGCAATAGCTGGCCTG 1155
DB 3144 AGTAACGTTCCCTATGTCCTCGTGTATTTATTCCTGCTTGAAGCGCAATAGCTGGCCTG 3203
QY 1156 TATGTACTCAAAAGCCGAGGCGCACTTATACCAATCACTGATCAATCAAGTTCACT 1215
```





```
Db 2424 AGGGGGGAGACAGGGGGCGCTTATAGGCGCAATATTGGCGGTGTGCTTTGGGGTTGC 2483
Qy 436 AACTGCGGACAAATTAACAGGCGCGCAGCTCTGATATACAAAGCAAAATGTCTCCAA 495
Db 2484 AACTGCGGACAAATTAACAGGCGCGCAGCTCTGATATACAAAGCAAAATGTCTCCAA 2543
Qy 496 CATCTTCGACTTAAGAGACATTGGCCGAACCAATGAGGCTGTGCATGAGTCACTGA 555
Db 2544 CATCTTCGACTTAAGAGACATTGGCCGAACCAATGAGGCTGTGCATGAGTCACTGA 2603
Qy 556 CGGATTTATCGCACTAGAGATGGCAGTTGGGAAGATGAGCAGTTTGTATATGACCAAT 615
Db 2604 CGGATTTATCGCACTAGAGATGGCAGTTGGGAAGATGAGCAGTTTGTATATGACCAAT 2663
Qy 616 TAATTAATAACAGCTCAGAAATTAGACTGATCAAAATTGCAAGCAAGTTGGTGTAGAGCT 675
Db 2664 TAATTAATAACAGCTCAGAAATTAGACTGATCAAAATTGCAAGCAAGTTGGTGTAGAGCT 2723
Qy 676 CAACCTGTACTTAAACGAATTGACTACATATTCGGACCACAAAATCACTTCACTGCTTT 735
Db 2724 CAACCTGTACTTAAACGAATTGACTACATATTCGGACCACAAAATCACTTCACTGCTTT 2783
Qy 736 AAAACAGCTGACTTTTACAGGCACTTTACATCTAGCTGTGTGAATATGATTTACTTATT 795
Db 2784 AAAACAGCTGACTTTTACAGGCACTTTACATCTAGCTGTGTGAATATGATTTACTTATT 2843
Qy 796 GACTAAGTTAGGTATAGGGAAACATCAACTGAGCTCATTAATCGGTAGCGGCTTAATCAC 855
Db 2844 GACTAAGTTAGGTATAGGGAAACATCAACTGAGCTCATTAATCGGTAGCGGCTTAATCAC 2903
Qy 856 CGGTAACTCTATTTCTATACGACTCAGACACTCAACTCTTGGGTATACAGTAACTCTAAC 915
Db 2904 CGGTAACTCTATTTCTATACGACTCAGACACTCAACTCTTGGGTATACAGTAACTCTAAC 2963
Qy 916 TTTCGTGGGAACTTAAATTAATGCGTGGCACTACTTGGAAACCTTATCCGTAGACAC 975
Db 2964 TTTCGTGGGAACTTAAATTAATGCGTGGCACTACTTGGAAACCTTATCCGTAGACAC 3023
Qy 976 AACCAAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACAGTGGTCTGTAT 1035
Db 3024 AACCAAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACAGTGGTCTGTAT 3083
Qy 1036 AGAAGAACTTGAACACTTACTGTATGAATAGAACTGACTTAATTTATTTATACAGAAAT 1095
Db 3084 AGAAGAACTTGAACACTTACTGTATGAATAGAACTGACTTAATTTATTTATACAGAAAT 3143
Qy 1096 AGTAACTTCCCTATATGTCCTGCTGATTTATTTCTGCTTGAAGCGGCAATACGTGGCTG 1155
Db 3144 AGTAACTTCCCTATATGTCCTGCTGATTTATTTCTGCTTGAAGCGGCAATACGTGGCTG 3203
Qy 1156 TATGTACTCAAAAGCCGAAGGCGCACTTACACCAATGACTATCAAAAGGTTCACT 1215
Db 3204 TATGTACTCAAAAGCCGAAGGCGCACTTACACCAATGACTATCAAAAGGTTCACT 3263
Qy 1216 CATGCGCAACTGCAAGATGACATGATGATGATAACCCCGGGTATCATATCGCA 1275
Db 3264 CATGCGCAACTGCAAGATGACATGATGATGATAACCCCGGGTATCATATCGCA 3323
Qy 1276 AAATCTATGAGAACCCGTGTCTTAAATGATTAACAATCATGCAATGTTTTATCTTAA 1335
Db 3324 AAATCTATGAGAACCCGTGTCTTAAATGATTAACAATCATGCAATGTTTTATCTTAA 3383
Qy 1336 CGGATTAATCTTAAGGCTCATAGTGGGAATTTGATGTATCTTATCAGAAATATCTCAAT 1395
Db 3384 CGGATTAATCTTAAGGCTCATAGTGGGAATTTGATGTATCTTATCAGAAATATCTCAAT 3443
Qy 1396 ACAAGATTTCTCAAGTAAATTAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATG 1455
Db 3444 ACAAGATTTCTCAAGTAAATTAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATG 3503
Qy 1456 CAACCACTCGATCAATTAATGCTTTGAATTAAGTAAAGGAAAGCAACAGAAAATGACAA 1515
Db 3504 CAACCACTCGATCAATTAATGCTTTGAATTAAGTAAAGGAAAGCAACAGAAAATGACAA 3563
```

```
Qy 1516 AGTCAATGTCAAACTGACTAGACATCTGCTCTCATTAAGTATATGTTTTGACTATCAT 1575
Db 3564 AGTCAATGTCAAACTGACTAGACATCTGCTCTCATTAAGTATATGTTTTGACTATCAT 3623
Qy 1576 ATCTCTGTTTTTGGTATACTTACCTTGATTTCTGATGCTACTAATATGTAACAGCAAAA 1635
Db 3624 ATCTCTGTTTTTGGTATACTTACCTTGATTTCTGATGCTACTAATATGTAACAGCAAAA 3683
Qy 1636 GGCGCAACAAAAAAGCTTATATGAGCTTGGGAATATATCTAGATCAGATGAGAGCCAC 1695
Db 3684 GGCGCAACAAAAAAGCTTATATGAGCTTGGGAATATATCTAGATCAGATGAGAGCCAC 3743
Qy 1696 TACAAAAATGTGAACACAGATGAGAAAGAAAGTTTCCCTTAATAGTAATTTGTGAAG 1755
Db 3744 TACAAAAATGTGAACACAGATGAGAAAGAAAGTTTCCCTTAATAGTAATTTGTGAAG 3803
Qy 1756 TTCTGTAGTCTGTCACTTTCAGAGATGTAAGAAAAA 1792
Db 3804 TTCTGTAGTCTGTCACTTTCAGAGATGTAAGAAAAA 3840
```

## RESULT 13

AAC67862 ID AAC67862 standard; DNA; 4177 BP.

AAC67862;

06-AUG-2003 (revised)  
02-MAR-2001 (first entry)

Sfil fragment comprising NDV HN and F gene.

Fowlpox virus; FPV; antiviral; antibacterial; vaccine;  
Newcastle's disease virus; NDV; Marek's disease;  
infectious laryngotracheitis; Sfil fragment; HN glycoprotein;  
F glycoprotein; ds.

Newcastle disease virus.

US6136318-A.

24-OCT-2000.

07-JUN-1995; 95US-00486414.

26-FEB-1993; 93US-00024156.

28-FEB-1994; 94WO-US002252.

(JUNK/) JUNKER D E.

(COCH/) COCHRAN M D.

Cochran MD, Junker DE;

WPI; 2000-686071/67.

P-PSDB; AAB36038.

New recombinant fowlpox virus useful as vaccines contains foreign DNA

Inserted into specific non-essential region of the genome.

Disclousure; Col 59-68; 56pp; English.

The present sequence is provided in a specification relating to a recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted within a 3.5 kb EcoRI fragment of the FPV genomic DNA. The foreign DNA can be expressed in host cells infected with FPV. The recombinant FPV may be used in vaccines to protect animals (especially chickens) against fowlpox and, depending on the source of the foreign DNA, other diseases, particularly Newcastle's disease, Marek's disease or infectious laryngotracheitis. (Updated on 06-AUG-2003 to correct OS field.)

Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;

Query Match 51.9%; Score 1741.8; DB 3; Length 4177;  
 Best Local Similarity 98.8%; Pred. No. 0;  
 Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

16 TGAATCCCGGTTGGCGGCTCCAGATGAGATGGGCTCCAGACCTTCTACCAAGAACCC 75  
 Db TCGATCCCGGTTGGCGGCTCCAGATGAGATGGGCTCCAGACCTTCTACCAAGAACCC 2123

Qy 76 AGCACTATGATGCTGATCTATCCGGGTTGGCGCTGGCACTGAGTTGACTTGTCCGGGAAA 135  
 Db AGCACTATGATGCTGATCTATCCGGGTTGGCGCTGGCACTGAGTTGACTTGTCCGGGAAA 2183

Qy 136 CTCATTGATGAGCGGCTCTTGGCACTGCGAAGATTGGTTTCAAGAGCAAAAGCCCT 195  
 Db CTCATTGATGAGCGGCTCTTGGCACTGCGAAGATTGGTTTCAAGAGCAAAAGCAAGT 2243

Qy 196 CAACATATACACCTATCCCGAGACAGATGCAATGTTAAAGCTCCCGGAACTGCGC 255  
 Db CAACATATACACCTATCCCGAGACAGATGCAATGTTAAAGCTCCCGGAACTGCGC 2303

Qy 256 CAAGATTAAGAGGATGTCGGAAGCCCTCTTGATGCAATACAAAGACATTGACAC 315  
 Db CAAGATTAAGAGGATGTCGGAAGCCCTCTTGATGCAATACAAAGACATTGACAC 2363

Qy 316 TTGGCTACCCCTCTGCTGATCTTATCCGTAAGATACAGAGTCTGTGACTACATCTGG 375  
 Db TTGGCTACCCCTCTGCTGATCTTATCCGTAAGATACAGAGTCTGTGACTACATCTGG 2423

Qy 376 AGGGGGGAGACAGGGGGGCTTATAGGGCCATTAATGGGGGCTGTTGGGCTCTGGGGTTGC 435  
 Db AGGGGGGAGACAGGGGGGCTTATAGGGCCATTAATGGGGGCTGTTGGGCTCTGGGGTTGC 2483

Qy 436 AACTGCCGCACAATTAACAGGGGCGGAGCTCTGATACAAGCCAAACAAATGCTGCCAA 495  
 Db AACTGCCGCACAATTAACAGGGGCGGAGCTCTGATACAAGCCAAACAAATGCTGCCAA 2543

Qy 496 CATCTCCGACTTAAGAAGACATTTGGCGCAACAAAGAGCTGTGATGAGTCACTGA 555  
 Db CATCTCCGACTTAAGAAGACATTTGGCGCAACAAAGAGCTGTGATGAGTCACTGA 2603

Qy 556 CGGATTAATCCCACTAGACAGTGGAGTTGGGAATGACAGAGTTGTTATGACCAATT 615  
 Db CGGATTAATCCCACTAGACAGTGGAGTTGGGAATGACAGAGTTGTTATGACCAATT 2663

Qy 616 TAAATAAAGAGCTCAGGAATTAGACTGATCAAAATTGCAAGAGAGTTGGTGTAGACT 675  
 Db TAAATAAAGAGCTCAGGAATTAGACTGATCAAAATTGCAAGAGAGTTGGTGTAGACT 2723

Qy 676 CAACCTGTACTTAAACGAATTGACTACAGTATTCGACACCAATTCACCTTGCCTT 735  
 Db CAACCTGTACTTAAACGAATTGACTACAGTATTCGACACCAATTCACCTTGCCTT 2783

Qy 736 AAACAAGCTACTATTAGGCACTTACAACTTACGCTGGGGAATAATGATTACTTATT 795  
 Db AAACAAGCTACTATTAGGCACTTACAACTTACGCTGGGGAATAATGATTACTTATT 2843

Qy 796 GACTAAGTATGATGAGGAACAATCACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC 855  
 Db GACTAAGTATGATGAGGAACAATCACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC 2903

Qy 856 CGGTAAACCTATTCTATACGACTCACAAGACTCAACTCTGGGGTATACAGTAACTTACC 915  
 Db CGGTAAACCTATTCTATACGACTCACAAGACTCAACTCTGGGGTATACAGTAACTTACC 2963

Qy 916 TTCAAGTGGGAACCTAATAATATGCGTGGCACTTCTGGAACCTTAATCCGTAACGAC 975  
 Db TTCAAGTGGGAACCTAATAATATGCGTGGCACTTCTGGAACCTTAATCCGTAACGAC 3023

Qy 976 AACCAAGGAGTTTGGCTCGGCACTTGTCCCAAAAGGTGTGACACAGGTCGGTCTGTGAT 1035  
 Db AACCAAGGAGTTTGGCTCGGCACTTGTCCCAAAAGGTGTGACACAGGTCGGTCTGTGAT 3083

Qy 1036 AGAAGAACTTGACACCTCATCTGTATAGAAAGTGAAGTTGATTTATTTGTACAGAAAT 1095

Db 3084 AGAAGAACTTGACACCTCATCTGTATAGAAAGTGAAGTTGATTTATTTGTACAGAAAT 3143

Qy 1096 AGTAACGTTCCCTATGTCCTGCTGATTTATTCCTGCTTGAAGCGGCAATACGTCGCTG 1155

Db 3144 AGTAACGTTCCCTATGTCCTGCTGATTTATTCCTGCTTGAAGCGGCAATACGTCGCTG 3203

Qy 1156 TATGTACTCAAAAGACGGAAGCGGCACTTACTACACCATATCATGACTATCAAGGTTACGT 1215

Db 3204 TATGTACTCAAAAGACGGAAGCGGCACTTACTACACCATATCATGACTATCAAGGTTACGT 3263

Qy 1216 CATGCGCAATGGAAGAATGACATGATGATGTTAAACCCCGGGGTATCATGCA 1275

Db 3264 CATGCGCAATGGAAGAATGACATGATGATGTTAAACCCCGGGGTATCATGCA 3323

Qy 1276 AAACATAGGAAGCCGCTGCTCTAATAGATAAACAATCATGCAATGTTTATCTTACG 1335

Db 3324 AAACATAGGAAGCCGCTGCTCTAATAGATAAACAATCATGCAATGTTTATCTTACG 3383

Qy 1336 CGGGATTACTTTAAGGCTCAGTGGGGAATTCGATGTAATCTTATCAGAAGAAATATCTCAAT 1395

Db 3384 CGGGATTACTTTAAGGCTCAGTGGGGAATTCGATGTAATCTTATCAGAAGAAATATCTCAAT 3443

Qy 1396 ACAAGATTCACAGTATTAATTAACAGGCAATCTTGATATCTCACTGAGCTGGGAATGT 1455

Db 3444 ACAAGATTCACAGTATTAATTAACAGGCAATCTTGATATCTCACTGAGCTGGGAATGT 3503

Qy 1456 CAACAATCGATCAGTAATGCTTTGATAATAGTTAGAGAAAGCAAGAAACCTAGACAA 1515

Db 3504 CAACAATCGATCAGTAATGCTTTGATAATAGTTAGAGAAAGCAAGAAACCTAGACAA 3563

Qy 1516 AGTCATATGTAACCTGATGACATCTGCTCTCATTAATCTTATGCTTTGACTATCAT 1575

Db 3564 AGTCATATGTAACCTGATGACATCTGCTCTCATTAATCTTATGCTTTGACTATCAT 3623

Qy 1576 ATCTGTTGTTTGGTATTAATTAATGCTTATGAGTCTAGACGCTTACTTAATGTAACGAAA 1635

Db 3624 ATCTGTTGTTTGGTATTAATTAATGCTTATGAGTCTAGACGCTTACTTAATGTAACGAAA 3683

Qy 1636 GGGGCAACAAAACCTTATTAATGCTTGGGAATAATCTTATGATCAGATGAGAGCCAC 1695

Db 3684 GGGGCAACAAAACCTTATTAATGCTTGGGAATAATCTTATGATCAGATGAGAGCCAC 3743

Qy 1696 TACAAAATGTGAACACAGATGAGAAAGAAAGTTTCCCTTAATGTAATTTGTGTGAAG 1755

Db 3744 TACAAAATGTGAACACAGATGAGAAAGAAAGTTTCCCTTAATGTAATTTGTGTGAAG 3803

Qy 1756 TTCTGTAGTCTGTCAAGTTCAGAGATTAGAAAAA 1792

Db 3804 TTCTGTAGTCTGTCAAGTTCAGAGATTAGAAAAA 3840

RESULT 14  
 ABK90556  
 ID ABK90556 standard; cDNA; 3570 BP.  
 XX  
 AC ABK90556;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Newcastle disease virus (NDV) fusion gene.  
 XX  
 KW Newcastle disease virus; gene; ss; novel recombinant avian herpesvirus;  
 XX  
 KW NAHV; herpes virus of turkeys; HVT; Marek's disease; Newcastle disease;  
 XX  
 KW infectious laryngotracheitis; virucide; immunostimulant; vaccine; NDV.  
 XX  
 OS Newcastle disease virus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1194..2888  
 FT /\*tag= a  
 FT /product= "Newcastle disease virus protein"  
 FT /transl\_except= (pos:1353..1355, aa:1xaa)

FT /note= "Xaa= unknown"  
 XX US2002081316-A1.  
 XX 27-JUN-2002.  
 XX 14-JUN-2001; 2001US-00881457.  
 XX 12-JUN-1992; 92US-00898087.  
 XX 26-FEB-1993; 93US-00023610.  
 XX 14-JUN-1993; 93WO-US005681.  
 XX 09-AUG-1994; 94US-00288055.  
 XX 13-JUN-1995; 95WO-US010245.  
 XX 21-FEB-1997; 96US-00663566.  
 XX 25-OCT-1999; 99US-00426352.  
 XX (COCH/) COCHRAN M D.  
 XX (COOK/) COOK S M.  
 XX (WILD/) WILD M A.  
 XX Cochran MD, Cook SM, Wild MA;  
 XX WPI; 2002-635456/68.  
 XX P-PSDB; ABG31709.  
 XX Novel recombinant avian herpesvirus comprising unique long and repeat  
 PT genome regions of herpes virus of turkeys, unique short viral  
 PT genome region of Marek's disease virus, and optional foreign DNA  
 PT sequence.  
 XX Disclosure; Page 12-14; 26pp; English.  
 PS The invention relates to a novel recombinant avian herpesvirus (NAHV)  
 CC comprising a herpes virus of turkeys (HVT) unique long (UL) and repeat  
 CC viral genome region and a Marek's disease virus unique short (US) viral  
 CC genome region where at least one foreign DNA sequence is inserted within  
 CC a US2 gene of the US region of the NAHV, and is capable of being  
 CC expressed in a host cell. NAHV is useful for producing vaccines used for  
 CC immunizing an avian species against Newcastle disease, infectious  
 CC laryngotracheitis and Marek's disease. This sequence represents a  
 CC Newcastle disease virus (NDV) fusion gene  
 CC XX  
 SQ Sequence 3570 BP; 982 A; 857 G; 845 T; 0 U; 1 Other;  
 Query Match 50.7%; Score 1701.6; DB 6; Length 3570;  
 Best Local Similarity 98.4%; Pred. No. 0;  
 Matches 1749; Conservative 0; Mismatches 25; Indels 3; Gaps 3;  
 QY 16 TGAATCCCGGTTGGGCGCCCTCCAGATGCAAGTGGGCTCCAGACCTTCTACCAAGAACCC 75  
 Db 1199 TCGATCCCGGTTGGGCGCCCTCCAGATGCAAGTGGGCTCCAGACCTTCTACCAAGAACCC 1258  
 QY 76 AGCACTATGATGCTGACTATCCGGGTTGCGCTGCACTGATGTCATGTCCGGCAA 135  
 Db 1259 AGCACTATGATGCTGACTATCCGGGTTGCGCTGCACTGATGTCATGTCCGGCAA 1318  
 QY 136 CTCCTATGATGCGAGGCTCTTTCAGCTGCAAGAAATTGTGTTACAGAGAACAAAGCCGT 195  
 Db 1319 CTCCTATGATGCGAGGCTCTTTCAGCTGCAAGG-ACITGTGTTACAGAGAACAAAGCAAT 1377  
 QY 196 CAACATATACACTCATCCAGACAGATGCAATGATTAAGTCTTCCGGAATCTGCC 255  
 Db 1378 CAACATATACACTCATCCAGACAGG-TCAATCTTA-TTAAAGTCTTCCGGAATCTGCC 1435  
 QY 256 CAAGATTAAGAGGAGGATGCGAAAGCCCTTGATGATCAACAGAGCAATTGACAC 315  
 Db 1436 AAAGATTAAGAGGAGGATGCGAAAGCCCTTGATGATCAACAGAGCAATTGACAC 1495  
 QY 316 TTCTGTCACCCCTTGTGTAATCTATCCGTAAGATTAAGAGTGTGATCACTTAC 375  
 Db 1496 TTCTGTCACCCCTTGTGTAATCTATCCGTAAGATTAAGAGTGTGATCACTTAC 1555

QY 376 AGGGGGGAGACAGGGGCGCCCTTATAGGGCCATTAATGCGGTGCGCTTGGGGTTC 435  
 Db 1556 AGGGGGGAGACAGGGGCGCCCTTATAGGGCCATTAATGCGGTGCGCTTGGGGTTC 1615  
 QY 436 AACTGCGGACAAATTAACAGGGGCGGAGCTCTGATACAGAGCAAAATAATGCTGCCAA 495  
 Db 1616 AACTGCGGACAAATTAACAGGGGCGGAGCTCTGATACAGAGCAAAATAATGCTGCCAA 1675  
 QY 496 CATCTCCGACTTAAGAGACATTCGCGCAACCAATGAGGCTGTGATGAGCTCTGCA 555  
 Db 1676 CATCTCCGACTTAAGAGACATTCGCGCAACCAATGAGGCTGTGATGAGCTCTGCA 1735  
 QY 556 CGATTTATCGCACTAGACAGTGGCACTTGGGAAGATGACAGAGTTTGTATGACCAATT 615  
 Db 1736 CGATTTATCGCACTAGACAGTGGCACTTGGGAAGATGACAGAGTTTGTATGACCAATT 1795  
 QY 616 TAAATTAACAGCTGAGAAATTAAGTGTGATCAAGCAAGTGTGATGAGCT 675  
 Db 1796 TAAATTAACAGCTGAGAAATTAAGTGTGATCAAGCAAGTGTGATGAGCT 1855  
 QY 676 CAACCTGACCTTAACCGAATGACTACAGTATTCGACCAACCAATCACTTCACTGCTTT 735  
 Db 1856 CAACCTGACCTTAACCGAATGACTACAGTATTCGACCAACCAATCACTTCACTGCTTT 1915  
 QY 736 AAACAGCTGACTATTCAGGCACTTTACATCTAGCTGTGGAATAATGATTTACTTATT 795  
 Db 1916 AAACAGCTGACTATTCAGGCACTTTACATCTAGCTGTGGAATAATGATTTACTTATT 1975  
 QY 796 GACTAAGTTAGTGTAGGGAACAATCACTAGGCTCAATTAACGCTGAGCTTAATATC 855  
 Db 1976 GACTAAGTTAGTGTAGGGAACAATCACTAGGCTCAATTAACGCTGAGCTTAATATC 2035  
 QY 856 CGGTAACTCTATCTATACGACTCAAGACTCAACTCTTGGGATATACAGTAACTCTAAC 915  
 Db 2036 CGGTAACTCTATCTATACGACTCAAGACTCAACTCTTGGGATATACAGTAACTCTAAC 2095  
 QY 916 TTCACTGCGGAACTTAATTAATATGCGGCACTTCTGGAACCTTAATCGTAAAGAC 975  
 Db 2096 TTCACTGCGGAACTTAATTAATATGCGGCACTTCTGGAACCTTAATCGTAAAGAC 2155  
 QY 976 AACCAAGGGAATTCCTCCGCACTTGTCCCAAGGTGTGACAGGTCGGTTCGTAT 1035  
 Db 2156 AACCAAGGGAATTCCTCCGCACTTGTCCCAAGGTGTGACAGGTCGGTTCGTAT 2215  
 QY 1036 AGAAGACTTGAACACTGATCTGATAGAACTGACTTGAATTTATTTGATCAAGAT 1095  
 Db 2216 AGAAGACTTGAACACTGATCTGATAGAACTGACTTGAATTTATTTGATCAAGAT 2275  
 QY 1156 TATGATCTCAAAAGCCGAAGGCGCACTTACTACCAATCAATGACTATCAAAAGTTGAGT 1215  
 Db 2276 TATGATCTCAAAAGCCGAAGGCGCACTTACTACCAATCAATGACTATCAAAAGTTGAGT 2335  
 QY 1216 CATGCCCACTGCAAGATGACACATGTAGATGTGTAACCCCGGGGTATCATATGCA 1275  
 Db 2336 CATGCCCACTGCAAGATGACACATGTAGATGTGTAACCCCGGGGTATCATATGCA 2455  
 QY 1276 AAATATGAGAAACCGGTCTCTAATATAGATTAACATCATGCAATGTTTATCTTAAAG 1335  
 Db 2456 AAATATGAGAAACCGGTCTCTAATATAGATTAACATCATGCAATGTTTATCTTAAAG 2515  
 QY 1336 CGGATTAATCTTAAGGCTCACTGGGGAATTCGATGTAACTTATCAGAAATATCTCAAT 1395  
 Db 2516 CGGATTAATCTTAAGGCTCACTGGGGAATTCGATGTAACTTATCAGAAATATCTCAAT 2575  
 QY 1396 ACAAGATTCGAAGTAATTAATCAAGGCACTTGAATCTCAACTGAGCTTGGGAATGT 1455  
 Db 2576 ACAAGATTCGAAGTAATTAATCAAGGCACTTGAATCTCAACTGAGCTTGGGAATGT 2635  
 QY 1456 CAACAACTGATCAGTAATGCTTTGAATTAAGTGAAGAAAGCAACAGAAACTAGACAA 1515

Db	2636	CACAACTCCATCACTAATGCCCTTGAAATTAAGTTAGAGAAAGCAACAGAAAACCTAGACA	2635
Qy	1516	AGTCATGTCAAACTGACTAGACACATCTGCTCTCATTAACCTATATCGTTTGAATCAT	1575
Db	2696	AGTCATGTCAAACTGACACAGACATCTGCTCTCATTAACCTATATCGTTTGAATCAT	2755
Qy	1576	ATCTCTGTCTTTGGTATACCTTAGCCCTGATCTAGACGTCACCTAAATGTACAAAGCAAA	1635
Db	2756	ATCTCTGTCTTTGGTATACCTTAGCCCTGATCTAGACGTCACCTAAATGTACAAAGCAAA	2815
Qy	1636	GGCGCAACAAAAACCTATTATGGCTTGGGAATATATCTAGATCAGATGAGCCAC	1695
Db	2816	GGCGCAACAAAAACCTATTATGGCTTGGGAATATATCTAGATCAGATGAGCCAC	2875
Qy	1696	TACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAGTAATTTGTGTAAAG	1755
Db	2876	TACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAGTAATTTGTGTAAAG	2935
Qy	1756	TTCTGTGATGTCTGTCACTTCAGAGAGATTAAAGAAAAA	1792
Db	2936	TTCTGTGATGTCTGTCACTTCAGAGAGATTAAAGAAAAA	2972

RESULT 15	
AA18203	
ID	AA18203 standard; DNA; 1662 BP.
XX	
AC	AA18203;
XX	
DT	04-MAR-1997 (first entry)
XX	
DE	Newcastle disease virus F gene.
XX	
KW	Turkey herpes Virus; recombinant virus; vaccine; prophylaxis;
KW	immunisation; avian virus; infectious bronchitis virus;
KW	infectious bursal disease virus; Newcastle disease virus;
KW	Marek's disease virus; infectious laryngotracheitis virus; IBV; IBDV;
KW	NDV; MDV; ILV; ds.
XX	
OS	Newcastle disease virus.
XX	
PH	Key
FT	Location/Qualifiers
FT	1..1662
FT	/*tag= a
FT	/product= "NDV F gene product"
XX	
PN	W09605291-A1.
XX	
PD	22-FEB-1996.
XX	
PF	09-AUG-1995; 95WC-US010245.
XX	
PR	09-AUG-1994; 94US-00288065.
PR	22-DEC-1994; 94US-00362240.
XX	
PA	(SYTR ) SYNTRO CORP.
XX	
PI	Cochran MD, Junker DE, Wild MA, Singer PA;
XX	
DR	WPI; 1996-139689/14.
DR	P-PSDB; AAM06828.
XX	
PT	Recombinant turkey herpes viruses contg. foreign DNA encoding a cytokine
PT	- useful in vaccines to protect against Marek's disease virus and other
PT	avian viruses.
XX	
PS	Disclosure; Page 177-179; 249pp; English.
XX	
CC	Recombinant turkey herpes virus (rTH) which comprise a foreign DNA
CC	sequence encoding a cytokine inserted into a XhoI site within an EcoRI #9
CC	genomic fragment, where the cytokine can be expressed in host cells
CC	infected with the virus can be used in vaccines to protect turkeys

CC against avian viruses. The recombinant viruses can be used for immunising  
CC birds against infectious bronchitis virus (IBV), infectious bursal  
CC disease virus (IBDV), Marek's disease virus (MDV), infectious  
CC laryngotracheitis virus (ILT) and Newcastle disease virus (NDV). They may  
CC also be used in multivalent vaccines to protect against two or more of  
CC these avian viruses. This sequence is the F gene of the Newcastle disease  
CC virus and encodes an antigen which can be used in the recombinant  
CC vaccines  
XX  
SQ Sequence 1662 BP, 507 A, 390 C, 353 G, 412 T, 0 U, 0 Other,  
XX

Query Match	Similarity	48.6%	Score	1631.6	DB	2	Length	1662	
Best Local	Similarity	98.9%	Pred.	No. 0					
Match	1643	Conservative	0	Mismatches	19	Indels	0	Gaps	0
OY	47	ATGGGCTCCAGACCTTCTACCAAGAACCCAGACACTATGATGCTGACTATCCGGGTGCG	106						
Db	1	ATGGGCTCCAGACCTTCTACCAAGAACCCAGACACTATGATGCTGACTATCCGGGTGCG	60						
OY	107	CTGGCAGCTGAGTTGATCTGTCCCGCAAACTTCATTGATGCGCAGGCCCTCTTGCACTGCA	166						
Db	61	CTGGAGCTGAGTTGATCTGTCCCGCAAACTTCATTGATGCGCAGGCCCTCTTGCACTGCA	120						
OY	167	GGAATTGGTGTTACAGAGACAAAGCCGTCACATATACACCTCATCCAGACAGATCA	226						
Db	121	GGAATTGGTGTTACAGAGACAAAGCACTCAACATATACACTCTATCCAGACAGATCA	180						
OY	227	ATCATAGTTAAGCTCTCCGAAATCTGCGCAAGATTAAGAGAGATGTGCGAAACCCCC	286						
Db	181	ATCATAGTTAAGCTCTCCGAAATCTGCGCAAGATTAAGAGAGATGTGCGAAACCCCC	240						
OY	287	TTGGATGATACCAACAGACATTTGACCTTTCACCCCTTGATGACCTATACCGT	346						
Db	241	TTGGATGATACCAACAGACATTTGACCTTTCACCCCTTGATGACCTATACCGT	300						
OY	347	AGGATACCAAGAGTCTGTACTACATCTGAGAGGGGAGACAGGGCGGCTTTAAGCGCC	406						
Db	301	AGGATACCAAGAGTCTGTACTACATCTGAGAGGGGAGACAGGGCGGCTTTAAGCGCC	360						
OY	407	ATTATTTGGCGGTGTGGCTCTTGGGGTTGCCA CTGCGCGCAAAATTAACAGCGGCGCAGCT	466						
Db	361	ATTATTTGGCGGTGTGGCTCTTGGGGTTGCCA CTGCGCGCAAAATTAACAGCGGCGCAGCT	420						
OY	467	CTGATACCAAGCCAAACAAATGTCTGCCAATCTCCGCACTTAAAGAGAGCTTTCGCGA	526						
Db	421	CTGATACCAAGCCAAACAAATGTCTGCCAATCTCCGCACTTAAAGAGAGCTTTCGCGA	480						
OY	527	ACCAATGAGGCTGTGCATGAGGTCACTGACGGATTTATGCAACTAGCAGTGGCAAGTTGGG	586						
Db	481	ACCAATGAGGCTGTGCATGAGGTCACTGACGGATTTATGCAACTAGCAGTGGCAAGTTGGG	540						
OY	587	AAGATGACAGAGTTTGTTAATGACCAATTTTAATTAATAAGCTCAGAGATTTAACTGCAAC	646						
Db	541	AAGATGACAGAGTTTGTTAATGACCAATTTTAATTAATAAGCTCAGAGATTTAACTGCAAC	600						
OY	647	AAATTTGACACGAAAGTTGTGTAGAGCTCAACCTGTACTTAACCGAATTGACTACAGTA	706						
Db	601	AAATTTGACACGAAAGTTGTGTAGAGCTCAACCTGTACTTAACCGAATTGACTACAGTA	660						
OY	707	TTGCGACCAAAATCATCTTCACTGTCTTAAACAAAGCTGACTATTCAGGCACTTTACAT	766						
Db	661	TTGCGACCAAAATCATCTTCACTGTCTTAAACAAAGCTGACTATTCAGGCACTTTACAT	720						
OY	767	CTACTCGTGGAAATATGGAATTACTATTATGACTAAGTTAGGGTATGGGAAACAATCAATC	826						
Db	721	CTACTCGTGGAAATATGGAATTACTATTATGACTAAGTTAGGGTATGGGAAACAATCAATC	780						
OY	827	AGCTCATTAATCGGATGCGCTTAATCAACCGGTAAACCTATTTCTATAAGACTCAGACA	886						
Db	781	AGCTCATTAATCGGATGCGCTTAATCAACCGGTAAACCTATTTCTATAAGACTCAGACA	840						
OY	887	CAACTCTTGGGTATACAGTAACTCTTACCTTGAGTGGGAACTTAATTAATATGCGTGGC	946						

```
Db      841 CAACTCTGGGTATACAGGTACTTACCTTCAGTCGGGAACTTAATAATATGCGTCC 900
Qy      947 ACCTACTGGAAACCTTATCCGTAAAGCAAAACAGGGGATTTGCTCGGCACTGTCCCA 1006
Db      901 ACCTACTGGAAACCTTATCCGTAAAGCAAAACAGGGGATTTGCTCGGCACTGTCCCA 960
Qy      1007 AAAGTGTGACACAGGTGGTTCTGTGTATAGAGAACTTGACACTCTACTGTATAGAA 1066
Db      961 AAAGTGTGACACGGGTGGTTCTGTGTATAGAGAACTTGACACTCTACTGTATAGAA 1020
Qy      1067 ACTGACTTAAATTTATTTATTTAGCAAGATATGTAACGTTCCCTATGTCCCTGTATTTAT 1126
Db      1021 ACTGACTTAAATTTATTTATTTAGCAAGATATGTAACGTTCCCTATGTCCCTGTATTTAC 1080
Qy      1127 TCCTGCTTGAACGGCAATACGTCCGCTGTATGTACTCAAAAGCCGAAGCGCACTTACT 1186
Db      1081 TCCTGCTTGAACGGCAATACGTCCGCTGTATGTACTCAAAAGCCGAAGCGCACTTACT 1140
Qy      1187 ACACCATACATGACTATCAAAAGTTCACTCATCCGCAACTGCAAGATGACACATGTAGA 1246
Db      1141 ACACCATATATGACTATCAAAAGCTCAGTCATCCGTAACGCAAGATGACAAACATGTAGA 1200
Qy      1247 TGTGTAAACCCCGGGGTATCATATCGCAAAACTATGAGAAAGCCGTCCTCTAATAGAT 1306
Db      1201 TGTGTAAACCCCGGGGTATCATATCGCAAAACTATGAGAAAGCCGTCCTCTAATAGAT 1260
Qy      1307 AAACATCATGCAATGTTTATCTTATCGGTAGCGGSAATTACTTAAAGGCTCAGTGGGAATTC 1366
Db      1261 AAACATCATGCAATGTTTATCTTATCGGTAGCGGSAATTACTTAAAGGCTCAGTGGGAATTC 1320
Qy      1367 GATGTAACTTATCAGAAAGATATCTCAATACAAAGTTCTCAAGTAAATATTAACAGGCAAT 1426
Db      1321 GATGTAACTTATCAGAAAGATATCTCAATACAAAGTTCTCAAGTAAATATTAACAGGCAAT 1380
Qy      1427 CTTGATATCTCAACTGAGCTTGGGAATGTCAACAACCTGATCAAGTATGCTTTGAATAG 1486
Db      1381 CTTGATATCTCAACTGAGCTTGGGAATGTCAACAACCTGATCAAGTATGCTTTGAATAG 1440
Qy      1487 TTAGAGAAAGCAACAGAAACTAGACAAAGTCAATGTCAAACTGACTAGCACAATCTGCT 1546
Db      1441 TTAGAGAAAGCAACAGAAACTAGACAAAGTCAATGTCAAACTGACTAGCACAATCTGCT 1500
Qy      1547 CTCAATTACCTATATCGTTTGACTATCAATATCTCTGTGTTTGGTATACTTAGCCTGAT 1606
Db      1501 CTCAATTACCTATATCGTTTGACTATCAATATCTCTGTGTTTGGTATACTTAGCCTGAT 1560
Qy      1607 CTAGCATGCTTACTTATGTATCAAGCAAAAGCGCAACAAAACCTTATTTATGCTTGGG 1666
Db      1561 CTAGCATGCTTACTTATGTATCAAGCAAAAGCGCAACAAAACCTTATTTATGCTTGGG 1620
Qy      1667 AATAATCTCTAGATCAGATGAGAGCCACTAATAAATGTGA 1708
Db      1621 AATAATCTCTAGATCAGATGAGAGCCACTAATAAATGTGA 1662
```

Search completed: February 4, 2006, 22:04:25  
Job time : 1908 secs

This Page Blank (use for)



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 21:39:14 ; Search time 569 Seconds  
(without alignments)  
10490.425 Million cell updates/sec

Title: US-10-800-256-1

Perfect score: 3358  
Sequence: 1 acgggtagaagattctggat.....cctaactctatagaacc 3358

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/1.COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5.COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/H.COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/PTUS.COMB.seq.\*  
7: /cgn2\_6/ptodata/1/ina/PP.COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE.COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3353.2	99.9	15186	3	US-09-741-744A-134
2	3196.4	95.2	3825	9	5310678-2
3	1741.8	51.9	4177	2	US-08-484-575A-12
4	1741.8	51.9	4177	3	US-08-477-459-12
5	1741.8	51.9	4177	3	US-08-479-869-12
6	1741.8	51.9	4177	3	US-08-486-414-12
7	1741.8	51.9	4177	6	PCT-US94-01826A-12
8	1741.8	51.9	4177	6	PCT-US94-02252A-12
9	1701.6	50.7	3570	3	US-09-881-457A-1
10	1631.6	48.6	1662	2	US-08-663-566A-12
11	1631.6	48.6	1662	2	US-08-023-610-12
12	1631.6	48.6	1662	2	US-08-288-065A-12
13	1631.6	48.6	1662	2	US-08-362-240A-12
14	1631.6	48.6	1662	3	US-08-804-372A-10
15	1631.6	48.6	1662	6	PCT-US95-10245-12
16	1511	45.0	1907	2	US-07-820-154A-29
17	1511	45.0	1907	2	US-08-097-554A-29
18	1511	45.0	1907	3	US-08-480-640A-29
19	1511	45.0	1907	3	US-08-295-802-29
20	1511	45.0	1907	3	US-08-488-237A-29
21	1511	45.0	1907	3	US-08-375-992A-29
22	1511	45.0	1907	3	US-08-472-679H-29
23	1511	45.0	1907	6	PCT-US93-00324-29
24	1448	43.1	2176	2	US-07-778-890A-2

25	1421.6	42.3	1734	2	US-08-663-566A-10	Sequence 10, Appl
26	1421.6	42.3	1734	2	US-08-023-610-10	Sequence 10, Appl
27	1421.6	42.3	1734	2	US-08-288-065A-10	Sequence 10, Appl
28	1421.6	42.3	1734	2	US-08-362-240A-10	Sequence 8, Appl1
29	1421.6	42.3	1734	2	US-08-804-372A-8	Sequence 10, Appl1
30	1421.6	42.3	1734	6	PCT-US95-10245-10	Sequence 1, Appl1
31	1414	42.1	1662	3	US-10-725-841-1	Sequence 16, Appl
32	1368.4	40.8	2521	2	US-08-368-803-16	Sequence 18, Appl
33	1368.4	40.8	2521	2	US-08-578-096A-18	Sequence 8, Appl1
34	1368.4	40.8	2521	3	US-08-750-517-8	Sequence 18, Appl
35	1368.4	40.8	2521	3	US-09-240-426-18	Sequence 14, Appl
36	1368.4	40.8	2521	3	US-09-219-932-14	Sequence 8, Appl1
37	1368.4	40.8	2521	3	US-09-362-831-8	Sequence 10, Appl
38	1362.8	40.6	1662	3	US-09-232-479-10	Sequence 10, Appl
39	1362.8	40.6	1662	3	US-09-784-990-10	Sequence 7, Appl1
40	1160.8	34.6	1716	3	US-09-232-479-7	Sequence 14, Appl
41	1160.8	34.6	1716	3	US-09-784-990-7	Sequence 370, App
42	127.2	3.8	1685	2	US-08-105-483-370	Sequence 370, App
43	127.2	3.8	1685	2	US-08-709-209-370	Sequence 370, App
44	127.2	3.8	1685	2	US-08-458-101-370	Sequence 3, Appl1
45	120.2	3.6	1656	2	US-08-700-548-3	

#### ALIGNMENTS

RESULT 1  
US-09-741-744A-134  
Sequence 134, Application US/09741744A  
Patent No. 6719979  
GENERAL INFORMATION:  
APPLICANT: Peeters, Bernadus  
APPLICANT: de Leeuw, Olav  
APPLICANT: Klaus, Guus  
APPLICANT: Arroud, Gielkens  
TITLE OR INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnostic  
FILE REFERENCE: 2183-464US  
CURRENT FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: 2000-12-19  
PRIOR FILING DATE: 1999-06-17  
NUMBER OF SEQ ID NOS: 148  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 134  
LENGTH: 15186  
TYPE: DNA  
ORGANISM: Newcastle disease virus LaSota  
US-09-741-744A-134

Query Match 99.9%; Score 3353.2; DB 3; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	ACGGGTGAAAGATTCTGGATCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60
DB	4498	ACGGGTGAAAGATTCTGGATCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	4557
QY	61	TTTACCAAGAACCCAGACCTATGATGCTGACTATCCGGTGGCGTGGCTGAGTTG	120
DB	4558	TTTACCAAGAACCCAGACCTATGATGCTGACTATCCGGTGGCGTGGCTGAGTTG	4617
QY	121	CATCTGTCGGCAACTCCATTGATGAGGCTCTTGCAGCTGCAGAAATGGTTAC	180
DB	4618	CATCTGTCGGCAACTCCATTGATGAGGCTCTTGCAGCTGCAGAAATGGTTAC	4677
QY	181	AGGAGCAAAAGCCGTCAATATACCTTATCCCAAGAGATCAATCAATTAAGCT	240
DB	4678	AGGAGCAAAAGCCGTCAATATACCTTATCCCAAGAGATCAATCAATTAAGCT	4737
QY	241	CTCTCCGAATCTGCCAAGGTAAGAGGAGGATGTCGGAAGCCCTCTTGATGATACAA	300
DB	4738	CTCTCCGAATCTGCCAAGGTAAGAGGAGGATGTCGGAAGCCCTCTTGATGATACAA	4797

```
QY 301 CAGGACATTGACCACTTTCCTCAACCCCTTGGTGACTCTATCCGTAAGATACAGAGTC 360
DB 4798 CAGGACATTGACCACTTTCCTCAACCCCTTGGTGACTCTATCCGTAAGATACAGAGTC 4857
QY 361 TGTGACATACATCTTGGAGGGGGAGACAGGGGCGCTTATATAGCCCATTTATTTGGCGGTGT 420
DB 4858 TGTGACATACATCTTGGAGGGGGAGACAGGGGCGCTTATATAGCCCATTTATTTGGCGGTGT 4917
QY 421 GGCCTTTGGGGTTGCAACTGCGCGACAAATTAACGCGCGGAGCTCTGATTAACGCCAA 480
DB 4918 GGCCTTTGGGGTTGCAACTGCGCGACAAATTAACGCGCGGAGCTCTGATTAACGCCAA 4977
QY 481 ACAAATATGCTGCCAAATCTCCGACTTAAAGAGAGCATTTGCCCAACCAATGAGGCTGT 540
DB 4978 ACAAATATGCTGCCAAATCTCCGACTTAAAGAGAGCATTTGCCCAACCAATGAGGCTGT 5037
QY 541 GCATGAGGTCATGACGGAATTATGCAACCTAGCAGTGGCAGTTGGGAAGATGACAGAGTT 600
DB 5038 GCATGAGGTCATGACGGAATTATGCAACCTAGCAGTGGCAGTTGGGAAGATGACAGAGTT 5097
QY 601 TGTTAATGACCAATTTATATAAAACAGCTCAGAAATTAGCTGCATCAAAATTTGCACAGCA 660
DB 5098 TGTTAATGACCAATTTATATAAAACAGCTCAGAAATTAGCTGCATCAAAATTTGCACAGCA 5157
QY 661 AGTTGGTGTAGAGCTCAACCTGTACCTTAACCGAAATTGACTAGATTTCCGACCAAAAT 720
DB 5158 AGTTGGTGTAGAGCTCAACCTGTACCTTAACCGAAATTGACTAGATTTCCGACCAAAAT 5217
QY 721 CACTTCACTGCTTTAAACAAGCTGATTTAGGCACTTTAACATCTAGCTGGTGGAAA 780
DB 5218 CACTTCACTGCTTTAAACAAGCTGATTTAGGCACTTTAACATCTAGCTGGTGGAAA 5277
QY 781 TATGATTAATCTTATTTGACTAAGTTAGGTGTAGGGAAACATCAACTGACTATTAAATCGG 840
DB 5278 TATGATTAATCTTATTTGACTAAGTTAGGTGTAGGGAAACATCAACTGACTATTAAATCGG 5337
QY 841 TAGCGGCTTATATCAACCGGTAAACCTTATTCTATACGACTCACAGACTCAACTCTTGGGTAT 900
DB 5338 TAGCGGCTTATATCAACCGGTAAACCTTATTCTATACGACTCACAGACTCAACTCTTGGGTAT 5397
QY 901 ACAGGTAACTCTACCTTCAAGTCGGGAAACCTTAATATAGTCGACCTACTTGGAAAC 960
DB 5398 ACAGGTAACTCTACCTTCAAGTCGGGAAACCTTAATATAGTCGACCTACTTGGAAAC 5457
QY 961 CTTATCCGTAGACACAACAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020
DB 5458 CTTATCCGTAGACACAACAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 5517
QY 1021 GGTTCGGTCTGTGTATAGAAAGACTTGAACCTCATACTGTATAGAAACTGACTTAGATTT 1080
DB 5518 GGTTCGGTCTGTGTATAGAAAGACTTGAACCTCATACTGTATAGAAACTGACTTAGATTT 5577
QY 1081 ATATTTGTAACAAGATATGTAAGCTTCCCTATGTCCCCCTGATTTTATTCCTGCTTGAACGG 1140
DB 5578 ATATTTGTAACAAGATATGTAAGCTTCCCTATGTCCCCCTGATTTTATTCCTGCTTGAACGG 5637
QY 1141 CAATACGTCGGGCTGTATGTACTCAAAAGACGAAAGGCGCACTTACTACACCATCATGAC 1200
DB 5638 CAATACGTCGGGCTGTATGTACTCAAAAGACGAAAGGCGCACTTACTACACCATCATGAC 5687
QY 1201 TATCAAAAGTTCACTCATGCGCAACTGCAGATGACAAACATGTAGATGTGTAAACCCCC 1260
DB 5698 TATCAAAAGTTCACTCATGCGCAACTGCAGATGACAAACATGTAGATGTGTAAACCCCC 5757
QY 1261 GGGTATCATATCCGAAAACCTATGGAAGACCGGTGTCTCTAATATAGATAAACAATATGCAA 1320
DB 5758 GGGTATCATATCCGAAAACCTATGGAAGACCGGTGTCTCTAATATAGATAAACAATATGCAA 5817
QY 1321 TGTTTTATCCTTTGGGGGGAATCTTAAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 1380
DB 5818 TGTTTTATCCTTTGGGGGGAATCTTAAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 5877
QY 1381 GAAGAAATATCTCAATACAAAGATTCTCAAGTAATATAACAGGCAATCTTGTATATCTCAAC 1440
```

---

```
DB 5878 GAAGAAATATCTCAATACAAAGATTCTCAAGTAATATAACAGGCAATCTTGTATATCTCAAC 5937
QY 1441 TGAAGTTGGGAATGTCAACAACCTCGATCAGTAATGCTTTGAATATAGTTAAGAGAAACAA 1500
DB 5938 TGAAGTTGGGAATGTCAACAACCTCGATCAGTAATGCTTTGAATATAGTTAAGAGAAACAA 5997
QY 1501 CAGAAAACCTAGCAAAATCTAATGTCAAACTGACTAGACACATCTGCTCTCATTAACCTATAT 1560
DB 5998 CAGAAAACCTAGCAAAATCTAATGTCAAACTGACTAGACACATCTGCTCTCATTAATATAT 6057
QY 1561 CGTTTGACTATCATCTCTGTTTGGTAATCTTAGCCTGATTTAGCATCTACTCT 1620
DB 6058 CGTTTGACTATCATCTCTGTTTGGTAATCTTAGCCTGATTTAGCATCTACTCT 6117
QY 1621 AATGTACAAAGCAAAAGCGCAACAAAACCTTATATATGAGCTTGGAAATATATCTAGA 1680
DB 6118 AATGTACAAAGCAAAAGCGCAACAAAACCTTATATATGAGCTTGGAAATATATCTAGA 6177
QY 1681 TCAGATGAGACCACTACAAAATTTGTGAACAACAGATGAGAACAGAGTTTCCCTAATAG 1740
DB 6178 TCAGATGAGACCACTACAAAATTTGTGAACAACAGATGAGAACAGAGTTTCCCTAATAG 6237
QY 1741 TAAATTTGTGAAAAGTTCTGGTAGTCTGTGAGTTCAAGAGATTAAAGAAAACCTACCGGT 1800
DB 6238 TAAATTTGTGAAAAGTTCTGGTAGTCTGTGAGTTCAAGAGATTAAAGAAAACCTACCGGT 6297
QY 1801 TGTATGATGACCAAAAGACGATATACGGGTAGAAACGTTAAGAGAGGCGCCCTCAATTGC 1860
DB 6298 TGTATGATGACCAAAAGACGATATACGGGTAGAAACGTTAAGAGAGGCGCCCTCAATTGC 6357
QY 1861 GAGCGAGCTTCAACAACCTCGTTCTTACCGCTTCAACGACCAACAGTCTCAATCATAGAC 1920
DB 6358 GAGCGAGCTTCAACAACCTCGTTCTTACCGCTTCAACGACCAACAGTCTCAATCATAGAC 6417
QY 1921 CGGCGGCTTAGCCAGTGGGTTTAGAATATGATGAAAGAGCAAAATTAACATGCGCG 1980
DB 6418 CGGCGGCTTAGCCAGTGGGTTTAGAATATGATGAAAGAGCAAAATTAACATGCGCG 6477
QY 1981 TTGATATTCGGGATTTGCAATCTTATTCTTAAACAGTATGACCTTGGCTATATCTGTAGCC 2040
DB 6478 TTGATATTCGGGATTTGCAATCTTATTCTTAAACAGTATGACCTTGGCTATATCTGTAGCC 6537
QY 2041 TCCCTTTATATATAGCATGGGGCGCTAGACACCTAGCGATCTTGTAGGCAATACCGACTAGG 2100
DB 6538 TCCCTTTATATATAGCATGGGGCGCTAGACACCTAGCGATCTTGTAGGCAATACCGACTAGG 6597
QY 2101 ATTTCCAGGGCAGAGAAAAGATTACATCTACACTTGTTCCAATCAAGATGTATGAT 2160
DB 6598 ATTTCCAGGGCAGAGAAAAGATTACATCTACACTTGTTCCAATCAAGATGTATGAT 6657
QY 2161 AGGATATATTAAGCAAGTGGGCTTGTAGTCTCCGTTGGCACTTGTAAATATCTGAGACACA 2220
DB 6658 AGGATATATTAAGCAAGTGGGCTTGTAGTCTCCGTTGGCACTTGTAAATATCTGAGACACA 6717
QY 2221 ATTATGAAACCAATTAACATCTCTCTTATCAGATTAATGAGCTGTCAACCAACAGTGGG 2280
DB 6718 ATTATGAAACCAATTAACATCTCTCTTATCAGATTAATGAGCTGTCAACCAACAGTGGG 6777
QY 2281 TGGGGGGCACCTATTCATGACCAAGATATATAGGGGGGATAGGCAAAAGACTCATTTGTA 2340
DB 6778 TGGGGGGCACCTATTCATGACCAAGATATATAGGGGGGATAGGCAAAAGACTCATTTGTA 6837
QY 2341 GATGATGCTATGATATGTCATGATCTATCCCTGTGCACTTCAAGAACTGAATTTT 2400
DB 6838 GATGATGCTATGATATGTCATGATCTATCCCTGTGCACTTCAAGAACTGAATTTT 6897
QY 2401 ATCCCGGCGCTACTACAGGATCAGGTGCACTCGAATACCTCATTTGACATGAGTGTCT 2460
DB 6898 ATCCCGGCGCTACTACAGGATCAGGTGCACTCGAATACCTCATTTGACATGAGTGTCT 6957
QY 2461 ACCCATTAATGCTACACCACTAATATATATTTGTCTGATGACAGAGATCTCACTTCA 2520
```

Db 6958 ACCATTACTGCTACACCCATATATATATCTGAGTCAGAGATCACTCAATTCA 7017  
Qy 2521 TATCAGATTATTAAGCACTTGGTGTCTCCGGAATCTGCAACAGGAGGATTTCTTTCT 2580  
Db 7018 TATCAGATTATTAAGCACTTGGTGTCTCCGGAATCTGCAACAGGAGGATTTCTTTCT 7077  
Qy 2581 ACTCTGCTTCCATCAACTGAGACGACCCCAAAATGGAAAGTCTTGACGTGTAGTGA 2640  
Db 7078 ACTCTGCTTCCATCAACTGAGACGACCCCAAAATGGAAAGTCTTGACGTGTAGTGA 7137  
Qy 2641 ACTCCCTGGGTGTGATATGCTGTGCTGAAAGTCAACGAGACAGAGAAAGATTAT 2700  
Db 7138 ACTCCCTGGGTGTGATATGCTGTGCTGAAAGTCAACGAGACAGAGAAAGATTAT 7197  
Qy 2701 AACTCAGCTGTCCCTAGCGGATGATCATGAGAGTTAGGTTGACGCGCAGTACAC 2760  
Db 7198 AACTCAGCTGTCCCTAGCGGATGATCATGAGAGTTAGGTTGACGCGCAGTACAC 7257  
Qy 2761 GAAAAGACCTAGATGTCACAACTTATCGGGGACTGGGTGGCCAACTACCCAGAGTA 2820  
Db 7258 GAAAAGACCTAGATGTCACAACTTATCGGGGACTGGGTGGCCAACTACCCAGAGTA 7317  
Qy 2821 GGGGGTGTATCTTTATGACGCGGATGATGTTCTCAGTCTACGAGGTTAAACCC 2880  
Db 7318 GGGGGTGTATCTTTATGACGCGGATGATGTTCTCAGTCTACGAGGTTAAACCC 7377  
Qy 2881 AATTCACTCAGTGAATGATGAGAGGAAATATGATATATCAAGCAGTATCAATGAC 2940  
Db 7378 AATTCACTCAGTGAATGATGAGAGGAAATATGATATATCAAGCAGTATCAATGAC 7437  
Qy 2941 ACATGCCAGATGACAACTACCAAGTTGAAATGGCAAGTCTTGATTAAGCTTGA 3000  
Db 7438 ACATGCCAGATGACAACTACCAAGTTGAAATGGCAAGTCTTGATTAAGCTTGA 7497  
Qy 3001 CGGTTTGTGGGAAACGATACAGAGGCTATCTTATCTATCAAGTGTCAACTCTTA 3060  
Db 7498 CGGTTTGTGGGAAACGATACAGAGGCTATCTTATCTATCAAGTGTCAACTCTTA 7557  
Qy 3061 GGGGAAACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120  
Db 7558 GGGGAAACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7617  
Qy 3121 AGAATTCACAGTACGAGGACATCTTCTTGTATCAACGAGGATCACTACTTCTCT 3180  
Db 7618 AGAATTCACAGTACGAGGACATCTTCTTGTATCAACGAGGATCACTACTTCTCT 7677  
Qy 3181 CCGCGTTATTAATATCTATGACAGTACAGCAAAACAGCCACTTTCATATGCTTAT 3240  
Db 7678 CCGCGTTATTAATATCTATGACAGTACAGCAAAACAGCCACTTTCATATGCTTAT 7737  
Qy 3241 ACATTCAGTCTTCACTCGGCGAGTATGATGATGATGATGATGATGATGATGATGAT 3300  
Db 7738 ACATTCAGTCTTCACTCGGCGAGTATGATGATGATGATGATGATGATGATGATGAT 7797  
Qy 3301 AACTGATGTTTACGAGTCTATACAGATCCATATCCCTAATCTTCTATAGAAAC 3358  
Db 7798 AACTGATGTTTACGAGTCTATACAGATCCATATCCCTAATCTTCTATAGAAAC 7855

RESULT 2  
5310678-2  
APPLICANT: Birmingham, Richard W.; Chambers, Philip; Emmerston, Peter  
T. Millar, Neil S.  
TITLE OF INVENTION: NEWCASTLE DISEASE VIRUS GENE CLONES  
NUMBER OF SEQUENCES: 3  
CURRENT APPLICATION NUMBER:  
FILING DATE: 17-NOV-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 885,765  
FILING DATE: 15-JUL-1986  
SEQ ID NO:2:

5310678-2  
LENGTH: 3825  
Query Match 95.2%; Score 3196.4; DB 9; Length 3825;  
Best Local Similarity 97.0%; Pred. No. 0;  
Matches 3257; Conservative 0; Mismatches 101; Indels 0; Gaps 0;  
Qy 1 ACGGTTGAAAGATTTCTGATTCCTGGTGGGCGCTCCAGGTGCAAGATGGCTCCACACC 60  
Db 1 ACGGTTGAAAGATTTCTGATTCCTGGTGGGCGCTTCAGGTGCAAGATGGGCGCTCCACACC 60  
Qy 61 TTCTACAGAGAACCCAGACCTATGATGCTGACTATCGGGTTGCGCTGGCACTGAGTTG 120  
Db 61 TTCTACAGAGAACCCAGATCTATGATGCTGACTATCGGATCGCGTGGATCTGAGTTG 120  
Qy 121 CATCTGTCCGCAAACTCCATGATGCAAGGCTCTTGACGTGCAAGAAATGGTTAC 180  
Db 121 CATCTGTCCGCAAACTCCATGATGCAAGGCTCTTGACGTGCAAGAAATGGTTAC 180  
Qy 181 AGGAGCAAAAGCGGTCAACATATACCTCATCCAGACAGATCATCATAGTTAAGCT 240  
Db 181 AGGAGCAAAAGCGGTCAACATATACCTCATCCAGACAGATCATCATAGTTAAGCT 240  
Qy 241 CCTCCGAATCTGCGCAAGGATAGAGGCAATGCGAAAGCCCTTGATGATGATCA 300  
Db 241 CCTCCGAATCTGCGCAAGGATAGAGGCAATGCGAAAGCCCTTGATGATGATCA 300  
Qy 301 CAGGACATTTGACCACTTTGCTCACCCCTTGATGATGATGATGATGATGATGATGATGAT 360  
Db 301 CAGGACATTTGACCACTTTGCTCACCCCTTGATGATGATGATGATGATGATGATGATGAT 360  
Qy 361 TGTGACTATCATTTGAGAGGAGAGACAGGCGCTTATAGGCGCCATTAATTTGGCGGT 420  
Db 361 TGTGACTATCATTTGAGAGGAGAGACAGGCGCTTATAGGCGCCATTAATTTGGCGGT 420  
Qy 421 GGCCTTTGGGTTGCACTGCGGCAAAATPACGCGCGCACTCTGATPACAGCCAA 480  
Db 421 GGCCTTTGGGTTGCACTGCGGCAAAATPACGCGCGCACTCTGATPACAGCCAA 480  
Qy 481 ACAAAATGCTGCAACATCTCCGACTTAAAGAGAGATTTGCCCAACCAATGAGGCTGT 540  
Db 481 ACAAAATGCTGCAACATCTCCGACTTAAAGAGAGATTTGCCCAACCAATGAGGCGGT 540  
Qy 541 GCATGAGGTCACTACGAGATTTATGCAACTAGCAGTGGCAGTTGGAAAGTACAGCTT 600  
Db 541 GCATGAGGTCACTACGAGATTTATGCAACTAGCAGTGGCAGTTGGAAAGTACAGCTT 600  
Qy 601 TGTTAATGACCAATTTAATAAACAAGTCAAGATTTAGCTGATCAAAATTTGACACGCA 660  
Db 601 TGTTAATGACCAATTTAATAAACAAGTCAAGATTTAGCTGATCAAAATTTGACACGCA 660  
Qy 661 AGTTGATGAGAGTCAACCTGATCACTAACCGAATTTAGTCACTATTTGGACCAAAAT 720  
Db 661 AGTTGATGAGAGTCAACCTGATCACTAACCGAATTTAGTCACTATTTGGACCAAAAT 720  
Qy 721 CACTTCACTGCTTTAAACAAGCTGATATTCAGGCACTTTACATCTAGCTGTGAAA 780  
Db 721 CACTTCACTGCTTTAAACAAGCTGATATTCAGGCACTTTACATCTAGCTGTGAAA 780  
Qy 781 TATGATTAATCTTATTAATTAAGTTAGTGTAGGGAACAATTAATCACTCACTAATTCG 840  
Db 781 TATGATTAATCTTATTAATTAAGTTAGTGTAGGGAACAATTAATCACTCACTAATTCG 840  
Qy 841 TAGGCGCTATATCAACCGCAACCTATATCTGTAGACCTCAAGACTCACTGTGGAT 900  
Db 841 TAGGCGCTATATCAACCGCAACCTATATCTGTAGACCTCAAGACTCACTGTGGAT 900  
Qy 901 ACAGTAATCTTACTTCACTGATGCGGAACCTTAATATATGCGTCCACTTATGGAAC 960  
Db 901 ACAGTAATCTTACTTCACTGATGCGGAACCTTAATATATGCGTCCACTTATGGAAC 960  
Qy 961 CTATTCGTAAGCAACACAGGGAATTTGCTCGGCACTTGTCCAAAAGTGTGACCA 1020  
Db 961 CTATTCGTAAGCAACACAGGGAATTTGCTCGGCACTTGTCCAAAAGTGTGACCA 1020

Db 961 CTTATCTGTAGCAACACAGGGATTGCTCGGCACTGTGCCAAAAGGTGACACA 1020  
Qy 1021 GGTGGTCTGTGTATAGAGAACTTGCACCTCATCTGTATAGAAACTGATGATTT 1080  
Db 1021 GGTGGTCTGTGTATAGAGAACTTGCACCTCATCTGTATAGAAAAGCACTTGATTT 1080  
Qy 1081 ATATTGTACAGAATAGTAACGTTCCCTATGTCCCTGGTATTTTATTTCTGCTTGAGCGG 1140  
Db 1081 ATATTGTACAGAATAGTAACGTTCCCTATGTCCCTGGTATTTTATTTCTGCTTGAGCGG 1140  
Qy 1141 CAATAGCTGGGCGGTATGTACTCAAAAGACCGAAGGGGCACTTCTACCATCATGAC 1200  
Db 1141 CAATAGCTGGGCGGTATGTACTCAAAAGACCGAAGGGGCACTCTACGCCATCATGAC 1200  
Qy 1201 TATCAAGGTTCACTCATCCGCAACTGCAAGATGACAAACATGTAGTGTGTAACCCCC 1260  
Db 1201 TATCAAGGCTCACTCATCCGTAATGCAAGATGACAAACATGTAGTGTGTAACCCCC 1260  
Qy 1261 GGGTATCATATCGCAAACTATGAGAAAGCCGTGCTCTAATAGATAGCATCATGCAA 1320  
Db 1261 GGGTATCATATCGCAAACTATGAGAAAGCCGTGCTCTAATAGATAGCATCATGCAA 1320  
Qy 1321 TGTTTATCCTTATAGCGGAACTTAAAGCTCAGTGGGAAATTCAGTGCATCTATCA 1380  
Db 1321 TGTTTATCCTTATAGCGGAACTTAAAGCTCAGTGGGAAATTCAGTGCATCTATCA 1380  
Qy 1381 GAAGAATATCTCAATACAGAATCTCAAGTAAATATAACAGCAATCTTGATCTCAAC 1440  
Db 1381 GAAGAATATCTCAATACAGAATCTCAAGTAAATATAACAGCAATCTTGATCTCAAC 1440  
Qy 1441 TGAAGTTGGAAATGTCAACAATCGATCAATGCTTTGAAATAGTTAAGAGAAACAA 1500  
Db 1441 TGAAGTTGGAAATGTCAACAATCGATCAATGCTTTGAAATAGTTAAGAGAAACAA 1500  
Qy 1501 CAGAAAATAGCAAAAGTCAATGTCAAACTGACAGCAATCTGCTCTCATTAATCTAT 1560  
Db 1501 CAGCAAACTAGCAAAAGTCAATGTCAAACTGACAGCAATCTGCTCTCATTAATCTAT 1560  
Qy 1561 CGTTTACTATCATATCTCTGTGTTTGGTATCTTACCTGATTTAGAGATCTACT 1620  
Db 1561 CGTTTACTATCATATCTCTGTGTTTGGTATCTTACCTGATTTAGAGATCTACT 1620  
Qy 1621 AATGTACAGCAAAAGGCGCAACAAAACCTTATATGCTTGGAAATATATCTTGA 1680  
Db 1621 AATGTATACCAAAAGGCGCAACAAAAGCCTTATATGCTTGGAAATATATCTTGA 1680  
Qy 1681 TCAGATAGAGCCCACTCAAAAATGTGAACACAGATAGAGAACAGAGTTCCCTATAG 1740  
Db 1681 TCAGATAGAGCCCACTCAAAAATGTGAACACAGATAGAGAACAGAGTTCCCTATAG 1740  
Qy 1741 TAAATTTGTGAAAGTTCTGTAGTCTGTCACTCAGAGATTAAAGAAAACCTAACGGT 1800  
Db 1741 TAAATTTGTGAAAGTTCTGTAGTCTGTCACTCAGAGATTAAAGAAAACCTAACGGT 1800  
Qy 1801 TGTAGATGACCAAGAGAGATATCGGGTAGAAAGGTAGAGAGCCGCCCTCAATTTGC 1860  
Db 1801 TGTAGATGACCAAGAGAGATATCGGGTAGAAAGGTAGAGAGCCGCCCTCAATTTGC 1860  
Qy 1861 GAGCCAGGCTTTCACAACTCCGTTCTTACCGCTTACCGAACAAGTCTCAATATGAC 1920  
Db 1861 GAGCCAGGCTTTCACAACTCCGTTCTTACCGCTTACCGAACAAGTCTCAATATGAC 1920  
Qy 1921 CGGGCGGTATGCAAGTTGGTTAGAGATGAGAAAGAGGAAAAATATCATGTGGCG 1980  
Db 1921 CGGGCGGTATGCAAGTTGGTTAGAGATGAGAAAGAGGAAAAATATCATGTGGCG 1980  
Qy 1981 TTGATATTCGGATTTGCAATCTTATTTCTTAAACAGTATGACCTTGGCTATATCTGAGCC 2040  
Db 1981 TTGATATTCGGATTTGCAATCTTATTTCTTAAACAGTATGACCTTGGCTATATCTGAGCC 2040  
Qy 2041 TCCCTTTATATAGATGGGGGCTAGCAACCTAGCGACTTGTAGGCATATCGACTAGG 2100  
Db 2041 TCCCTTTATATAGATGGGGGCTAGCAACCTAGCGACTTGTAGGCATATCGACTAGG 2100

Qy 2101 ATTTCCAGGCGAGAGAAAAGATTACATCTACCTGTTCCATCAATCAAGTATGATGAT 2160  
Db 2101 ATTTCTTAGGCGAGAGAAAAGATTACATCTGCACTTGTTCCATCAAGTATGATGAT 2160  
Qy 2161 AGGATATATAGAGAGGCGCTTGAGTCTCCGTTGGCACTTGTAAATATCTGAGACACA 2220  
Db 2161 AGGATATATAGAGAGGCGCTTGAGTCTCCGTTGGCACTTGTAAACATCTGAGACACA 2220  
Qy 2221 ATTAGAGCGCAATTAACATCTCTCTTATCAGATTAATAGAGCTGCAACACAGTGGG 2280  
Db 2221 ATTAGAGCGCAATTAACATCTCTCTTATCAGATTAATAGAGCTGCAACACAGTGGG 2280  
Qy 2281 TGGGGGCACTATTCATGACCAAGATTATAGGGGGGATAGGCAAGAACTCATTTGA 2340  
Db 2281 TGGGGGCACTATTCATGACCAAGATTATAGGGGGGATAGGCAAGAACTCATTTGA 2340  
Qy 2341 GATGATGCTAGTATGTCACATCTATTCCTCTGCACTTTCAAGAAACATGAAATTT 2400  
Db 2341 GATGATGCTAGTATGTCACATCTATTCCTCTGCACTTTCAAGAAACATGAAATTT 2400  
Qy 2401 ATCCGGCGCTACTACAGGATCAGGTTGCACTGAAATACCTCATTTGACATGATGCT 2460  
Db 2401 ATCCGGCGCTACTACAGGATCAGGTTGCACTGGAATACCTCATTTGACATGATGCT 2460  
Qy 2461 ACCCATTACTGCTACACCCATTAATGTAATTTGTGATGACAGATCACTCAATTTCA 2520  
Db 2461 ACCCATTACTGCTACACCTTAATGTAATTTGTGATGACAGATCACTCAATTTCA 2520  
Qy 2521 TATCAGATTTAGACATTTGTTGCTCCGCAATCTGCAACAGGAGGGATTTCTTTCT 2580  
Db 2521 TATCAGATTTAGACATTTGTTGCTCCGCAATCTGCAACAGGAGGGATTTCTTTCT 2580  
Qy 2581 ACTCTGGTTCATCAACCTGAGACACCAAAATCGAAAGTCTTGCACTGATGAGTGA 2640  
Db 2581 ACTCTGGTTCATCAACCTGAGTACAGGACCAAAATCGAAAGTCTTGCACTGATGAGTGA 2640  
Qy 2641 ACTCCCTGGGTTGTATGATGCTGTGCTCGAAAGTCAAGGACAGAGAAAGATTAT 2700  
Db 2641 ACTCCCTGGGTTGTATGATGCTGTGCTCGAAAGTCAAGGACAGAGAAAGATTAT 2700  
Qy 2701 AACTCAGCTGCTCCCTACCGGAGTGTACATGGAAGTTAGGTTTCCAGCGCCAGTACAC 2760  
Db 2701 AACTCAGCTGCTCCCTACCGGAGTGTACATGGAAGTTAGGTTTCCAGCGCCAGTACAC 2760  
Qy 2761 GAAAGGACCTAGATGTCAACATTTATGAGGGAAGTGGGCACTACCCAGAGATGA 2820  
Db 2761 GAAAGGACCTAGATGTCAACATTTATGAGGGAAGTGGGCACTACCCAGAGATGA 2820  
Qy 2821 GGGGGTGAATCTTTATTTGACAGCCGCTATGTTGCTCACTTACGAGGGCTGAAACC 2880  
Db 2821 GGGGGTGAATCTTTATTTGACAGCCGCTATGTTGCTCACTTACGAGGGCTGAAACC 2880  
Qy 2881 AATTCAACCGATGACCTGTACAGAAAGGAAATATGTGATATACAGCATACATGAC 2940  
Db 2881 AATTCAACCGATGACCTGTACAGAAAGGAAATATGTGATATACAGCATACATGAC 2940  
Qy 2941 ACATGCCAGATAGAGCAAGCTACAGATTCAGATGGCCAAAGTCTTGTAAGCCCTGGA 3000  
Db 2941 ACATGCCAGATAGAGCAAGCTACAGATTCAGATGGCCAAAGTCTTGTAAGCCCTGGA 3000  
Qy 3001 CGGTTTGTGGGAAAGCATACAGAGGCTATCTTATCTTCAAGGTTGCAACATCTTTA 3060  
Db 3001 CGGTTTGTGGGAAAGCATACAGAGGCTATCTTATCTTCAAGGTTGCAACATCTTTG 3060  
Qy 3061 GGGGAAAGCCGGTACTGATCCGCCAACAAGTCACTCATGAGGGGCTGAAAGGC 3120  
Db 3061 GGGGAAAGCCAGTACTGATCCGCCAACAAGTCACTCATGAGGGGCTGAAAGGC 3120  
Qy 3121 AGAATTTCAAGATAGGAGACATCTATTTCTTGTATCAAGAGGCTCATATCTTCTCT 3180  
Db 3121 AGAATTTCAAGATAGGAGACATCTATTTCTTGTATCAAGAGGCTCATATCTTCTCT 3180



QY 1276 AAACATGAGAAACCGTGTCTCTAATAGATAAACAATCATGCAATGTTTATCTTAGG 1335  
DB 3324 AAACATGAGAAACCGTGTCTCTAATAGATAAACAATCATGCAATGTTTATCTTAGG 3383  
QY 1336 CGGATTAACCTTTAAGGCTCAGTGGGAAATTCAGATGAACCTTATCAGAAATATCTCAAT 1395  
DB 3384 CGGATTAACCTTTAAGGCTCAGTGGGAAATTCAGATGAACCTTATCAGAAATATCTCAAT 3443  
QY 1396 ACAAGATTCCTCAAGTAATTAATAACAGCAATCTTGATATCTCAACTGAGCTGGGAATGT 1455  
DB 3444 ACAAGATTCCTCAAGTAATTAATAACAGCAATCTTGATATCTCAACTGAGCTGGGAATGT 3503  
QY 1456 CAACAACTGATCAGTAATGCTTTGAATTAAGTAAAGAAAGCAAGAAACCTAGACAA 1515  
DB 3504 CAACAACTGATCAGTAATGCTTTGAATTAAGTAAAGAAAGCAAGAAACCTAGACAA 3563  
QY 1516 AGTCATATGTAACCTGACATGACATCTGCTCTCATTAACCTATATGCTTTGACTATCAT 1575  
DB 3564 AGTCATATGTAACCTGACATGACATCTGCTCTCATTAACCTATATGCTTTGACTATCAT 3623  
QY 1576 ATCTCTGTTTGGTATACCTTAGCTGATCTGATCTAGCATGCTAATGTAACAAGCAAAA 1635  
DB 3624 ATCTCTGTTTGGTATACCTTAGCTGATCTGATCTAGCATGCTAATGTAACAAGCAAAA 3683  
QY 1636 GGGCAACCAAAAAACCTTATATGCTTGGGAATATATCTCTAGATCAGATGAGAGCCAC 1695  
DB 3684 GGGCAACCAAAAAACCTTATATGCTTGGGAATATATCTCTAGATCAGATGAGAGCCAC 3743  
QY 1696 TACAAAAATGTGAACACAGATGAGAAACGAAGTTTCCCTAATATGTAATTTGTGTGAAG 1755  
DB 3744 TACAAAAATGTGAACACAGATGAGAAACGAAGTTTCCCTAATATGTAATTTGTGTGAAG 3803  
QY 1756 TTCTGGTAGTCTGTCACTGATCAGAGAGTTAAGAAAAA 1792  
DB 3804 TTCTGGTAGTCTGTCACTGATCAGAGAGTTAAGAAAAA 3840

RESULT 4

US-08-477-459-12  
Sequence 12, Application US/08477459  
Patent No. 6001369  
GENERAL INFORMATION:  
APPLICANT: Mark D. Cochran  
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,459  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White Beq, John P.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 115..1860  
NAME/KEY: CDS  
LOCATION: 2095..3756  
US-08-477-459-12

Query Match 51.9%; Score 1741.8; DB 3; Length 4177;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 16 TGGATCCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACAGAAACCC 75  
DB 2064 TCGATCCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACAGAAACCC 2123  
QY 76 AGCACCCTATGATCTGATCTATCCGGGTGGCGCTGGCACTGAGTTGCACTGTCCGGCAA 135  
DB 2124 AGCACCCTATGATCTGATCTATCCGGGTGGCGCTGGCACTGAGTTGCACTGTCCGGCAA 2183  
QY 136 CTCATTTGATGGCAGGCTCTTTCAGCTGCGAGAAATTTGTGTTACAGAGAACAAAGCCGT 195  
DB 2184 CTCATTTGATGGCAGGCTCTTTCAGCTGCGAGAAATTTGTGTTACAGAGAACAAAGCAGT 2243  
QY 196 CAACATTAACCTCCTCCAGACAGGATCAATGATTAAGTCTCCCGAATCTGCC 255  
DB 2244 CAACATTAACCTCCTCCAGACAGGATCAATGATTAAGTCTCCCGAATCTGCC 2303  
QY 2256 CAAGATTAAGAGAGCAGTGTGCAAAACCCCTTGTGATGATCAACAGACATTTGACAC 315  
DB 2304 AAAGATTAAGAGAGCAGTGTGCAAAACCCCTTGTGATGATCAACAGACATTTGACAC 2363  
QY 316 TTGCTCAACCCCTTGTGATCTATCCGTAGAGATCAAGAGTCTGTGACTCATCTGG 375  
DB 2364 TTGCTCAACCCCTTGTGATCTATCCGTAGAGATCAAGAGTCTGTGACTCATCTGG 2423  
QY 376 AGGGGGGAGACAGGGGCGCTTATAGCGCATTAATGGCGGTGGCTTGGGGGTGC 435  
DB 2424 AGGGGGGAGACAGGGGCGCTTATAGCGCATTAATGGCGGTGGCTTGGGGGTGC 2483  
QY 436 AACTGCGCAAAATTAACAGCGGCGCAGCTGATATCAAGCCAAACAAATCTGCGCAA 495  
DB 2484 AACTGCGCAAAATTAACAGCGGCGCAGCTGATATCAAGCCAAACAAATCTGCGCAA 2543  
QY 496 CATCTCCGACTTAAGAGAGCAATTCGCGCAACCAATGAGCTGTGATGAGTCACTGA 555  
DB 2544 CATCTCCGACTTAAGAGAGCAATTCGCGCAACCAATGAGCTGTGATGAGTCACTGA 2603  
QY 556 CGGATTAATGCAACTAGCAGTGGCAATTTGGGAAAGATGCGACATTTGTTAATGCAAT 615  
DB 2604 CGGATTAATGCAACTAGCAGTGGCAATTTGGGAAAGATGCGACATTTGTTAATGCAAT 2663  
QY 616 TAATTAACAGCTCAGAAATTTAGCTGATCAAAATTTGCAACAGATTGGTGTAGAGCT 675  
DB 2664 TAATTAACAGCTCAGAAATTTAGCTGATCAAAATTTGCAACAGATTGGTGTAGAGCT 2723  
QY 676 CAACCTGTACTAACCGAATTTGACTAGTATTCGAGCAACAAATCACTTCACTGCTTT 735  
DB 2724 CAACCTGTACTAACCGAATTTGACTAGTATTCGAGCAACAAATCACTTCACTGCTTT 2783  
QY 736 AAACAGCTGACTAATTCAGGCACTTTAACAATCTAGCTGTGGGAATATGATTAATTAAT 795  
DB 2784 AAACAGCTGACTAATTCAGGCACTTTAACAATCTAGCTGTGGGAATATGATTAATTAAT 2843  
QY 796 GACTAAGTTAGGTGTGGGAAACAATCACTCAGCTCATTAATGGTGTAGCGGCTTAATCAC 855  
DB 2844 GACTAAGTTAGGTGTGGGAAACAATCACTCAGCTCATTAATGGTGTAGCGGCTTAATCAC 2903  
QY 856 CGGTAAACCTAATCTATAAGACTCAGACACTCAACTTGGGTATACAGGTAACTCTAAC 915



```
|||||
Db 2904 CGGTAACTTCTATTCGACTCAGACTCAAGCTCAACTCTTGGGTATACAGGTAACCTAAC 2963
Qy 916 TTCAAGTGGGAACTTAATATATATGCGGCAACCTACTGGAACTTAATCGTAAGAC 975
Db 2964 TTCAAGTGGGAACTTAATATATATGCGGCAACCTACTGGAACTTAATCGTAAGAC 3023
Qy 976 AACCAAGGGAATTTGCTCGGCACTTGTCCCAAAAGGTGACAGAGGTGCTGTGTAT 1035
Db 3024 AACCAAGGGAATTTGCTCGGCACTTGTCCCAAAAGGTGACAGAGGTGCTGTGTAT 3083
Qy 1036 AGAAGAACTTGACACTCTATCTGTATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1095
Db 3084 AGAAGAACTTGACACTCTATCTGTATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3143
Qy 1096 AGTAACTTCCCTATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1155
Db 3144 AGTAACTTCCCTATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3203
Qy 1156 TATGTACTCAAAAGACCGAAGGCGCACTTACACACATGACTGACTATCAAGGTTCACT 1215
Db 3204 TATGTACTCAAAAGACCGAAGGCGCACTTACACACATGACTGACTATCAAGGTTCACT 3263
Qy 1216 CATGCCAACTGCAAGATGACACATGTGATGTGTAACCCCGGGTATCATATGCA 1275
Db 3264 CATGCCAACTGCAAGATGACACATGTGATGTGTAACCCCGGGTATCATATGCA 3323
Qy 1276 AAATCTATGAGAGACCGGTGTCTCTATATGATTAACAATCAATGCAATGTTTATCTT 1335
Db 3324 AAATCTATGAGAGACCGGTGTCTCTATATGATTAACAATCAATGCAATGTTTATCTT 3383
Qy 1336 CGGATTAATCTTAAGGCTCAGTGGGGAATTTGATGTAATCTTATGAGAAATATCTCAT 1395
Db 3384 CGGATTAATCTTAAGGCTCAGTGGGGAATTTGATGTAATCTTATGAGAAATATCTCAT 3443
Qy 1396 ACAAGATTTCTCAAGTAATTAATACAGGCAATCTTGAATCTCAACTGAGCTTGGAA 1455
Db 3444 ACAAGATTTCTCAAGTAATTAATACAGGCAATCTTGAATCTCAACTGAGCTTGGAA 3503
Qy 1456 CAACAACTCGATCAGTAATGCTTGAATTAAGTGAAGAAAGCAACAGAAACCTAGACA 1515
Db 3504 CAACAACTCGATCAGTAATGCTTGAATTAAGTGAAGAAAGCAACAGAAACCTAGACA 3563
Qy 1516 AGTCAATGTCAAAGCTAGACATGCTCTCATTAATCTATATCTGTTGATGATCAT 1575
Db 3564 AGTCAATGTCAAAGCTAGACATGCTCTCATTAATCTATATCTGTTGATGATCAT 3623
Qy 1576 ATCTCTGTTTGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1635
Db 3624 ATCTCTGTTTGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3683
Qy 1636 GGGGCAACAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1695
Db 3684 GGGGCAACAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3743
Qy 1696 TACAAAAATGGAACAGATGAGAGAAAGTTTCCCTAATAGTATTTTGTGAAG 1755
Db 3744 TACAAAAATGGAACAGATGAGAGAAAGTTTCCCTAATAGTATTTTGTGAAG 3803
Qy 1756 TTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAAA 1792
Db 3804 TTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAAA 3840
```

```
RESULT 5
US-08-479-869-12
: Sequence 12, Application US/08479869
: Patent No. 6123949
: GENERAL INFORMATION:
: APPLICANT: Cochran Ph.D, Mark D
: TITLE OF INVENTION: Recombinant Powjox Virus S-PPV-043 and
: TITLE OF INVENTION: Uses thereof
: NUMBER OF SEQUENCES: 20
```

```

CORRESPONDENCE ADDRESS:
ADDRESS: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,869
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/024,156
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4177 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 115..1860
FEATURE:
NAME/KEY: CDS
LOCATION: 2095..3756
US-08-479-869-12

Query Match 51.9%; Score 1741.8; DB 3; Length 4177;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

16 TGAATCCCGGTTGGCGCCCTTCAAGTGCAGATGAGGCTCCAGACTTACCAAGAACCC 75
Db 2064 TGAATCCCGGTTGGCGCCCTTCAAGTGCAGATGAGGCTCCAGACTTACCAAGAACCC 2123
Qy 76 AGCACTATGATGCTGATCTATCCGGGTTGGCTGCACTGAGTTGATCTGTCCGGCAAA 135
Db 2124 AGCACTATGATGCTGATCTATCCGGGTTGGCTGCACTGAGTTGATCTGTCCGGCAAA 2183
Qy 136 CTCATTGATGAGGAGGCGCTCTTGCAGCTGCAAGAAATTTGGTTACAGAGACAAAGCCGT 195
Db 2184 CTCATTGATGAGGAGGCGCTCTTGCAGCTGCAAGAAATTTGGTTACAGAGACAAAGCAGT 2243
Qy 196 CAACATATACCTCTATCTCCAGACAGATCAATATAGTTAAAGTCTCTCCGGAATCTGCC 255
Db 2244 CAACATATACCTCTATCTCCAGACAGATCAATATAGTTAAAGTCTCTCCGGAATCTGCC 2303
Qy 256 CAAGATTAAGGAGGATGTCGAAAGCCCTTGGATGATCAACAGACAGATTAAGCCAC 315
Db 2304 CAAGATTAAGGAGGATGTCGAAAGCCCTTGGATGATCAACAGACAGATTAAGCCAC 2363
Qy 316 TTGCTCAACCCCTTGGTGACTATCTATCCGTAGATACAAAGTCTGTACTATCATCTGG 375
Db 2364 TTGCTCAACCCCTTGGTGACTATCTATCCGTAGATACAAAGTCTGTACTATCATCTGG 2423
Qy 376 AGGGGGGAGACAGGGGCGCTTATAGGGGCAATATTGCGGTGTGCTCTTGGGGTTGC 435
Db 2424 AGGGGGGAGACAGGGGCGCTTATAGGGGCAATATTGCGGTGTGCTCTTGGGGTTGC 2483
```

QY 436 AACTGCCGACAAATTAACAGCGCGCAGCTCTGTATACAGCCAAACAAATGCTGCCAA 495  
DB 2484 AACTGCCGACAAATTAACAGCGCGCAGCTCTGTATACAGCCAAACAAATGCTGCCAA 2543  
QY 496 CATCTCCGACCTTAAAGAGAGCATTTGCCGCAACCAATAGAGCTGAGCATGACATGA 555  
DB 2544 CATCTCCGACCTTAAAGAGAGCATTTGCCGCAACCAATAGAGCTGAGCATGAGCTGAC 2603  
QY 556 CGAGTTATCGCAATAGAGAGCATTTGCCGCAACCAATAGAGCTGAGCATGAGCTGAC 615  
DB 2604 CGAGTTATCGCAATAGAGAGCATTTGCCGCAACCAATAGAGCTGAGCATGAGCTGAC 2663  
QY 616 TAAATAAAACAGCTAGAGATTTAGCTGATCAAAATTTGCAACAGAGTTGGTGTAGAGCT 675  
DB 2664 TAAATAAAACAGCTAGAGATTTAGCTGATCAAAATTTGCAACAGAGTTGGTGTAGAGCT 2723  
QY 676 CAACCTGTACCTAACCGAATTGACAGCTATTCGAGACCAAAATTCATTCACCTGCTTT 735  
DB 2724 CAACCTGTACCTAACCGAATTGACAGCTATTCGAGACCAAAATTCATTCACCTGCTTT 2783  
QY 736 AAACAAGCTGACTATTCAGGACCTTTACATCTAGCTGGTGAATAATGATTTACTTAT 795  
DB 2784 AAACAAGCTGACTATTCAGGACCTTTACATCTAGCTGGTGAATAATGATTTACTTAT 2843  
QY 796 GACTAAGTTAGGTAGAGGAACTAACTCACTCAGCTCATTAATCGGTAGCGGCTTAATCAC 855  
DB 2844 GACTAAGTTAGGTAGAGGAACTAACTCACTCAGCTCATTAATCGGTAGCGGCTTAATCAC 2903  
QY 856 CGGTAAACCTATTTCTATACGACTCAAGACTCACTCTGGGTATACAGGTAACTCAACC 915  
DB 2904 CGGTAAACCTATTTCTATACGACTCAAGACTCACTCTGGGTATACAGGTAACTCAACC 2963  
QY 916 TTCAGTCGGGAACCTTAAATATATAGCGTCCAGCTACTTGGAAACCTTAATCCGTAAAGCAC 975  
DB 2964 TTCAGTCGGGAACCTTAAATATATAGCGTCCAGCTACTTGGAAACCTTAATCCGTAAAGCAC 3023  
QY 976 AACGAGGGGATTTTGCCTCGGACCTTGTCCAAAGGTGTGACACAGGTCCGTTCTGTAT 1035  
DB 3024 AACGAGGGGATTTTGCCTCGGACCTTGTGTCCAAAGGTGTGACACAGGTCCGTTCTGTAT 3083  
QY 1036 AGAAGAACTTGAACACTCTATCTGTATAGAACTGACCTTAATTTATTTATGTAAGAAT 1095  
DB 3084 AGAAGAACTTGAACACTCTATCTGTATAGAACTGACCTTAATTTATTTATGTAAGAAT 3143  
QY 1096 AGTAACGTTCCCTATGTCCTCGTATTTATTCCTGCTTGAAGCGGCAATAGTCCGCTG 1155  
DB 3144 AGTAACGTTCCCTATGTCCTCGTATTTATTCCTGCTTGAAGCGGCAATAGTCCGCTG 3203  
QY 1156 TATGTACTCAAAAGACCGAAGGCGCATTAACACCATATGACCTATCAAAAGGCTCAGT 1215  
DB 3204 TATGTACTCAAAAGACCGAAGGCGCATTAACACCATATGACCTATCAAAAGGCTCAGT 3263  
QY 1216 CATGCCCACTGCAAGATGACACATGTAGTGTGTAAACCCCGCGGTATCATATGCGCA 1275  
DB 3264 CATGCCCACTGCAAGATGACACATGTAGTGTGTAAACCCCGCGGTATCATATGCGCA 3323  
QY 1276 AAATCTATGAGAGACCGGTGTCTCTAATAGATTAACAATCATGCAATGTTTATCTTAA 1335  
DB 3324 AAATCTATGAGAGACCGGTGTCTCTAATAGATTAACAATCATGCAATGTTTATCTTAA 3383  
QY 1336 CGGGATTAACCTTTAAGGCTCAGTGGGGAATTGATGTAACTTATCAGAAAGATATCTCAAT 1395  
DB 3384 CGGGATTAACCTTTAAGGCTCAGTGGGGAATTGATGTAACTTATCAGAAAGATATCTCAAT 3443  
QY 1396 ACAAGATTTCTCAAGTAAATATAACAGGCAATCTTGATATCTCAACTGAGCTTGGAAATGT 1455  
DB 3444 ACAAGATTTCTCAAGTAAATATAACAGGCAATCTTGATATCTCAACTGAGCTTGGAAATGT 3503  
QY 1456 CAACAACCTGATCGATATGCTTGAATAGTTAGAGAAAGCAAGAAACCTAGACAA 1515  
DB 3504 CAACAACCTGATCGATATGCTTGAATAGTTAGAGAAAGCAAGAAACCTAGACAA 3563

QY 1516 AGTCAATGTCAAACTGACTGACATCTGCTCATTAACCTAATGCTTTGACTATCAT 1575  
DB 3564 AGTCAATGTCAAACTGACTGACATCTGCTCATTAACCTAATGCTTTGACTATCAT 3623  
QY 1576 ATCTCTGTTTTTGGTATTAAGCTGATCTGATTTAGATGCTACTTAATGTAAGCAAAA 1635  
DB 3624 ATCTCTGTTTTTGGTATTAAGCTGATCTGATTTAGATGCTACTTAATGTAAGCAAAA 3683  
QY 1636 GGGCGCAACAAAACTTTATTTATGCTTGGGAATTAATCTTATGATCAGATGAGAGCCAC 1695  
DB 3684 GGGCGCAACAAAACTTTATTTATGCTTGGGAATTAATCTTATGATCAGATGAGAGCCAC 3743  
QY 1696 TACAAAATGTGAACACAGATGAGGAAGCAAGTTTCCCTAATATGTAATTTGTGTAAG 1755  
DB 3744 TACAAAATGTGAACACAGATGAGGAAGCAAGTTTCCCTAATATGTAATTTGTGTAAG 3803  
QY 1756 TTCTGTAGTCTGTCACTTACAGAGATTAAGAAAAA 1792  
DB 3804 TTCTGTAGTCTGTCACTTACAGAGATTAAGAAAAA 3840

RESULT 6  
US-08-486-414-12  
; Sequence 12, Application US/08486414B  
; Patent No. 6136318  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D.  
; APPLICANT: Junker, David E.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF  
; FILE REFERENCE: 42771D  
; CURRENT APPLICATION NUMBER: US/08/486,414B  
; CURRENT FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 4177  
; TYPE: DNA  
; ORGANISM: Fowlpox virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (115)..(1857)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2095)..(3753)  
US-08-486-414-12

Query Match 51.9%; Score 1741.8; DB 3; Length 4177;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 16 TGGATCCCGGTTGGCGCCTTCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75  
DB 2064 TGGATCCCGGTTGGCGCCTTCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 2123  
QY 76 AGCACTATGATGCTGACTATCCGGGTTGCGCTGGGCACTGAGTTGCATCTGTCCGCAAA 135  
DB 2124 AGCACTATGATGCTGACTATCCGGGTTGCGCTGGGCACTGAGTTGCATCTGTCCGCAAA 2183  
QY 136 CTCATTTGATGAGAGGCGCTTTCAGCTGCAAGAAATTTGGTTTACAGGAACAAAGCGT 135  
DB 2184 CTCATTTGATGAGAGGCGCTTTCAGCTGCAAGAAATTTGGTTTACAGGAACAAAGCGT 2243  
QY 196 CAACATTTACACCTCATCCAGACAGGATCAATCATAGTTAAGCTCTCCGAATCTGCC 255  
DB 2244 CAACATTTACACCTCATCCAGACAGGATCAATCATAGTTAAGCTCTCCGAATCTGCC 2303  
QY 256 CAAGATTAAGAGGAGCATGTGCGAAAGCCCTTGGATGCTATCAACAGACATTGACAC 315  
DB 2304 CAAGATTAAGAGGAGCATGTGCGAAAGCCCTTGGATGCTATCAACAGACATTGACAC 2363  
QY 316 TTGTCCTACCCCTTGGTGTGATCTATCCGTAGATTAAGAGATCTGCTGATCATCTGG 375  
DB 2364 TTGTCCTACCCCTTGGTGTGATCTATCCGTAGATTAAGAGATCTGCTGATCATCTGG 2423

QY 376 AGGGGGGAGACAGGGGGCCTTATAGGCCATTATGGCGGTGTGCTTTGGGGTTC 435  
DB 2424 AGGGGGGAGACAGGGGGCCTTATAGGGCCATTATGGCGGTGTGCTTTGGGGTTC 2483  
QY 436 AACTGCGCACAAATTAACAGCGCGCCGAGCTCTGTATACAGCCAAACAAATGCTGCCAA 495  
DB 2484 AACTGCGCACAAATTAACAGCGCGCGCAGCTCTGTATACAGCCAAACAAATGCTGCCAA 2543  
QY 496 CATCTCCGACTTAAAGAGACATTTGCCGAACCAATGAGGCTGTGATGAGTCACTGA 555  
DB 2544 CATCTCCGACTTAAAGAGACATTTGCCGAACCAATGAGGCTGTGATGAGTCACTGA 2603  
QY 556 CGGATTAACGCACTAGAGTGGCAGTTGGGAGATGACAGATTTGTTAAATGACCAAT 615  
DB 2604 CGGATTAACGCACTAGAGTGGCAGTTGGGAGATGACAGATTTGTTAAATGACCAAT 2663  
QY 616 TAATTAACAGCTCAGGAATTAGACTGCATCAAAATTTGACACAGCAAGTTGGTGTAGACT 675  
DB 2664 TAATTAACAGCTCAGGAATTAGACTGCATCAAAATTTGACACAGCAAGTTGGTGTAGACT 2723  
QY 676 CAACCTGTACTTAACCGAATTGATCAAGTATTTGGGACCAATATCACTTCACTGCTTT 735  
DB 2724 CAACCTGTACTTAACCGAATTGATCAAGTATTTGGGACCAATATCACTTCACTGCTTT 2783  
QY 736 AAACAGCTGACTATTGAGGACCTTTACATCTAGCTGTGGAAATATGATTAATTATT 795  
DB 2784 AAACAGCTGACTATTGAGGACCTTTACATCTAGCTGTGGAAATATGATTAATTATT 2843  
QY 796 GACTAATGATAGTGTAGGGAAACAAATCACTAGCTCATTAATCGGTAGCGGCTTAATGAC 855  
DB 2844 GACTAATGATAGTGTAGGGAAACAAATCACTAGCTCATTAATCGGTAGCGGCTTAATGAC 2903  
QY 856 CGGTAAACCTTATTTATACACTCAAGACTCAACTCTTGGGTATACAGTATCTTACC 915  
DB 2904 CGGTAAACCTTATTTATACACTCAAGACTCAACTCTTGGGTATACAGTATCTTACC 2963  
QY 916 TTTCAGTGGGAAACCTTAATATATATATGCGGACCACTTGGAAACCTTATCGGTAGGAC 975  
DB 2964 TTTCAGTGGGAAACCTTAATATATATATGCGGACCACTTGGAAACCTTATCGGTAGGAC 3023  
QY 976 AACGAGGGGATTTTGCCTGCGCACTTGTCCCAAAATGTGTGACACAGGTTCGTGTAT 1035  
DB 3024 AACGAGGGGATTTTGCCTGCGCACTTGTCCCAAAATGTGTGACACAGGTTCGTGTAT 3083  
QY 1036 AGAAGAACTTGAACACTTATATGTATGAAATGACTTAAATTTATTTGTACAAAGAT 1095  
DB 3084 AGAAGAACTTGAACACTTATATGTATGAAATGACTTAAATTTATTTGTACAAAGAT 3143  
QY 1096 AGTAACTTCCCTATATGTCCTGATTTATTTCCCTGCTTGAAGCGGCAATAGCTGGGCTG 1155  
DB 3144 AGTAACTTCCCTATATGTCCTGATTTATTTCCCTGCTTGAAGCGGCAATAGCTGGGCTG 3203  
QY 1156 TATGTACTCAAGACCGAAGGCGCACTTACTACACCATATACATCAAGGTTCACT 1215  
DB 3204 TATGTACTCAAGACCGAAGGCGCACTTACTACACCATATACATCAAGGTTCACT 3263  
QY 1216 CATGCGCAACTGCAAGATGACCAACATGTATGTATAAATGTTGTTATCTTATAGG 1275  
DB 3264 CATGCGCAACTGCAAGATGACCAACATGTATGTATAAATGTTGTTATCTTATAGG 3323  
QY 1276 AAATCTATGAGAGAGCGGTCTCTTATATAGTAAACAAATCAAGCAATTTATCTTATAGG 1335  
DB 3324 AAATCTATGAGAGAGCGGTCTCTTATATAGTAAACAAATCAAGCAATTTATCTTATAGG 3383  
QY 1336 CGGGATTACTTTAAGGCTCAGTGGGGAATTCGATTAATCTTATCAGAAATATCTCAAT 1395  
DB 3384 CGGGATTACTTTAAGGCTCAGTGGGGAATTCGATTAATCTTATCAGAAATATCTCAAT 3443  
QY 1396 ACAAGATTTCTCAAGTAAATTAATACAGGCAATCTTGTATATCTCACTGAGCTTGGGAATGT 1455  
DB 3444 ACAAGATTTCTCAAGTAAATTAATACAGGCAATCTTGTATATCTCACTGAGCTTGGGAATGT 3503

QY 1456 CAACACTCGATCGTATATGCTTTGAATTAAGTAAAGCAACAGAAACTAGACAA 1515  
DB 3504 CAACACTCGATCGTATATGCTTTGAATTAAGTAAAGCAACAGAAACTAGACAA 3563  
QY 1516 AGTCAATGTCAAACTGATAGACACATCTGCTCTCATTAATCTTATCTGTTTGAATCAT 1575  
DB 3564 AGTCAATGTCAAACTGATAGACACATCTGCTCTCATTAATCTTATCTGTTTGAATCAT 3623  
QY 1576 ATCTCTGTTTTTGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1635  
DB 3624 ATCTCTGTTTTTGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3683  
QY 1636 GGGCGCAACAAAACCTTATTTATGCTTGGGAAATTAATTAATTAATTAATTAATTAAT 1695  
DB 3684 GGGCGCAACAAAACCTTATTTATGCTTGGGAAATTAATTAATTAATTAATTAATTAATTAAT 3743  
QY 1696 TACAAAATGTGAACACAGATGAGAAAGGTTTCCCTATATAGTATTTGTGAAAG 1755  
DB 3744 TACAAAATGTGAACACAGATGAGAAAGGTTTCCCTATATAGTATTTGTGAAAG 3803  
QY 1756 TTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAAA 1792  
DB 3804 TTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAAA 3840

RESULT 7  
PCT-US94-01826A-12  
; Sequence 12, Application PC/TUS9401826A  
; GENERAL INFORMATION:  
; APPLICANT: Syntro Corporation, et al.  
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and Uses Thereof  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/01826A  
; FILING DATE: 28-FEB-1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White Bsq, John P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)977-9550  
; TELEFAX: (212)664-0525  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 115..1860  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 2095..3756  
PCT-US94-01826A-12  
Query Match 51.9%; Score 1741.8; DB 6; Length 4177;  
Best Local Similarity 98.8%; Pred. No. 0;

Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy	16	TGATCCCGGTTGGCGCCCTCAGAGTGCAGATGGGCTCCAGACCTTCTACCAAGAACCC	75
Db	2064	TGATCCCGGTTGGCGCCCTCAGAGTGCAGATGGGCTCCAGACCTTCTACCAAGAACCC	2123
Qy	76	AGCAGCTATGATGCTGATATCCGGGTTGGCTGGCACTGAGTTGCACTCTCCGGCAA	135
Db	2124	AGCAGCTATGATGCTGATATCCGGGTTGGCTGGCACTGAGTTGCACTCTCCGGCAA	2183
Qy	136	CTTCATTGATGGAGGCGCTTTCAGCTGAGAAATTTGGTTACAGAGACAAAGCCGT	195
Db	2184	CTTCATTGATGGAGGCGCTTTCAGCTGAGAAATTTGGTTACAGAGACAAAGCCGT	2243
Qy	196	CAACATATACCTCATCCAGACAGATCAATCATAGTTAAGCTCTCCGAAATCTGCC	255
Db	2244	CAACATATACCTCATCCAGACAGATCAATCATAGTTAAGCTCTCCGAAATCTGCC	2303
Qy	256	CAAGATPAGAGGAGGATGCGAAAGCCCTTGGATGATACAAAGAGCAATTGACAC	315
Db	2304	CAAGATPAGAGGAGGATGCGAAAGCCCTTGGATGATACAAAGAGCAATTGACAC	2363
Qy	316	TTTGTCAACCCCTTGGTGACTCATCCGTAGGATACAGAGTCTGTGCTACATCTGG	375
Db	2364	TTTGTCAACCCCTTGGTGACTCATCCGTAGGATACAGAGTCTGTGCTACATCTGG	2423
Qy	376	AGGGGGGAGACAGGGGCGCTTATAGGCGCATATTATGGCGGTGTGGCTTGGGGTTGC	435
Db	2424	AGGGGGGAGACAGGGGCGCTTATAGGCGCATATTATGGCGGTGTGGCTTGGGGTTGC	2483
Qy	436	AACGCGGACAAATACAGCGGCGCGCTGTGTATACAGCCAAACAAATGCTGCCAA	495
Db	2484	AACGCGGACAAATACAGCGGCGCGCTGTGTATACAGCCAAACAAATGCTGCCAA	2543
Qy	496	CATCTCCGACTTAAAGAGACATTTCCGCAACCAAGAGGCTGTGATGAGTCACTGA	555
Db	2544	CATCTCCGACTTAAAGAGACATTTCCGCAACCAAGAGGCTGTGATGAGTCACTGA	2603
Qy	556	CGGATTTATCGCAATAGAGAGTGGAGATGGGAAATGAGACAGTTCTTATATGACAAAT	615
Db	2604	CGGATTTATCGCAATAGAGAGTGGAGATGGGAAATGAGACAGTTCTTATATGACAAAT	2663
Qy	616	TAAATAAACAGCTCAGAGATTTAGCTGATCAAAATTTGCACAGACAGTTGTTGAGACT	675
Db	2664	TAAATAAACAGCTCAGAGATTTAGCTGATCAAAATTTGCACAGACAGTTGTTGAGACT	2723
Qy	676	CAACCTGTACTAACCGAATTTGATCAAGTATTTGGACACAAATCACTTCACTGCTTT	735
Db	2724	CAACCTGTACTAACCGAATTTGATCAAGTATTTGGACACAAATCACTTCACTGCTTT	2783
Qy	736	AAACAGAGTGACTATTGAGGCACTTTACAATCTAGCTGTGGAATATATGATTTACTTAT	795
Db	2784	AAACAGAGTGACTATTGAGGCACTTTACAATCTAGCTGTGGAATATATGATTTACTTAT	2843
Qy	796	GACTAATGATAGTGTAGGGAACAATCACTCAGCTCATTAATCGGTAGCGGCTTAATCAC	855
Db	2844	GACTAATGATAGTGTAGGGAACAATCACTCAGCTCATTAATCGGTAGCGGCTTAATCAC	2903
Qy	856	CGGTAAACCTTATTTATACAGCTCAAGATCTCAACTCTTGGGTATACAGTTAATCTTACC	915
Db	2904	CGGTAAACCTTATTTATACAGCTCAAGATCTCAACTCTTGGGTATACAGTTAATCTTACC	2963
Qy	916	TTTCAGTGGGGAACCTAATAATATATGCGTGCACCACTAGTGGAACTTAATCGTAAAGAC	975
Db	2964	TTTCAGTGGGGAACCTAATAATATATGCGTGCACCACTAGTGGAACTTAATCGTAAAGAC	3023
Qy	976	AACCAAGGGAATTTGCTCGGCACTTTGCCAAAAGTGTTGACAGAGTGGTTCTGTGAT	1035
Db	3024	AACCAAGGGAATTTGCTCGGCACTTTGCCAAAAGTGTTGACAGAGTGGTTCTGTGAT	3083
Qy	1036	AGAAAGAACTTGACACTCTCATCTGTATAGAAAGTGAATTTATTTATTTATCAAGAT	1095
Db	3084	AGAAAGAACTTGACACTCTCATCTGTATAGAAAGTGAATTTATTTATTTATCAAGAT	3143

Qy	1096	AGTAACTTCCCTATATGTCCTGCTGATTTATCTCTGTTGAGCGGCAATACCTGCGCTG	1155
Db	3144	AGTAACTTCCCTATATGTCCTGCTGATTTATCTCTGTTGAGCGGCAATACCTGCGCTG	3203
Qy	1156	TATGTACTCAAAAGCGGAGCGGCACTTACTACACCAATACATGATCTATCAAGGTTAGT	1215
Db	3204	TATGTACTCAAAAGCGGAGCGGCACTTACTACACCAATACATGATCTATCAAGGTTAGT	3263
Qy	1216	CATGCCCACTGCAAGATGACCAACATGTAGTGTAAACCCCGGGATATCATATGCA	1275
Db	3264	CATGCCCACTGCAAGATGACCAACATGTAGTGTAAACCCCGGGATATCATATGCA	3323
Qy	1276	AACTATGAGAGGCGGTGTCTTAATATATTAACAATCATGCAATGTTTATCTTAAG	1335
Db	3324	AACTATGAGAGGCGGTGTCTTAATATATTAACAATCATGCAATGTTTATCTTAAG	3393
Qy	1336	CGGATTAACCTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATACAGAAATATCTCAAT	1395
Db	3384	CGGATTAACCTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATACAGAAATATCTCAAT	3443
Qy	1396	ACAAGATTTCAAGTAAATTAATACAGGCAATCTTATATCTCAACTGAGCTTGGGAATGT	1455
Db	3444	ACAAGATTTCAAGTAAATTAATACAGGCAATCTTATATCTCAACTGAGCTTGGGAATGT	3503
Qy	1456	CAACACTCGATCAGTATGCTTTGAATTAAGTTAGAGAAAGCAAGAAACTAGACAA	1515
Db	3504	CAACACTCGATCAGTATGCTTTGAATTAAGTTAGAGAAAGCAAGAAACTAGACAA	3563
Qy	1516	AGTCAATGTCAAACTGACTGACCATCTGCTCATTAAGTTAGAGAAAGCAAGAAACTAGAC	1575
Db	3564	AGTCAATGTCAAACTGACTGACCATCTGCTCATTAAGTTAGAGAAAGCAAGAAACTAGAC	3623
Qy	1576	ATCTGTTGTTTGGTATCTTACCTGATTTAGCTGATCTACATTAATGTACAAACAA	1635
Db	3624	ATCTGTTGTTTGGTATCTTACCTGATTTAGCTGATCTACATTAATGTACAAACAA	3683
Qy	1636	GGCGCAACAAACAACTTATTTATGCTTGGAAATTAATCTCTAGATCAGATGAGAGCAC	1695
Db	3684	GGCGCAACAAACAACTTATTTATGCTTGGAAATTAATCTCTAGATCAGATGAGAGCAC	3743
Qy	1696	TACAAAATGTGAACACAGATGAGGAAAGGATTTCCCTTAATATTTGTTGTGAAG	1755
Db	3744	TACAAAATGTGAACACAGATGAGGAAAGGATTTCCCTTAATATTTGTTGTGAAG	3803
Qy	1756	TTCTGTAGTCTGTCACTGAGAGTTAAGAAAAA	1792
Db	3804	TTCTGTAGTCTGTCACTGAGAGTTAAGAAAAA	3840

RESULT 8  
PCT-US94-02252A-12  
Sequence 12, Application PC/TUS9402252A  
GENERAL INFORMATION:  
APPLICANT: Syntro Corporation, et al.  
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/02252A  
FILING DATE: 28-FEB-1994  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: White Esq, John P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 115..1860  
NAME/KEY: CDS  
LOCATION: 2095..3756  
PCT-US94-02252A-12

Query Match 51.9%; Score 1741.8; DB 6; Length 4177;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 16 TGGATCCCGGTGGGCGCCCTCCAGGTGCAAGATGGGGCTCCAGACCTTCTACCAAGAACCC 75  
DB 2064 TCGATCCCGGTGGGCGCCCTCCAGGTGCAAGATGGGGCTCCAGACCTTCTACCAAGAACCC 2123

QY 76 AGCACTATGATGCTGATCTATCCGGGTGCGCTGGCACTGATGTCATCTGTCCGGCAAA 135  
DB 2124 AGCACTATGATGCTGATCTATCCGGGTGCGCTGGCACTGATGTCATCTGTCCGGCAAA 2183

QY 136 CTCATTGATGCGCAGGCGCTTTGCAAGCTGCAAGAAATTGTGTTACAGAGAACAAAGCCGT 195  
DB 2184 CTCATTGATGCGCAGGCGCTTTGCAAGCTGCAAGAAATTGTGTTACAGAGAACAAAGCCGT 2243

QY 196 CAACATATACCTTCATCCCAAGACAGATTCATATCTATTAAAGCTCCCTCCGAATCTGCC 255  
DB 2244 CAACATATACCTTCATCCCAAGACAGATTCATATCTATTAAAGCTCCCTCCGAATCTGCC 2303

QY 256 CAAGATTAAGAGGCGATGCGAAAGCCCTTGGATGATCAACAGAGCACTTACAC 315  
DB 2304 AAAGATTAAGAGGCGATGCGAAAGCCCTTGGATGATCAACAGAGCACTTACAC 2363

QY 316 TTTCCTCACCCCCTTGGTGACTCTATCCGTAGATACAAAGTCTGTGACTACATCTGG 375  
DB 2364 TTTCCTCACCCCCTTGGTGACTCTATCCGTAGATACAAAGTCTGTGACTACATCTGG 2423

QY 376 AGGGGGGAGACAGGGGGCCCTTATAGGGCCATTTATGGCGGTGTGGCTTTGGGGTTGC 435  
DB 2424 AGGGGGGAGACAGGGGGCCCTTATAGGGCCATTTATGGCGGTGTGGCTTTGGGGTTGC 2483

QY 436 AACTGCCGCAAAATTAACAGGGCGCGAGCTCTGTATCAAGCCAAACAAATGTGCCAA 495  
DB 2484 AACTGCCGCAAAATTAACAGGGCGCGAGCTCTGTATCAAGCCAAACAAATGTGCCAA 2543

QY 496 CATCTCCGACTTAAAGAGACATTCGCGCAACCAATAGGCTGTGATGAGTCACTGA 555  
DB 2544 CATCTCCGACTTAAAGAGACATTCGCGCAACCAATAGGCTGTGATGAGTCACTGA 2603

QY 556 CGGATTTACGCACTAGACAGTGGCAGTTGGGAAGTGCAGCAGTTTGTATGACCAATT 615  
DB 2604 CGGATTTACGCACTAGACAGTGGCAGTTGGGAAGTGCAGCAGTTTGTATGACCAATT 2663

QY 616 TAAATAAACAGCTCAGAAATTAAGATGATCAAAATTTGCAACAGAAAGTTGGTGAAGT 675  
DB 2664 TAAATAAACAGCTCAGAAATTAAGATGATCAAAATTTGCAACAGAAAGTTGGTGAAGT 2723

QY 676 CAACCTGACTTAACGAATTTGACTAGATTCGGAACCAAAATCACTTCACTGCTTT 735  
DB 735

DB 2724 CAACCTGACTTAACGAATTTGACTAGATTCGGAACCAAAATCACTTCACTGCTTT 2783

QY 736 AAACAGCTGACTATTCAGGACCTTTTCAATCTAGCTGGTGGAAATATGATTTACTTAT 795  
DB 2784 AAACAGCTGACTATTCAGGACCTTTTCAATCTAGCTGGTGGAAATATGATTTACTTAT 2843

QY 796 GACTAAGTTAGGTAGGAAACATCAACTGACTCATTTATCGGTAGCGGCTTAATCAC 855  
DB 2844 GACTAAGTTAGGTAGGAAACATCAACTGACTCATTTATCGGTAGCGGCTTAATCAC 2903

QY 856 CGGTAAACCTTATTCATACGCTCAGACACTCACTGTGGGTATACAGTAACTTACC 915  
DB 2904 CGGTAAACCTTATTCATACGCTCAGACACTCACTGTGGGTATACAGTAACTTACC 2963

QY 916 TTCACTCGGAACTTAATATATATGCGTCCACCTACTTGGAAACTTATCCGTAAGCAC 975  
DB 2964 TTCACTCGGAACTTAATATATATGCGTCCACCTACTTGGAAACTTATCCGTAAGCAC 3023

QY 976 AACCAAGGAAATTTGCTCGGCACTTGTCCAAAGTGTGACACAGTTCGGTTCTGTAT 1035  
DB 3024 AACCAAGGAAATTTGCTCGGCACTTGTCCAAAGTGTGACACAGTTCGGTTCTGTAT 3083

QY 1036 AGAAGACTTGACACCTCATCTGTATATGAATGACCTTAGATTTATATGTAACAAGAT 1095  
DB 3084 AGAAGACTTGACACCTCATCTGTATATGAATGACCTTAGATTTATATGTAACAAGAT 3143

QY 1096 AGTAACGTTCCCTATATGTCCTCGTATTTATTCCTGTCTGAGCGGCAATAGCTGGCCTG 1155  
DB 3144 AGTAACGTTCCCTATATGTCCTCGTATTTATTCCTGTCTGAGCGGCAATAGCTGGCCTG 3203

QY 1156 TATGTACTCAAAAGCCGAGGCGCACTTATCAACCATATGACTATCAAAAGTTCACT 1215  
DB 3204 TATGTACTCAAAAGCCGAGGCGCACTTATCAACCATATGACTATCAAAAGTTCACT 3263

QY 1216 CATGGCCAACTGCAAGATGACAAATGATGTGTAAACCCCGGGGTATCATTTGCCA 1275  
DB 3264 CATGGCCAACTGCAAGATGACAAATGATGTGTAAACCCCGGGGTATCATTTGCCA 3323

QY 1276 AAACATAGGAAACCGGTCTCTAATAGATTAACAATCATGCAATGTTTTATCCTTAG 1335  
DB 3324 AAACATAGGAAACCGGTCTCTAATAGATTAACAATCATGCAATGTTTTATCCTTAG 3383

QY 1336 CGGATTAACCTTAAAGCTCACTGAGGGAATTCATGTAACTTATCAGAAATATCTCAAT 1395  
DB 3384 CGGATTAACCTTAAAGCTCACTGAGGGAATTCATGTAACTTATCAGAAATATCTCAAT 3443

QY 1396 ACAAGATTCCTAAGTATTAATTAACAGGCATCTTGAATTCACACTGACTGCTGGAAATG 1455  
DB 3444 ACAAGATTCCTAAGTATTAATTAACAGGCATCTTGAATTCACACTGACTGCTGGAAATG 3503

QY 1456 CAACAACTCGATCAGTAATGCTTTGAATATGATTAAGAGAAAGCAACAGAAAATAGACAA 1515  
DB 3504 CAACAACTCGATCAGTAATGCTTTGAATATGATTAAGAGAAAGCAACAGAAAATAGACAA 3563

QY 1516 AGTCATGTCAAACTGACTAGACATCTGCTCATTAACCTATATCGTTTTGACTATCAT 1575  
DB 3564 AGTCATGTCAAACTGACTAGACATCTGCTCATTAACCTATATCGTTTTGACTATCAT 3623

QY 1576 ATCTCTGTTTTTGGTATTAAGCTGATCTTACAGTCACTCACTTAATAGTCAAGCAAAA 1635  
DB 3624 ATCTCTGTTTTTGGTATTAAGCTGATCTTACAGTCACTCACTTAATAGTCAAGCAAAA 3683

QY 1636 GGGCGCAAAAAACCTTATATGAGCTTGGGAATTAATCTAGATGAGTGAAGGCCAC 1695  
DB 3684 GGGCGCAAAAAACCTTATATGAGCTTGGGAATTAATCTAGATGAGTGAAGGCCAC 3743

QY 1696 TACAAAATGTGAACACAGATGAGGAAGAAAGTTTCCCTAATAGTAATTTGTGAAAG 1755  
DB 3744 TACAAAATGTGAACACAGATGAGGAAGAAAGTTTCCCTAATAGTAATTTGTGAAAG 3803

QY 1756 TTCTGTAGTCTGTCAAGTTCAAGAGTTTAAGAAAAA 1792  
DB 3804 TTCTGTAGTCTGTCAAGTTCAAGAGTTTAAGAAAAA 3840

```
RESULT 9
US-09-881-457A-1
; Sequence 1, Application US/09881457A
; Patent No. 6913751
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Cook, Stephanie M
; APPLICANT: Wild, Martha A
; TITLE OF INVENTION: No. 6913751e1 Avian Herpes Virus and Uses Thereof
; FILE REFERENCE: SY01105X1OKOK
; CURRENT APPLICATION NUMBER: US/09/881,457A
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/426,352
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/804,372
; PRIOR FILING DATE: 1997-02-21
; PRIOR APPLICATION NUMBER: PCT/US95/10245
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: 08/663,566
; PRIOR FILING DATE: 1996-06-13
; PRIOR APPLICATION NUMBER: 08/288,065
; PRIOR FILING DATE: 1994-08-09
; PRIOR APPLICATION NUMBER: PCT/US93/05681
; PRIOR FILING DATE: 1993-06-14
; PRIOR APPLICATION NUMBER: 08/023,610
; PRIOR FILING DATE: 1993-02-26
; PRIOR APPLICATION NUMBER: 07/898,087
; PRIOR FILING DATE: 1992-06-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3570
; TYPE: DNA
; ORGANISM: Newcastle disease virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1194)..(2888)
; OTHER INFORMATION: NDV Fusion Protein
; NAME/KEY: misc feature
; LOCATION: (1355)
; OTHER INFORMATION: n = any nucleotide
US-09-881-457A-1

Query Match      50.7%; Score 1701.6; DB 3; Length 3570;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 25; Indels 3; Gaps 3;

QY      16 TGGATCCGCGTGGCGCCCTTCAGAGTGCAGAGTGGGCTCCAGACCTTCTACCAAGAAACC 75
DB      1199 TCGATCCCGGTTGGCGCCCTTCAGAGTGCAGAGTGGGCTCCAGACCTTCTACCAAGAAACC 1258
QY      76 AGCACCTATGATGCTGACTATCCGGGTTGGCGCTGGCACTGAGTTGCATCTGTCCGGCAA 135
DB      1259 AGCACCTATGATGCTGACTATCCGGGTTGGCGCTGGCACTGAGTTGCATCTGTCCGGCAA 1318
QY      136 CTCATTGATGGGCGGCTCTTGGAGCTGAGGAATTGGTTACAGGAAGCAAAAGCGT 195
DB      1319 CTCATTGATGGGCGGCTCTTGGAGCTGAGGAATTGGTTACAGGAAGCAAAAGCGT 1377
QY      196 CAACATATTAACCTCATCCAGACAGATCAATCATATTAAAGCTCCTCCGAATCTGCC 255
DB      1378 CAACATATTAACCTCATCCAGACAGATCAATCATATTAAAGCTCCTCCGAATCTGCC 1435
QY      256 CAAGGATTAAGAGGAGCATGTGGGAAAGCCCTTGGATGCATACAAGACATTGACCAAC 315
DB      1436 AAAGGATTAAGAGGAGCATGTGGGAAAGCCCTTGGATGCATACAAGACATTGACCAAC 1495
QY      316 TTGGCTCAACCCCTTGGTGACTCTATCCGTAAGATCAAGAGCTGTGACTATCATCTGG 375
DB      1496 TTGGCTCAACCCCTTGGTGACTCTATCCGTAAGATCAAGAGCTGTGACTATCATCTGG 1555
```

```
QY      376 AGGGGGAGACAGGGGGCCCTTATAGCCCATATTATGGCGGTGGCTCTTGGGGTTGC 435
DB      1556 AGGGGGAGACAGGGGGCCCTTATAGCCCATATTATGGCGGTGGCTCTTGGGGTTGC 1615
QY      436 AACTGCCGCACAATTAACAGGGGCGGAGCTCTGATCAAGGCCAAACAAATGTCTGCCAA 495
DB      1616 AACTGCCGCACAATTAACAGGGGCGGAGCTCTGATCAAGGCCAAACAAATGTCTGCCAA 1675
QY      496 CATCCTCCGACTTAAGAGAGCATTTGGCGCAACCAATGAGGCTGTGCATGAGTCACTGA 555
DB      1676 CATCCTCCGACTTAAGAGAGCATTTGGCGCAACCAATGAGGCTGTGCATGAGTCACTGA 1735
QY      556 CGGATTTCCGCACTACAGTGGGAGTTGGGGAATGCAGAGTTTGTATATGCAATT 615
DB      1736 CGGATTTCCGCACTACAGTGGGAGTTGGGGAATGCAGAGTTTGTATATGCAATT 1795
QY      616 TAATTAACAGCTCAGGAATTTAGCTGCATCAAAATTGCAACAGCAAGTGGTGAAGCT 675
DB      1796 TAATTAACAGCTCAGGAATTTAGCTGCATCAAAATTGCAACAGCAAGTGGTGAAGCT 1855
QY      676 CAACCTGTACTTAACCGAATTTGACTACAGTATTCGACCAACCAATCACTTCACTGCTTT 735
DB      1856 CAACCTGTACTTAACCGAATTCGACTACAGTATTCGACCAACCAATCACTTCACTGCTTT 1915
QY      736 AAACAGCTGACTATTAGGCACTTTACAACTTACCTGCTGGGAATATGCAATTCTATT 795
DB      1916 AAACAGCTGACTATTAGGCACTTTACAACTTACCTGCTGGGAATATGCAATTCTATT 1975
QY      796 GACTAAGTATAGGTATAGGAAACAATCACTCAGCTCAATTAATGGTGGCGCTTAATCAC 855
DB      1976 GACTAAGTATAGGTATAGGAAACAATCACTCAGCTCAATTAATGGTGGCGCTTAATCAC 2035
QY      856 CGGTAAACCTTATTTCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACCTTACC 915
DB      2036 CGGTAAACCTTATTTCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACCTTACC 2095
QY      916 TTCACTGGGAAACCTTAATTAATATGCTGCCAAGCTTATGGAAACCTTATCCGTAAACAC 975
DB      2096 TTCACTGGGAAACCTTAATTAATATGCTGCCAAGCTTATGGAAACCTTATCCGTAAACAC 2155
QY      976 AACGAGGGGATTTGGCCCTGGGCACTTGGCCCAAAAGGTGTGACACAGGTCGGTCTGTGAT 1035
DB      2156 AACGAGGGGATTTGGCCCTGGGCACTTGGCCCAAAAGGTGTGACACAGGTCGGTCTGTGAT 2215
QY      1036 AGAAGAACTTGACACTCATATCTGTATAGAACTGACTTATGATTTATATGTACAAAGAT 1095
DB      2216 AGAAGAACTTGACACTCATATCTGTATAGAACTGACTTATGATTTATATGTACAAAGAT 2275
QY      1096 AGTAACGTTCCCTATGTCCCTGGTATTTATCTGCTTGAAGGCAATACGTGGCCCTG 1155
DB      2276 AGTAACGTTCCCTATGTCCCTGGTATTTATCTGCTTGAAGGCAATACGTGGCCCTG 2315
QY      1156 TATGTACTCAAAAGCGAAGGCGCACTTACACCAATGATGATCTTCAAGGTCAGT 1215
DB      2316 TATGTACTCAAAAGCGAAGGCGCACTTACACCAATGATGATGATCTTCAAGGTCAGT 2395
QY      1216 CATCGCAACTGCAAGATGACCAATGTATGTATTAACCCCGGGGTATCATATGCA 1275
DB      2396 CATCGCAACTGCAAGATGACCAATGTATGTATTAACCCCGGGGTATCATATGCA 2455
QY      1276 AAACATATGAGAAAGCCGTGTCTTAATATGATTAACAATCATGCAATGTTTATCTTAGG 1335
DB      2456 AAACATATGAGAAAGCCGTGTCTTAATATGATTAACAATCATGCAATGTTTATCTTAGG 2515
QY      1336 CGGGATTAACCTTTAAGGCTCAGTGGGAAATTCATGTAACCTTAACAAGAAATTCGAAT 1395
DB      2516 CGGGATTAACCTTTAAGGCTCAGTGGGAAATTCATGTAACCTTAACAAGAAATTCGAAT 2575
QY      1396 ACAAGATTTCAAGTATTAATTAACAGGCAATCTTGAATCTCAACGAGCTTGGGAATGT 1455
DB      2576 ACAAGATTTCAAGTATTAATTAACAGGCAATCTTGAATCTCAACGAGCTTGGGAATGT 2635
QY      1456 CAACAACTCGATCAGTAATGCTTTGAATTAATGATGAAGAAAGCAAGAAACTTAGACAA 1515
```



|||||  
Db 2636 CAACACCTCGATCGATATGCTTGAATTAAGTTAGAGAAAGCAACGAAAACTTAGCAAA 2695  
Qy 1516 AGTCAATGTCAAACTGATGACACATCGCTCTCATTAACCTATATCGTTTGACATCAT 1515  
Db 2696 AGTCAATGTCAAACTGATGACACATCGCTCTCATTAACCTATATCGTTTGACATCAT 2755  
Qy 1576 ATCTCTGTTTTTGGTATCTACTTACCTGATTTCTAGCATGCTACTAATGTACAAGCAAAA 1635  
Db 2756 ATCTCTGTTTTTGGTATCTACTTACCTGATTTCTAGCATGCTACTAATGTACAAGCAAAA 2815  
Qy 1636 GGGCGCAACAAAACTTATATGCGCTTGGAAATATCTTAATGATGAGAGGCCAC 1635  
Db 2816 GGGCGCAACAAAACTTATATGCGCTTGGAAATATCTTAATGATGAGAGGCCAC 2875  
Qy 1696 TACAAAATGTGACACAGATGAGAAAGGATTTCCCTAATAGTAAATTTGTGGAAG 1755  
Db 2876 TACAAAATGTGACACAGATGAGAAAGGATTTCCCTAATAGTAAATTTGTGGAAG 2935  
Qy 1756 TTCTGTAGTCTGTCACTTCAAGATGAGATTAAGAAAAA 1792  
Db 2936 TTCTGTAGTCTGTCACTTCAAGATGAGATTAAGAAAAA 2972

RESULT 10  
US-08-663-566A-12  
; Sequence 12, Application US/08663566A  
; Patent No. 5853733  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D  
; APPLICANT: Macdonald, Richard D  
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys  
; TITLE OF INVENTION: and Uses Thereof  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/663,566A  
; FILING DATE: June 13, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P  
; REGISTRATION NUMBER: 28,678  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0526  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1662 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1662  
; US-08-663-566A-12  
Query March 48.6%; Score 1631.6; DB 2; Length 1662;  
Best Local Similarity 98.9%; Pred. No. 0;

	Matches	1643; Conservative	0; Mismatches	19; Indels	0; Gaps	0;
Qy	47	ATGGGCTCCAGACCTTCTACCAAGACCCAGACCTATGATGCTGACTATCCGGGTTCCG				106
Db	1	ATGGGCTCCAGACCTTCTACCAAGACCCAGACCTATGATGCTGACTATCCGGGTTCCG				60
Qy	107	CTGGCACTGAGTTGCACTCTGTCGGGCAAACTCCATTTGAATGGCAGGCGCTTTGGACCTGCA				166
Db	61	CTGGTACTGAGTTGCACTCTGTCGGGCAAACTCCATTTGAATGGCAGGCGCTTTGGACCTGCA				120
Qy	167	GGAATGTGGTTACAGGAGCAAAAGCCGTCAACATATACCTATCCAGACAGATATCA				226
Db	121	GGAATGTGGTTACAGGAGCAAAAGCCGTCAACATATACCTATCCAGACAGATATCA				180
Qy	227	ATCATAGTTAAAGCTCTCCGGAATCTGCCAAGGATTAAGAGGAGATGTGCAAAAGCCGCC				286
Db	181	ATCATAGTTAAAGCTCTCCGGAATCTGCCAAGGATTAAGAGGAGATGTGCAAAAGCCGCC				240
Qy	287	TTGGATGCAATACACAGACATTTGACCACTTTCCTACCCCTTGGTGAATCTTATCGGT				346
Db	241	TTGGATGCAATACACAGACATTTGACCACTTTCCTACCCCTTGGTGAATCTTATCGGT				300
Qy	347	AGGATACAGAGCTGTGACCTACATCTGAGGGGGGAGACAGGGGGCGCTTATAGGGGCC				406
Db	301	AGGATACAGAGCTGTGACCTACATCTGAGGGGGGAGACAGGGGGCGCTTATAGGGGCC				360
Qy	407	ATTATTTGGCGGTGTGGCTCTTGGGGTTGCACTCCGACCAAAATACAGCGGCGCAGCT				466
Db	361	ATTATTTGGCGGTGTGGCTCTTGGGGTTGCACTCCGACCAAAATACAGCGGCGCAGCT				420
Qy	467	CTGATACAGGCAAAATATGCTGCCAATCTCTCCGACTTAAAGAGAGCATTTGCCGCA				526
Db	421	CTGATACAGGCAAAATATGCTGCCAATCTCTCCGACTTAAAGAGAGCATTTGCCGCA				480
Qy	527	ACCAATGAGGCTGTGATGAGGTCATCGACGGAATTAACGCAATACAGGAGTTGGG				586
Db	481	ACCAATGAGGCTGTGATGAGGTCATCGACGGAATTAACGCAATACAGGAGTTGGG				540
Qy	587	AAGATGACAGAGTTGTTAATGACCAATTTAATAACAGCTCAGGAATTAGACTGCATC				646
Db	541	AAGATGACAGAGTTGTTAATGACCAATTTAATAACAGCTCAGGAATTAGACTGCATC				600
Qy	647	AAAATGCAACAGAGTTGTTGTAAGCTCAACCTGTACCTAACCGAATTGACTACAGTA				706
Db	601	AAAATGCAACAGAGTTGTTGTAAGCTCAACCTGTACCTAACCGAATTGACTACAGTA				660
Qy	707	TTGGACCACAAAATCACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTACAT				766
Db	661	TTGGACCACAAAATCACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTACAT				720
Qy	767	CTAGCTGGTGAATATGATGATTACTTATTTGACTAAGTTAGGTAGGGAACAATCAATC				826
Db	721	CTAGCTGGTGAATATGATGATTACTTATTTGACTAAGTTAGGTAGGGAACAATCAATC				780
Qy	827	AGCTCATTTAATCGGTAGCGGCTTATACACCGGTAACTTATATAGCACTCACAGACT				886
Db	781	AGCTCATTTAATCGGTAGCGGCTTATACACCGGTAACTTATATAGCACTCACAGACT				840
Qy	887	CAACTTTGGGTATACAGGTACTTACCTTCACTGAGTGGGAACTTAATATATCGTGGC				946
Db	841	CAACTTTGGGTATACAGGTACTTACCTTCACTGAGTGGGAACTTAATATATCGTGGC				900
Qy	947	ACCTACTTGAACCTTATCGGTATAGCAACAGGGGATTTGGCTGGGCACTTGTCCCA				1006
Db	901	ACCTACTTGAACCTTATCGGTATAGCAACAGGGGATTTGGCTGGGCACTTGTCCCA				960
Qy	1007	AAAGTGTGACACAGTCCGTTCTGTGATAGAGAACTTGACACCTCATCTGATAGAA				1066
Db	961	AAAGTGTGACACAGTCCGTTCTGTGATAGAGAACTTGACACCTCATCTGATAGAA				1020
Qy	1067	ACTGACTTAGATTATATTTGATCAAGAAATAGTAACGTTCCCTATAGTCCCTGGTATTTAT				1126
Db	1021	ACTGACTTAGATTATATTTGATCAAGAAATAGTAACGTTCCCTATAGTCCCTGGTATTTAT				1080

QY 1127 TCCTGCTTGAGCGGCAATACGTCGGCCTGTATGTACTCAAGACGGAAGCGCACTTACT 1186  
DB 1081 TCCTGCTTGAGCGGCAATACGTCGGCCTGTATGTACTCAAGACGGAAGCGCACTTACT 1140  
QY 1187 ACACCATACATGATATCAAAAGGTTCACTATCGCCCACTGCAAGATGACAACTGTAGA 1246  
DB 1141 ACACCATATATGACTATCAAAAGGCTCACTATCGCTCAAGATGACAACTGTAGA 1200  
QY 1247 TGTATAACCCCGGGGTATCATATCGCAAAACTATGAGAGAGCGGTCTCTAATAGAT 1306  
DB 1201 TGTATAACCCCGGGGTATCATATCGCAAAACTATGAGAGAGCGGTCTCTAATAGAT 1260  
QY 1307 AAACCAATCATGCAATGTTTTATCCTTAGCGCGGATTAATTAGGCTCAAGTGGGAAATTC 1366  
DB 1261 AAACCAATCATGCAATGTTTTATCCTTAGCGCGGATTAATTAGGCTCAAGTGGGAAATTC 1320  
QY 1367 GATGTAACTTATCAAGAAATATCTCAATACAAATTTCTCAAGTAAATATTAACAGGCAAT 1426  
DB 1321 GATGTAACTTATCAAGAAATATCTCAATACAAATTTCTCAAGTAAATATTAACAGGCAAT 1380  
QY 1427 CTGATATCTCAACTGAGCTTGGGAATGTCAACAATCGATCAGTAAATGCTTGAATAG 1486  
DB 1381 CTGATATCTCAACTGAGCTTGGGAATGTCAACAATCGATCAGTAAATGCTTGAATAG 1440  
QY 1487 TTAAGGAAAGCAACAGAAAATAGACAAAGTCAATGTCAAACTGACTAGCAACTGTCT 1546  
DB 1441 TTAAGGAAAGCAACAGAAAATAGACAAAGTCAATGTCAAACTGACTAGCAACTGTCT 1500  
QY 1547 CTGATTAACCTATATCGTTTGGTATCATATCTCTGTTTTTGGTAAATCTTAAGCTGAT 1606  
DB 1501 CTGATTAACCTATATCGTTTGGTATCATATCTCTGTTTTTGGTAAATCTTAAGCTGAT 1560  
QY 1607 CTAGCATGCTACCAATATGTAACAAGCAAAAGCGCAACAAATCTTATTATGCTTGGG 1666  
DB 1561 CTAGCATGCTACCAATATGTAACAAGCAAAAGCGCAACAAATCTTATTATGCTTGGG 1620  
QY 1667 AATAATCTCTAGATCAGATGAGAGCCATCAAAAATGTGA 1708  
DB 1621 AATAATCTCTAGATCAGATGAGAGCCATCAAAAATGTGA 1662

RESULT 11  
US-08-023-610-12  
; Sequence 12, Application US/08023610  
; Patent No. 5928648  
; GENERAL INFORMATION:  
; APPLICANT: Cochran Ph.D., Mark D  
; APPLICANT: Macdonald Ph.D., Richard D  
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: John P. White  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/023,610  
; FILING DATE: February 26, 1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White Esq., John P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 977-9550  
; TELEFAX: (212) 664-0525

TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1662 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1662  
; US-08-023-610-12

Query Match 48.6%; Score 1631.6; DB 2; Length 1662;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 47 ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTTCG 106  
DB 1 ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTTCG 60  
QY 107 CTGCAACTGAGTTCATCTGTCCGGCAACTCATTTGATGAGAGGCGCTTTGACAGTGA 166  
DB 61 CTGCAACTGAGTTCATCTGTCCGGCAACTCATTTGATGAGAGGCGCTTTGACAGTGA 120  
QY 167 GGAATGTGTTACAGAGACAAGCCGTCACATATACCTCATTCGCCAGACAGATCA 226  
DB 121 GGAATGTGTTACAGAGACAAGCCGTCACATATACCTCATTCGCCAGACAGATCA 180  
QY 227 ATCATATTAAGTCTCTCCGGAATCTGCCAAGATTAAGAGGCAATGTGGAAAGCCCC 286  
DB 181 ATCATATTAAGTCTCTCCGGAATCTGCCAAGATTAAGAGGCAATGTGGAAAGCCCC 240  
QY 287 TTGGATGATACAAACAGAAATGACCACTTTGCTCAACCCCTTGGTGACTATCCGT 346  
DB 241 TTGGATGATACAAACAGAAATGACCACTTTGCTCAACCCCTTGGTGACTATCCGT 300  
QY 347 AGGATCAAGAGTCTGTGACTATCATCTGAGAGGAGGAGACAGGGGCGCTTATAGGCGC 406  
DB 301 AGGATCAAGAGTCTGTGACTATCATCTGAGAGGAGGAGACAGGGGCGCTTATAGGCGC 360  
QY 407 ATTATGGCGGTGTGGCTCTTGGGGTTGCACTGCGCACAAATTAACGCGCGCAGCT 466  
DB 361 ATTATGGCGGTGTGGCTCTTGGGGTTGCACTGCGCACAAATTAACGCGCGCAGCT 420  
QY 467 CTGATACAGCCCAAAATGCTGCGCAATCTCTCGACTTAAAGAGACATTTGCCGA 526  
DB 421 CTGATACAGCCCAAAATGCTGCGCAATCTCTCGACTTAAAGAGACATTTGCCGA 480  
QY 527 ACCAATGAGCTGTGATGAGTCACTGACGATTTATGCACTAGACAGTGGCAGTTGGG 586  
DB 481 ACCAATGAGCTGTGATGAGTCACTGACGATTTATGCACTAGACAGTGGCAGTTGGG 540  
QY 587 AAGATGAGCAGTTTGTAAATGAACAATTTAATAACAGCTCAGAAATTAAGCTGATC 646  
DB 541 AAGATGAGCAGTTTGTAAATGAACAATTTAATAACAGCTCAGAAATTAAGCTGATC 600  
QY 647 AAAATGCAAGCAAGTTGTGTGAGCTCAACCTGTACTTAACCGAATGTACTACAGTA 706  
DB 601 AAAATGCAAGCAAGTTGTGTGAGCTCAACCTGTACTTAACCGAATGTACTACAGTA 660  
QY 707 TTGGAACCAAAATCACTTCACTGCTTTAAACAAGTGACTAATGAGGCACTTTACAAT 766  
DB 661 TTGGAACCAAAATCACTTCACTGCTTTAAACAAGTGACTAATGAGGCACTTTACAAT 720  
QY 767 CTAGCTGTGGAATATGATTAATTAATGATCAATGATGATGAGGAAATCAATCACTC 826  
DB 721 CTAGCTGTGGAATATGATTAATTAATGATCAATGATGATGAGGAAATCAATCACTC 780  
QY 827 AGCTCATTAATCGGTAGCGGCTTAATCAACGGTAACCTTATTTATACGACTCAAGACT 886

Db 781 AGCTCATTAATCGGTAGCGGCTTAATCAACGGTAACCTTAATTTCTATAGCACTCAAGACT 840  
Qy 887 CAACCTTGGGTATACAGGTAACTTACCTTCACTGCGGAACTTAATATATATGCTGCC 946  
Db 841 CAACCTTGGGTATACAGGTAACTTACCTTCACTGCGGAACTTAATATATATGCTGCC 900  
Qy 947 ACCTACTTGGAAACCTTATCCGTAAAGCAACACGAGGATTTGGCTCGGCACTTGTCCCA 1006  
Db 901 ACCTACTTGGAAACCTTATCCGTAAAGCAACACGAGGATTTGGCTCGGCACTTGTCCCA 960  
Qy 1007 AAAGTGGGACACAGTCCGCTTCTGTATAGAAAGTCACTGACCTCATCTATAGTAA 1066  
Db 961 AAAGTGGGACACAGGCTCGTCTGTATAGAAAGTCACTGACCTCATCTATAGTAA 1020  
Qy 1067 ACTGACTTGAATTAATTTATTTGACAAAGTATGAAGTTCCTTATGTCCTGCTGATTTAT 1126  
Db 1021 ACTGACTTGAATTAATTTATTTGACAAAGTATGAAGTTCCTTATGTCCTGCTGATTTAT 1080  
Qy 1127 TCCTGCTTGAAGCGGCAATACGTCGCGCTGTATGTATCTCAAAAGACCGAAGCGCACTTACT 1186  
Db 1081 TCCTGCTTGAAGCGGCAATACGTCGCGCTGTATGTATCTCAAAAGACCGAAGCGCACTTACT 1140  
Qy 1187 AACACATATACAGTATTAAGTTCAGTCACTGCGCACTGCAAGATGACAAACATGTAGA 1246  
Db 1141 AACACATATATGACTATTAAGTTCAGTCACTGCGCACTGCAAGATGACAAACATGTAGA 1200  
Qy 1247 TGTGTAAACCCCGGGGTATCATATCGCAAACTATGAGAAGCCGTCTCTAATAGAT 1306  
Db 1201 TGTGTAAACCCCGGGGTATCATATCGCAAACTATGAGAAGCCGTCTCTAATAGAT 1260  
Qy 1307 AAACATATCATCAATGTTTATTCCTTGAAGCGGATTAACCTTGAAGCTCAGTGGGAATTC 1366  
Db 1261 AAACATATCATCAATGTTTATTCCTTGAAGCGGATTAACCTTGAAGCTCAGTGGGAATTC 1320  
Qy 1367 GATGTAACTTATCGAAGAAATATCTCAATACAAAGTTCGAAATTAATTAACAGGCAAT 1426  
Db 1321 GATGTAACTTATCGAAGAAATATCTCAATACAAAGTTCGAAATTAATTAACAGGCAAT 1380  
Qy 1427 CTGATATCTCAACGTAGCTGGGAATGTCAACACCTGATCAGTATGCTTGAATTAAG 1486  
Db 1381 CTGATATCTCAACGTAGCTGGGAATGTCAACACCTGATCAGTATGCTTGAATTAAG 1440  
Qy 1487 TTAGAGAAAGCAACAGAAACTAGACAAAGTCAATGTCAAACTGACTAGCAATCTGCT 1546  
Db 1441 TTAGAGAAAGCAACAGAAACTAGACAAAGTCAATGTCAAACTGACTAGCAATCTGCT 1500  
Qy 1547 CTCAATTAATTAATGCTTTTGAATCAATATCTCTGTTTGTGTAATCTTACCTGATTT 1606  
Db 1501 CTCAATTAATTAATGCTTTTGAATCAATATCTCTGTTTGTGTAATCTTACCTGATTT 1560  
Qy 1607 CTACATGCTCACTTAATGTATAGCAAAAGCGCAAAACCTTATTAATGCTTGGG 1666  
Db 1561 CTACATGCTCACTTAATGTATAGCAAAAGCGCAAAACCTTATTAATGCTTGGG 1620  
Qy 1667 AATATATCTAGATCAGATGAGAGCACTACAAAAATGTGA 1708  
Db 1621 AATATATCTAGATCAGATGAGAGCACTACAAAAATGTGA 1662

RESULT 12  
US-08-288-065A-12  
Sequence 12, Application US/08288065A  
Patent No. 5961982

GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D  
APPLICANT: Macdonald, Richard D  
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys S-  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York

STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/288,065A  
FILING DATE: Aug-09-94  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
TELEX: 422523  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1662 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1662  
US-08-288-065A-12

Query Match 48.6%; Score 1631.6; DB 2; Length 1662;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 47 ATGGGCTCCAGACCTTCTACCAAGAACCCAGCACTTATGATGCTGACTATCCGGGTGCG 106  
Db 1 ATGGGCTCCAGACCTTCTACCAAGAACCCAGCACTTATGATGCTGACTATCCGGGTGCG 60  
Qy 107 CTGGCACTGATTTGATCTGTCCCGGCAAACTCCATTTGATGSCAGCCCTTGGAGCTGCA 166  
Db 61 CTGGCACTGATTTGATCTGTCCCGGCAAACTCCATTTGATGSCAGCCCTTGGAGCTGCA 120  
Qy 167 GGAATTTGTTTACAGGAGACAAAGCCGTCAACATATACACTTATCCCAAGAGATCA 226  
Db 121 GGAATTTGTTTACAGGAGACAAAGCCGTCAACATATACACTTATCCCAAGAGATCA 180  
Qy 227 ATCATATGTTAAGCTCTCCGAAATCTGCCAAGATAAGAGCATGTGCCAAAGCCGCC 286  
Db 181 ATCATATGTTAAGCTCTCCGAAATCTGCCAAGATAAGAGCATGTGCCAAAGCCGCC 240  
Qy 287 TTGATGCTATCAACAGGACATTTGACCACTTGTCTCAACCCCTTGGTGAATCTATCCGT 346  
Db 241 TTGATGCTATCAACAGGACATTTGACCACTTGTCTCAACCCCTTGGTGAATCTATCCGT 300  
Qy 347 AGGATTAAGAGTCTGTGACTATCACTGAGGAGGAGAGCAAGGAGCCCTTATAGAGGCC 406  
Db 301 AGGATTAAGAGTCTGTGACTATCACTGAGGAGGAGAGCAAGGAGCCCTTATAGAGGCC 360  
Qy 407 ATTATTTGGCGGTGTGGCTCTTGGGTTGCACTGCGGCACAAATTAACAGCGCGCAGCT 466  
Db 361 ATTATTTGGCGGTGTGGCTCTTGGGTTGCACTGCGGCACAAATTAACAGCGCGCAGCT 420  
Qy 467 CTGATTAAGGCAAAACAAATGCTGCGCAATCTCTCGAATTAAAGAGAGATTTGCCCA 526  
Db 421 CTGATTAAGGCAAAACAAATGCTGCGCAATCTCTCGAATTAAAGAGAGATTTGCCCA 480  
Qy 527 ACCAATGAGCTGTGCAATGAGGTCACTGACGGAATTTATCGCACTAGCAGTGGAGTTGGG 586  
Db 481 ACCAATGAGCTGTGCAATGAGGTCACTGACGGAATTTATCGCACTAGCAGTGGAGTTGGG 540  
Qy 587 AAGATGACGAGTTTGTAAATGACCAATTTAATAAAAAGCTCAGGAATTAAGACTGCATC 646

Db 541 AAGATGAGCGATTGTTAATGACCAATTTAATAAACAAGTCCGAAATGACTGCATC 600  
Qy 647 AAATTCGACAGCAAGTTGTGTAGAGCTCAACCTGTACTACCGAATGTGACTACAGTA 706  
Db 601 AAAATTCGACAGCAAGTTGTGTAGAGCTCAACCTGTACTACCGAATGTGACTACAGTA 660  
Qy 707 TTGGAGCCACAATCACTTCACTGCTTTTAAACAAGTACTGACTATTGAGCACTTTACAT 766  
Db 661 TTGGAGCCACAATCACTTCACTGCTTTTAAACAAGTACTGACTATTGAGCACTTTACAT 720  
Qy 767 CTACTGCTGGAATATATGATTTACTATATGACTAGTTAGTGTAGGGAACAATCAATC 826  
Db 721 CTACTGCTGGAATATATGATTTACTATATGACTAGTTAGTGTAGGGAACAATCAATC 780  
Qy 827 AGCTCAATTAATCGGTAGCGGCTTAATCAACCGTAACTCTATTCTATAGACTCAGACT 886  
Db 781 AGCTCAATTAATCGGTAGCGGCTTAATCAACCGTAACTCTATTCTATAGACTCAGACT 840  
Qy 887 CAATCTTTGGGTATATACAGTAACTCTACTTCACTCGGGAACCTAAATATATGCGTCC 946  
Db 841 CAATCTTTGGGTATATACAGTAACTCTACTTCACTCGGGAACCTAAATATATGCGTCC 900  
Qy 947 ACCTACTTGGAAACCTTATCCGTAAAGCAACAGGGGATTTGCTCGGCACTTGCCCA 1006  
Db 901 ACCTACTTGGAAACCTTATCCGTAAAGCAACAGGGGATTTGCTCGGCACTTGCCCA 960  
Qy 1007 AAAGTGGGACAGAGTCCGTTCTGTGATTAAGAACTGTACCTCACTGATATGAA 1066  
Db 961 AAAGTGGGACAGAGTCCGTTCTGTGATTAAGAACTGTACCTCACTGATATGAA 1020  
Qy 1067 ACTGACTTGAATTTATATTTGTACAGAAATAGTAAAGTCCCTATGTCCCTGTATTTAT 1126  
Db 1021 ACTGACTTGAATTTATATTTGTACAGAAATAGTAAAGTCCCTATGTCCCTGTATTTAT 1080  
Qy 1127 TCTGCTTGAAGCGCAATACGTCCGCTGTATGTATCTCAAAAGACCGAAGGCGCACTTACT 1186  
Db 1081 TCTGCTTGAAGCGCAATACGTCCGCTGTATGTATCTCAAAAGACCGAAGGCGCACTTACT 1140  
Qy 1187 ACACATATATGATATATCAAGAGTTCACTGCTCAATCCGCAAGATGACAAATGTAGA 1246  
Db 1141 ACACATATATGATATATCAAGAGTTCACTGCTCAATCCGCAAGATGACAAATGTAGA 1200  
Qy 1247 TGTGTAAACCCCGGGTATCATATCGCAAAACTATGAGAGGCGGTCTCTATATAGAT 1306  
Db 1201 TGTGTAAACCCCGGGTATCATATCGCAAAACTATGAGAGGCGGTCTCTATATAGAT 1260  
Qy 1307 AAACATATATGATATTTTATCTTATGAGCGGGAATTAATTAGGCTCAGTGGGGAATTC 1366  
Db 1261 AAACATATATGATATTTTATCTTATGAGCGGGAATTAATTAGGCTCAGTGGGGAATTC 1320  
Qy 1367 GATGTACTTATGAGAGAAATATCTCAATACAAAGTCTCAAGTATATATACAGGCAAT 1426  
Db 1321 GATGTACTTATGAGAGAAATATCTCAATACAAAGTCTCAAGTATATATACAGGCAAT 1380  
Qy 1427 CTGTATATCTCACTGAGCTTGGAAATGTCAACAAGTCAATCAGTAAATGCTTGAATAG 1486  
Db 1381 CTGTATATCTCACTGAGCTTGGAAATGTCAACAAGTCAATCAGTAAATGCTTGAATAG 1440  
Qy 1487 TTAGAGAAAGCAACAGAAACTATGACAAAGTCAATGTCAACTGACTAGCAATCTGCT 1546  
Db 1441 TTAGAGAAAGCAACAGAAACTATGACAAAGTCAATGTCAACTGACTAGCAATCTGCT 1500  
Qy 1547 CTGATTAATCTATATCGTTTGAATGATATATCTGTTTGTATATCTTATAGCTGAT 1606  
Db 1501 CTGATTAATCTATATCGTTTGAATGATATATCTGTTTGTATATCTTATAGCTGAT 1560  
Qy 1607 CTAGCATGTACTAATGTATCAAGCAAAAGGCGCAACAAATCTTATATGCTTGGG 1666  
Db 1561 CTAGCATGTACTAATGTATCAAGCAAAAGGCGCAACAAATCTTATATGCTTGGG 1620  
Qy 1667 AATATATCTTATGATGATGAGGCACTTCAAAAATGTGA 1708

Db 1621 AATATATCCCTAGATGATGAGGCACTTACAAAATGTGA 1662  
RESULT 13  
US-08-362-240A-12  
; Sequence 12. Application US/08362240A  
; Patent No. 5965138  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D  
; APPLICANT: Junker, David  
; APPLICANT: Wild, Martha A  
; TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: Dec-22-94  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P  
; REGISTRATION NUMBER: 28,678  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)278-0400  
; TELEFAX: (212)391-0526  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1662 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1662  
; US-08-362-240A-12  
Query Match 48.6%; Score 1631.6; DB 2; Length 1662;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 47 ATGGGCTCCAGACCTTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTGCG 106  
Db 1 ATGGGCTCCAGACCTTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTGCG 60  
Qy 107 CTGGCACTGAGTGTGATCTGTCCGGGCAAACTCCATTTGATGAGGAGGCGCTTTGACGCTGCA 166  
Db 61 CTGGTACTGAGTGTGATCTGTCCGGGCAAACTCCATTTGATGAGGAGGCGCTTTGACGCTGCA 120  
Qy 167 GGAATGTGGTTACAGGAGCAAAAGCGGTCAACATATACCTCATCCAGACAGATCA 226  
Db 121 GGAATGTGGTTACAGGAGCAAAAGCGGTCAACATATACCTCATCCAGACAGATCA 180  
Qy 227 ATCATAGTTAAGCTCTCCGAAATCTGCGCAAGATTAAGGAGGCAATGTGGAAGCCGCC 286  
Db 181 ATCATAGTTAAGCTCTCCGAAATCTGCGCAAGATTAAGGAGGCAATGTGGAAGCCGCC 240  
Qy 287 TTGGATGCAATACACAGAGCAATTTGACCACTTTGTCTACCCCCCTTTGTGACTATTCCT 346  
Db 241 TTGGATGCAATACACAGAGCAATTTGACCACTTTGTCTACCCCCCTTTGTGACTATTCCT 300

QY 347 AGATACAAAGTCTGTGCTACATCTGAGGGGGAGACAGGGGCGCTTATAGCGCC 406  
DB 301 AGGATACAAAGTCTGTGCTACATCTGAGGGGGAGACAGGGGCGCTTATAGCGCC 360  
QY 407 ATTATTTGGGGGTGGCTCTTGGGGTTCGAATGCGCGCAAAATTAACGCGCGCGACGT 466  
DB 361 ATTATTTGGGGGTGGCTCTTGGGGTTCGAATGCGCGCAAAATTAACGCGCGCGACGT 420  
QY 467 CTGATACAGGCAAAACAAATGCTCCAAACATCTCCGACTTAAAGAGACATTCGCCA 526  
DB 421 CTGATACAGGCAAAACAAATGCTCCAAACATCTCCGACTTAAAGAGACATTCGCCA 480  
QY 527 ACCAATGAGGCTGTGCTGATGAGGTCACTGACGATTAATGCGCAATGACAGTGGCAGTTGGG 586  
DB 481 ACCAATGAGGCTGTGCTGATGAGGTCACTGACGATTAATGCGCAATGACAGTGGCAGTTGGG 540  
QY 587 AAGATGACGAGCTTTGTTAATGACCAATTTAATAAAGCTCAGAGATTAAGCTGCATC 646  
DB 541 AAGATGACGAGCTTTGTTAATGACCAATTTAATAAAGCTCAGAGATTAAGCTGCATC 600  
QY 647 AAAATGACAGCAAGTTGGTGTAGAGCTCAACCTGTACTTAACGGAATTGACTACAGTA 706  
DB 601 AAAATGACAGCAAGTTGGTGTAGAGCTCAACCTGTACTTAACGGAATTGACTACAGTA 660  
QY 707 TTGCGACCACAAAATCACTTCACTGCTTTAAACAAAGCTGACTATTCAAGCACTTTACAT 766  
DB 661 TTGCGACCACAAAATCACTTCACTGCTTTAAACAAAGCTGACTATTCAAGCACTTTACAT 720  
QY 767 CTAGCTGTGGAATATGATATTAATTAATTAAGTTAGGTGAGGACAAATTAATC 826  
DB 721 CTAGCTGTGGAATATGATATTAATTAATTAAGTTAGGTGAGGACAAATTAATC 780  
QY 827 AGCTCATTAATCGGAGCGGCTTAATCAACGGTAACCTTAATCTTAAGACTCAGACT 886  
DB 781 AGCTCATTAATCGGAGCGGCTTAATCAACGGTAACCTTAATCTTAAGACTCAGACT 840  
QY 887 CAACCTTTGGGTATACAGTAATCTTACCTTCACTGCGGAACTTAATTAATGCGTCC 946  
DB 841 CAACCTTTGGGTATACAGTAATCTTACCTTCACTGCGGAACTTAATTAATGCGTCC 900  
QY 947 ACCTACTTGGAAACCTTATCCGTAAAGCAACCAAGGGGATTTGCTCGGCACTTGTCCA 1006  
DB 901 ACCTACTTGGAAACCTTATCCGTAAAGCAACCAAGGGGATTTGCTCGGCACTTGTCCA 960  
QY 1007 AAAGTGGGACAGGTCGGTCTGTGATAGAAAGCTTGAACCTCACTCATCTGATTAAG 1066  
DB 961 AAAGTGGGACAGGTCGGTCTGTGATAGAAAGCTTGAACCTCACTCATCTGATTAAG 1020  
QY 1067 ACTGACTTAGATTTATATTTGTAACAAGATTAAGTCCCTATGTCCTGATATTAT 1126  
DB 1021 ACTGACTTAGATTTATATTTGTAACAAGATTAAGTCCCTATGTCCTGATATTAT 1080  
QY 1127 TCCTGCTTGAACGGCAATACGTGGCTGTATGTAATCAAGACCGAAGCGGCACTTACT 1186  
DB 1081 TCCTGCTTGAACGGCAATACGTGGCTGTATGTAATCAAGACCGAAGCGGCACTTACT 1140  
QY 1187 ACACCATACATGACTATTAAGAGTTCACTCATCGCAACTGCAAGATTAACAATGTGA 1246  
DB 1141 ACACCATACATGACTATTAAGAGTTCACTCATCGCAACTGCAAGATTAACAATGTGA 1200  
QY 1247 TGTGTAACCCCGGGGTATCATATCGCAAACTATGAGAAGCGGTCTCTATATAT 1306  
DB 1201 TGTGTAACCCCGGGGTATCATATCGCAAACTATGAGAAGCGGTCTCTATATAT 1260  
QY 1307 AAACATATCATGCAATGTTTATCTTATGCGGAGATTAATTTAAGCTCAGTGGGAAATTC 1366  
DB 1261 AAACATATCATGCAATGTTTATCTTATGCGGAGATTAATTTAAGCTCAGTGGGAAATTC 1320  
QY 1367 GATGTAACTTATCGAAGAAATATCTCAATACAGATTCTCAAGTAATTAATACAGGCAAT 1426  
DB 1321 GATGTAACTTATCGAAGAAATATCTCAATACAGATTCTCAAGTAATTAATACAGGCAAT 1380

QY 1427 CTGATATCTCACTGAGCTTGGGAATGTCAACAACCTGATCAGTAATGCTTGAATAG 1486  
DB 1391 CTGATATCTCACTGAGCTTGGGAATGTCAACAACCTGATCAGTAATGCTTGAATAG 1440  
QY 1487 TTAGAGAAAGCAACAGAAAACTAGACAAAGTCAATGTCAACTGACTAGACATCTGCT 1546  
DB 1441 TTAGAGAAAGCAACAGAAAACTAGACAAAGTCAATGTCAACTGACTAGACATCTGCT 1500  
QY 1547 CTCATTAATCTATGCTTTTGTGATCATATCTCTGTTTGTGTAATCTTACCTGAT 1606  
DB 1501 CTCATTAATCTATGCTTTTGTGATCATATCTCTGTTTGTGTAATCTTACCTGAT 1560  
QY 1607 CTAGATCTTACCTTAATGATACAGCAAAAGCGGCAACAAAACCTTATTTAGCTTGGG 1666  
DB 1561 CTAGATCTTACCTTAATGATACAGCAAAAGCGGCAACAAAACCTTATTTAGCTTGGG 1620  
QY 1667 AATAATCTTACCTTAATGATAGAGCCACTCAAAAATGTGA 1708  
DB 1621 AATAATCTTACCTTAATGATAGAGCCACTCAAAAATGTGA 1662

RESULT 14  
US-08-804-372A-10  
; Sequence 10, Application US/08804372A  
; Patent No. 6183753  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D.  
; APPLICANT: Wild, Martha A.  
; APPLICANT: Winslow, Barbara J.  
; TITLE OF INVENTION: Recombinant Chimeric Viruses and Uses  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/804,372A  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 2552/39115E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1662 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1662  
; US-08-804-372A-10

Query Match 48.6%; Score 1631.6; DB 3; Length 1662;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 47 ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTATGATGCTGACTATTCGGGTTGCG 106  
DB 1 ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTATGATGCTGACTATTCGGGTTGCG 60  
QY 107 CTGGCACTGAGTTCATCTGTCGGGCAAACTCCATTTGACAGGCGCTTTCAGACTGCA 166  
DB 61 CTGGTACTGAGTTCATCTGTCGGGCAAACTCCATTTGACAGGCGCTTTCAGACTGCA 120  
QY 167 GGAATTTGGTTTACAGAGAACAAAGCCGTCAACATATACCTGATCCAGACAGATCA 226  
DB 121 GGAATTTGGTTTACAGAGAACAAAGCACTCAATATACCTGATCCAGACAGATCA 180  
QY 227 ATCATAGTTAACTCTCCGGAATCTGCGCAAGATTAAGAGCAATGTGCGAAAGCCGCC 286  
DB 181 ATCATAGTTAACTCTCTCCGGAATCTGCGCAAGATTAAGAGCAATGTGCGAAAGCCGCC 240  
QY 287 TTGGATGCTATCAACAGAGCAATTTGACCACTTTTGCTCAACCCCTTGGTGAATCATCTGCT 346  
DB 241 TTGGATGCTATCAACAGAGCAATTTGACCACTTTTGCTCAACCCCTTGGTGAATCATCTGCT 300  
QY 347 AGGATACAAAGACTCTGTGACTACATCTGAGGGGGGAGACAGGGGCGCTTATAGGCGCC 406  
DB 301 AGGATACAAAGACTCTGTGACTACATCTGAGGGGGGAGACAGGGGCGCTTATAGGCGCC 360  
QY 407 ATTAATGGCGGTGTGCTCTTGGGGTTGCAACTGCCGCACAATATACAGCGGCGCGAGCT 466  
DB 361 ATTAATGGCGGTGTGCTCTTGGGGTTGCAACTGCCGCACAATATACAGCGGCGCGAGCT 420  
QY 467 CTGATACAAAGCAAAATATGCTGCGCAACATCTCCGCACTTAAGAGAGATTTGCCGCA 526  
DB 421 CTGATACAAAGCAAAATATGCTGCGCAACATCTCCGCACTTAAGAGAGATTTGCCGCA 480  
QY 527 ACCAATAGGCTGTGCAATGAGGTCACTGACGATTTATTCGCAATGAGTGGCAGTTGGG 586  
DB 481 ACCAATAGGCTGTGCAATGAGGTCACTGACGATTTATTCGCAATGAGTGGCAGTTGGG 540  
QY 587 AAGATGAGCAGATTGTTAATGACCAATTTAATAAAACAGTCAAGATTAAGTGCATC 646  
DB 541 AAGATGAGCAGATTGTTAATGACCAATTTAATAAAACAGTCAAGATTAAGTGCATC 600  
QY 647 AAAATTCGACAGCAATTTGTTGATGACTCAACTGTATCCCTAACCGAATTTGATCACTGATA 706  
DB 601 AAAATTCGACAGCAATTTGTTGATGACTCAACTGTATCCCTAACCGAATTTGATCACTGATA 660  
QY 707 TTGGGACCAAAATCACTTCACTGCTTTAAACAAGCTGATATTCAGGCACTTTAACAT 766  
DB 661 TTGGGACCAAAATCACTTCACTGCTTTAAACAAGCTGATATTCAGGCACTTTAACAT 720  
QY 767 CTAGCTGTGAAAATGATGATTACTTATTTGACTAAGTTAGGTGAGGAAACATCAATCTC 826  
DB 721 CTAGCTGTGAAAATGATGATTACTTATTTGACTAAGTTAGGTGAGGAAACATCAATCTC 780  
QY 827 AGCTCATTAATCGGTAGCGGCTTAAATCAACCGGTAACTTATTCATAGACTCAACAAT 886  
DB 781 AGCTCATTAATCGGTAGCGGCTTAAATCAACCGGTAACTTATTCATAGACTCAACAAT 840  
QY 887 CAACCTTTGGGTATACAGGTAACTCTACCTTCAGTGGGAACTTAATTAATATCTGTCG 946  
DB 841 CAACCTTTGGGTATACAGGTAACTCTACCTTCAGTGGGAACTTAATTAATATCTGTCG 900  
QY 947 ACCTACTTTGAAACCTTATCCGTAGACCAACAGGGGATTTGCTCGGCACTTGTCCA 1006  
DB 901 ACCTACTTTGAAACCTTATCCGTAGACCAACAGGGGATTTGCTCGGCACTTGTCCA 960  
QY 1007 AAAGTGTGACACAGGTTCGTTCTGTGATTAAGAACTTGAACACTCATCTGTATAGAA 1066  
DB 961 AAAGTGTGACACAGGTTCGTTCTGTGATTAAGAACTTGAACACTCATCTGTATAGAA 1020  
QY 1067 ACTGACTTAAGTTATTAATTTGTAACAAGAAATAGTAAAGTTCCCTATGTCCTGCTGATTTAT 1126  
DB 1021 ACTGACTTAAGTTATTAATTTGTAACAAGAAATAGTAAAGTTCCCTATGTCCTGCTGATTTAT 1080  
QY 1127 TCTGCTTGAAGCGCAATACGTGCGCTGTATGTATCTCAAGAACGGAAGGCGCACTTACT 1186

DB 1081 TCTGCTTGAAGCGCAATACATGCGCTGTATGTATCTCAAGAACGGAAGGCGCACTTACT 1140  
QY 1187 ACAACATACATGACTATCAAGAGTTGAGTATGATGATGATGATGATGATGATGATGATGATGAT 1246  
DB 1141 ACACATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200  
QY 1247 TGTGTAAACCCCGGGGTATCATATGCGCAAACTATGAGAGAGCGGTGTCTTATATGAT 1306  
DB 1201 TGTGTAAACCCCGGGGTATCATATGCGCAAACTATGAGAGAGCGGTGTCTTATATGAT 1260  
QY 1307 AAACATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1366  
DB 1261 AAACATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320  
QY 1367 GATGTATCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1426  
DB 1321 GATGTATCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
QY 1427 CTGTATATCTCAACTGAGCTTGGGAAATGTCAACAATCTGATGATGATGATGATGATGATGATGAT 1486  
DB 1381 CTGTATATCTCAACTGAGCTTGGGAAATGTCAACAATCTGATGATGATGATGATGATGATGATGAT 1440  
QY 1487 TTAGAGAAAGCAACGAAACCTAGCAAGTCAATGATGATGATGATGATGATGATGATGATGATGAT 1546  
DB 1441 TTAGAGAAAGCAACGAAACCTAGCAAGTCAATGATGATGATGATGATGATGATGATGATGATGAT 1500  
QY 1547 CTGATTAATCTATATGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1606  
DB 1501 CTGATTAATCTATATGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
QY 1607 CTAGCATGCTACCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1666  
DB 1561 CTAGCATGCTACCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
QY 1667 AATTAATCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1708  
DB 1621 AATTAATCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1662

RESULT 15  
PCT-US95-10245-12  
Sequence 12, Application PC/TUS9510245  
GENERAL INFORMATION:  
APPLICANT: SYNTRO CORPORATION  
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys And Uses Thereof  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/10245  
FILING DATE: 09-AUG-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
REGISTRATION NUMBER: 28,678  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
TELEX: 422523  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1662 base pairs



TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1662  
PCT-US95-10245-12

Query Match 48.6%; Score 1631.6; DB 6; Length 1662;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```
Qy 47 ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTTATGATGCTGACATCCGGTTGG 106
Db 1 ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTTATGATGCTGACATCCGGTTGG 60

Qy 107 CTGGCACTGAGTTGCATCTGTCCGGCAAACTCAATTGATGGCAGGCTCTTGCAGCTGCA 166
Db 61 CTGGTACTGAGTTGCATCTGTCCGGCAAACTCAATTGATGGCAGGCTCTTGCAGCTGCA 120

Qy 167 GGAATTGTGTTTACAGAGACAAAGCCGTCAATATACCTCATCCCAAGCAGGATCA 226
Db 121 GGAATTGTGTTTACAGAGACAAAGCAGTCAATATACCTCATCCCAAGCAGGATCA 180

Qy 227 ATCATATTAACTGCTCTCCGGAATCTGCCAAGATTAAGGAGGATGTGCGAAGCCCC 286
Db 181 ATCATATTAACTGCTCTCCGGAATCTGCCAAGATTAAGGAGGATGTGCGAAGCCCC 240

Qy 287 TTGGATGCATACACAGGACATTTGACCACTTGTCTACCCCTTGTGTGATCTTATCCGT 346
Db 241 TTGGATGCATACACAGGACATTTGACCACTTGTCTACCCCTTGTGTGATCTTATCCGT 300

Qy 347 AGATACCAAGCTGTGACTACATCTGGAGGAGGAGACAGGAGCGCTTATAGGCGCC 406
Db 301 AGATACCAAGCTGTGACTACATCTGGAGGAGGAGACAGGAGCGCTTATAGGCGCC 360

Qy 407 ATTTATGGCGGTGTGGCTCTTGGGGTTGCACTGCCGCAAAATTAACGCGCGCGAGT 466
Db 361 ATTTATGGCGGTGTGGCTCTTGGGGTTGCACTGCCGCAAAATTAACGCGCGCGAGT 420

Qy 467 CTGATACAGGCAAAATGCTGCCAATCTCCGCACTTAAAGAGAGGATTTGCCGCA 526
Db 421 CTGATACAGGCAAAATGCTGCCAATCTCCGCACTTAAAGAGAGGATTTGCCGCA 480

Qy 527 ACCAATGAGCTGTGATGAGGTCATGACGGAATTAATCGCAATAGCAGTGGCAGTTGG 586
Db 481 ACCAATGAGCTGTGATGAGGTCATGACGGAATTAATCGCAATAGCAGTGGCAGTTGG 540

Qy 587 AAGATGACGAGCTTTGTTAATGACCAATTTAATAAACAAGCTCAGGAATTGACTGCATC 646
Db 541 AAGATGACGAGCTTTGTTAATGACCAATTTAATAAACAAGCTCAGGAATTGACTGCATC 600

Qy 647 AAAATTGCAACGCAAGTTGTGTAGAGCTCAACCTGTAACCTTAACGAATTGAACAGTA 706
Db 601 AAAATTGCAACGCAAGTTGTGTAGAGCTCAACCTGTAACCTTAACGAATTGAACAGTA 660

Qy 707 TTCGGAACCAAAATCACTTCACTGCTTTAAACAAGCTGACTAATTCAGGCACTTTACAA 766
Db 661 TTCGGAACCAAAATCACTTCACTGCTTTAAACAAGCTGACTAATTCAGGCACTTTACAA 720

Qy 767 CTAGCTGTGGAATAATGATTAATTAATGACTAAGTTAGGTGAGGAACTAATCAATC 826
Db 721 CTAGCTGTGGAATAATGATTAATTAATGACTAAGTTAGGTGAGGAACTAATCAATC 780

Qy 827 AGCTCATTAATCGGTAGCGCTTAATACCGGTAAACCTTATTAATGACTCAAGACT 886
Db 781 AGCTCATTAATCGGTAGCGCTTAATACCGGTAAACCTTATTAATGACTCAAGACT 840

Qy 887 CAATCTTGGGTATACAGGTAACTTACCTTCACTCGGGAACCTAAATATATGCTGCTC 946
Db 887 CAATCTTGGGTATACAGGTAACTTACCTTCACTCGGGAACCTAAATATATGCTGCTC 900
```

```
Db 841 CAATCTTGGGTATACAGGTAACTTACCTTCACTCGGGAACCTAAATATATGCTGCTC 900
Qy 947 ACTTACTTGGAAACCTTATCCGTAAGCAACAAGGAGATTGGCTCGGCACTTGCCCA 1006
Db 901 ACTTACTTGGAAACCTTATCCGTAAGCAACAAGGAGATTGGCTCGGCACTTGCCCA 960
Qy 1007 AAGTGGTACACAGTCCGTTCTGTGATGAGAGAACTTGAACCTCATTAATGATGAA 1066
Db 961 AAGTGGTACACAGTCCGTTCTGTGATGAGAGAACTTGAACCTCATTAATGATGAA 1020
Qy 1067 ACTGACTTAATTTATATGTAACAAGAAATAGTAAGTCCCTAATGTCCTGATTTAT 1126
Db 1021 ACTGACTTAATTTATATGTAACAAGAAATAGTAAGTCCCTAATGTCCTGATTTAT 1080
Qy 1127 TCTGCTTGAAGCGGCAATACGTCGGCTGTATGTACTCAAGAAGCGGCACTTACT 1186
Db 1081 TCTGCTTGAAGCGGCAATACGTCGGCTGTATGTACTCAAGAAGCGGCACTTACT 1140
Qy 1187 ACACCATATACATGACTATCAAAAGTTCAATCATGTCGCAACCTGCAAGATGACAACTGTA 1246
Db 1141 ACACCATATATGACTATCAAAAGCTCAAGTCACTGCAAGATGACAACTGTA 1200
Qy 1247 TGTGTAACCCCGGGTATATATGCGAATACTATGGAAGCCGTCTTATATAT 1306
Db 1201 TGTGTAACCCCGGGTATATATGCGAATACTATGGAAGCCGTCTTATATAT 1260
Qy 1307 AAACATCATGCAATGTTTATCTTATAGCGGGAATCTTAAAGGCTCAGTGGGAATTC 1366
Db 1261 AAACATCATGCAATGTTTATCTTATAGCGGGAATCTTAAAGGCTCAGTGGGAATTC 1320
Qy 1367 GATGTAACTTATCAGAAAGATATCTCAATACAGATTTCTAAGTATATTAACAGGCAAT 1426
Db 1321 GATGTAACTTATCAGAAAGATATCTCAATACAGATTTCTAAGTATATTAACAGGCAAT 1380
Qy 1427 CTGATATCTCACTGAGCTTGGGAATGTCAACAATCGATCAATTAATGCTTTGAATAG 1486
Db 1381 CTGATATCTCACTGAGCTTGGGAATGTCAACAATCGATCAATTAATGCTTTGAATAG 1440
Qy 1487 TTAGAGGAAGCAACAGAAACTAGACAAAGTCAATGCAACTGACTAGGACATCTGCT 1546
Db 1441 TTAGAGGAAGCAACAGAAACTAGACAAAGTCAATGCAACTGACTAGGACATCTGCT 1500
Qy 1547 CTCATTAATCTATATGTTTGAATATCTCTTGTGTTTGTATATCTTATAGCTGAT 1606
Db 1501 CTCATTAATCTATATGTTTGAATATCTCTTGTGTTTGTATATCTTATAGCTGAT 1560
Qy 1607 CTAGCATGCTACCTAATGTACAGCAAAAGCGGCAAAAACTTATATATGCTTGG 1666
Db 1561 CTAGCATGCTACCTAATGTACAGCAAAAGCGGCAAAAACTTATATATGCTTGG 1620
Qy 1667 AATAATATCTAGATCAGATGAGAGCACTTCAAAAAATGTGA 1708
Db 1621 AATAATATCTAGATCAGATGAGAGCACTTCAAAAAATGTGA 1662
```

Search completed: February 5, 2006, 02:50:00  
Job time : 577 secs

The Logo Blank (usps)

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 21:40:18 ; Search time 2548 Seconds  
(without alignments)  
10898.183 Million cell updates/sec

Title: US-10-800-256-1  
Perfect score: 3358  
Sequence: 1 acgggtgagaaatcttgat.....cctaactctatagaacc 3358

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pubdna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubdna/US08\_PUBCOMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubdna/US09\_PUBCOMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubdna/US09B\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubdna/US10A\_PUBCOMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubdna/US10B\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubdna/US10C\_PUBCOMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubdna/US10D\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubdna/US10E\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubdna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3358	100.0	3358	US-10-800-256-1	Sequence 1, Appli
2	3353.2	99.9	15186	US-09-741-744A-134	Sequence 134, App
3	3353.2	99.9	15186	US-10-377-718-3	Sequence 3, Appli
4	3353.2	99.9	15186	US-10-429-735-3	Sequence 3, Appli
5	3353.2	99.9	15186	US-10-824-782-134	Sequence 134, App
6	3353.2	99.9	15186	US-10-788-232-134	Sequence 134, App
7	3346.8	99.7	15900	US-10-440-419-55	Sequence 55, Appli
8	3198	95.2	15882	US-10-440-419-56	Sequence 56, Appli
9	1701.6	50.7	3570	US-09-881-457A-1	Sequence 1, Appli
10	1701.6	50.7	3570	US-11-126-465-1	Sequence 19, Appli
11	1434.4	42.7	1734	US-10-838-834-19	Sequence 19, Appli
12	1414	42.1	1662	US-10-725-841-1	Sequence 1, Appli
13	1414	42.1	1662	US-10-990-204-1	Sequence 1, Appli
14	1362.8	40.6	1662	US-09-784-990-10	Sequence 10, Appli
15	1362.8	40.6	1662	US-10-229-412-10	Sequence 10, Appli
16	1160.8	34.6	1716	US-09-784-990-7	Sequence 7, Appli
17	1160.8	34.6	1716	US-10-229-412-7	Sequence 7, Appli
18	831.2	24.8	1753	US-10-839-509-1	Sequence 1, Appli
19	819.2	24.4	4767	US-10-838-834-12	Sequence 12, Appli
20	819.2	24.4	10603	US-10-838-834-26	Sequence 26, Appli
21	819.2	24.4	10677	US-10-838-834-25	Sequence 25, Appli
22	816.2	24.3	1760	US-10-838-834-1	Sequence 1, Appli
23	149.6	4.5	15498	US-09-733-692A-61	Sequence 61, Appli

24	148	4.4	15654	8	US-10-667-141-60	Sequence 60, Appli
25	147.6	4.4	15654	8	US-10-667-141-59	Sequence 59, Appli
26	145.8	4.3	15492	3	US-09-733-692A-60	Sequence 60, Appli
27	145.8	4.3	15492	3	US-09-733-692A-62	Sequence 62, Appli
28	142.6	4.2	15654	8	US-10-667-141-58	Sequence 58, Appli
29	139.4	4.2	1500	6	US-10-377-718-9	Sequence 9, Appli
30	139.4	4.2	1500	6	US-10-429-735-9	Sequence 9, Appli
31	96.8	2.9	1617	9	US-10-842-032-25	Sequence 25, Appli
32	96.8	2.9	1844	7	US-10-842-032-1	Sequence 1, Appli
33	96	2.9	1986	9	US-10-670-695-15	Sequence 15, Appli
34	96	2.9	2113	3	US-09-951-061A-86	Sequence 86, Appli
35	96	2.9	4343	3	US-09-951-061A-91	Sequence 91, Appli
36	96	2.9	4604	3	US-09-951-061A-93	Sequence 93, Appli
37	96	2.9	15690	9	US-10-312-052B-1	Sequence 1, Appli
38	96	2.9	15690	9	US-10-312-052B-2	Sequence 2, Appli
39	96	2.9	18826	9	US-10-312-052B-3	Sequence 3, Appli
40	87.8	2.6	692	5	US-10-206-901B-50	Sequence 50, Appli
41	85	2.5	18967	10	US-11-013-786-82	Sequence 82, Appli
42	83.4	2.5	2384	6	US-10-397-635-8	Sequence 8, Appli
43	82	2.4	1653	3	US-09-873-233A-17	Sequence 17, Appli
44	79.4	2.4	1653	3	US-09-873-233A-19	Sequence 19, Appli
45	79.2	2.4	15456	3	US-09-900-112-35	Sequence 35, Appli

ALIGNMENTS

```
RESULT 1
US-10-800-256-1
; Sequence 1, Application US/10800256
; Publication No. US20050031642A1
; GENERAL INFORMATION:
; APPLICANT: Zakay-Rones, Zichria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF CANCER
; FILE REFERENCE: 85189-5900
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: IL 145397
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: IL 145397
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3358
; TYPE: DNA
; ORGANISM: Newcastle disease virus
; US-10-800-256-1

Query Match      100.0%; Score 3358; DB 8; Length 3358;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ACGGTTAGAAAGATTCTGGATCCGGTTGGCGGCTTCCAGGTGCAAGATGGGCTCCAGACC 60
DB      1  ACGGTTAGAAAGATTCTGGATCCGGTTGGCGGCTTCCAGGTGCAAGATGGGCTCCAGACC 60

QY      61  TTTCACCAAGAACCCAGACCTATGATGCTGACATATCCGGTTGGCGGCTGGAAGTGG 120
DB      61  TTTCACCAAGAACCCAGACCTATGATGCTGACATATCCGGTTGGCGGCTGGAAGTGG 120

QY      121 CATCTGTCGGCAAACTCCATTGATGGAGGCTCTTGACACTGAGGAATTGGTTAC 180
DB      121 CATCTGTCGGCAAACTCCATTGATGGAGGCTCTTGACACTGAGGAATTGGTTAC 180

QY      181 AGGAGCAAAAGCCGTCAACATATACACTCTCCAGACAGATCAATCATAGTTAACT 240
DB      181 AGGAGCAAAAGCCGTCAACATATACACTCTCCAGACAGATCAATCATAGTTAACT 240

QY      241 CCTCCGAAATTTGCCAAGATAGAGAGGATTTGCCAAACCCCTTGGATGATTAAC 300
DB      241 CCTCCGAAATTTGCCAAGATAGAGAGGATTTGCCAAACCCCTTGGATGATTAAC 300

QY      300 CCTCCGAAATTTGCCAAGATAGAGAGGATTTGCCAAACCCCTTGGATGATTAAC 300
DB      300 CCTCCGAAATTTGCCAAGATAGAGAGGATTTGCCAAACCCCTTGGATGATTAAC 300
```

QY 301 CAGGACATTGACCACTTTGCTCACCCCCCTTGATGACTCTATCCGTAGAGATACAGAGTC 360  
DB |||||  
DB 301 CAGGACATTGACCACTTTGCTCACCCCCCTTGATGACTCTATCCGTAGAGATACAGAGTC 360  
QY 361 TGTGACATCATCTGAGAGGGGGAGACAGGGGCGCTTATAGAGCGCATTTATTTGGCGGT 420  
DB |||||  
DB 361 TGTGACATCATCTGAGAGGGGGAGACAGGGGCGCTTATAGAGCGCATTTATTTGGCGGT 420  
QY 421 GGCCTTTGGGGTTTGCACCTGCGGACAAATTAACGGCGCGAGCTTGATTAACGCCAA 480  
DB |||||  
DB 421 GGCCTTTGGGGTTTGCACCTGCGGACAAATTAACGGCGCGAGCTTGATTAACGCCAA 480  
QY 481 ACAAAATGCTGCCAAACATCTCCGACTTTAAAGAGACATTCGGCAACCAATGAGCGT 540  
DB |||||  
DB 481 ACAAAATGCTGCCAAACATCTCCGACTTTAAAGAGACATTCGGCAACCAATGAGCGT 540  
QY 541 GCATGAGGTACATGACGGAATTAATGSCAACTGACGTGGAGTTGGGAAGATGACAGTT 600  
DB |||||  
DB 541 GCATGAGGTACATGACGGAATTAATGSCAACTGACGTGGAGTTGGGAAGATGACAGTT 600  
QY 601 TGTTAATGACCAATTTAATAAACAAGCTCAAGAAATTAGACTGCATCAAAATTGACAGCA 660  
DB |||||  
DB 601 TGTTAATGACCAATTTAATAAACAAGCTCAAGAAATTAGACTGCATCAAAATTGACAGCA 660  
QY 661 AGTTGGTGTAGAGCTCAACCTGTACTTAACGGAATTGACTAGATTTGGACCAAAAT 720  
DB |||||  
DB 661 AGTTGGTGTAGAGCTCAACCTGTACTTAACGGAATTGACTAGATTTGGACCAAAAT 720  
QY 721 CACTTCACTGCTTTAAACAAGCTGACATTCAGAGCACTTTAACAATCTAGCTGGTGA 780  
DB |||||  
DB 721 CACTTCACTGCTTTAAACAAGCTGACATTCAGAGCACTTTAACAATCTAGCTGGTGA 780  
QY 781 TATGATTAATCTTATTTGA CTAGTTAGGTGTAGGGAAACAATCACTCAGCTCATTTAT 840  
DB |||||  
DB 781 TATGATTAATCTTATTTGA CTAGTTAGGTGTAGGGAAACAATCACTCAGCTCATTTAT 840  
QY 841 TAGCGGCTTATTAACCGGTAAACCTTATTTCTATACGACTCAAGACTCACTCACTTGGGTAT 900  
DB |||||  
DB 841 TAGCGGCTTATTAACCGGTAAACCTTATTTCTATACGACTCAAGACTCACTCACTTGGGTAT 900  
QY 901 ACGGTAACTCTACCTCAGTCGGGAAACCTTAATTAATGCGTGCACCTACTTGGAAAC 960  
DB |||||  
DB 901 ACGGTAACTCTACCTCAGTCGGGAAACCTTAATTAATGCGTGCACCTACTTGGAAAC 960  
QY 961 CTTATCCGTAGACAAACAAGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
DB |||||  
DB 961 CTTATCCGTAGACAAACAAGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
QY 1021 GGTGCGTTCTGTGTATAGAGAACTTGACCTCTACTGTATAGAAA CTGACTTATGATTT 1080  
DB |||||  
DB 1021 GGTGCGTTCTGTGTATAGAGAACTTGACCTCTACTGTATAGAAA CTGACTTATGATTT 1080  
QY 1081 AATTTGTACAAAGATTAATAGTTCCCTATGTCCTCGGTATTTATCTCGTGTGAGCGG 1140  
DB |||||  
DB 1081 AATTTGTACAAAGATTAATAGTTCCCTATGTCCTCGGTATTTATCTCGTGTGAGCGG 1140  
QY 1141 CAATACGTCCGCTGTATGTACTCAAAAGACGAAAGGGGCACTTACATCACTACGAC 1200  
DB |||||  
DB 1141 CAATACGTCCGCTGTATGTACTCAAAAGACGAAAGGGGCACTTACATCACTACGAC 1200  
QY 1201 TATCAAAAGTTCACTGCTGCGCAACTGCAAGATGACCAATGTATGATGTGTAACCCCCC 1260  
DB |||||  
DB 1201 TATCAAAAGTTCACTGCTGCGCAACTGCAAGATGACCAATGTATGATGTGTAACCCCCC 1260  
QY 1261 GGGTATCATATCGCAAACTATGAGAAAGCGGTCTCTAATATATATATATATATATAT 1320  
DB |||||  
DB 1261 GGGTATCATATCGCAAACTATGAGAAAGCGGTCTCTAATATATATATATATATATAT 1320  
QY 1321 TGTTTTATCTTATAGGCGGATTAATTTAAGGCTCAGTGGGAAATTCATGTATCTTATCA 1380  
DB |||||  
DB 1321 TGTTTTATCTTATAGGCGGATTAATTTAAGGCTCAGTGGGAAATTCATGTATCTTATCA 1380  
QY 1381 GAAAGATATCTCAATACAAAGATTCAGATTAATTAACAAGCAATCTTGTATATCTCAAC 1440

DB |||||  
DB 1381 GAAAGATATCTCAATACAAAGATTCAGATTAATTAACAAGCAATCTTGTATATCTCAAC 1440  
QY 1441 TGAGCTTTGGGAATGTCAACAACCTCGATCAGTAATGCTTTGAATTAAGTTAGAGAAACAA 1500  
DB |||||  
DB 1441 TGAGCTTTGGGAATGTCAACAACCTCGATCAGTAATGCTTTGAATTAAGTTAGAGAAACAA 1500  
QY 1501 CAGAAAATCTAGCAAAAGTCAATGTCAAACTGACTAGACATCTGCTCTCATTAATCTAT 1560  
DB |||||  
DB 1501 CAGAAAATCTAGCAAAAGTCAATGTCAAACTGACTAGACATCTGCTCTCATTAATCTAT 1560  
QY 1561 GGTTTGACTATCATCTCTGTTTTTGGTAATCTTAAAGCTGATTTAGACATCTACT 1620  
DB |||||  
DB 1561 GGTTTGACTATCATCTCTGTTTTTGGTAATCTTAAAGCTGATTTAGACATCTACT 1620  
QY 1621 AATGTACAAACAAAGCGGCAACAAAACCTTATTAATGCTTTGGAAATTAATCTTAGA 1680  
DB |||||  
DB 1621 AATGTACAAACAAAGCGGCAACAAAACCTTATTAATGCTTTGGAAATTAATCTTAGA 1680  
QY 1681 TCAGATGAGAGCCA CTACAAAAATGTGAACA CAGATGAGGAAGAGGTTTCCCTAATAG 1740  
DB |||||  
DB 1681 TCAGATGAGAGCCA CTACAAAAATGTGAACA CAGATGAGGAAGAGGTTTCCCTAATAG 1740  
QY 1741 TAAATTTGTGAAAGTTCTGGTGTCTGTCAGTTCAAGAGTTAAGAAAAAATCTACCGGT 1800  
DB |||||  
DB 1741 TAAATTTGTGAAAGTTCTGGTGTCTGTCAGTTCAAGAGTTAAGAAAAAATCTACCGGT 1800  
QY 1801 TGTAGATGACCAAAAGACGATATACGGGTAGAA CAGTAAAGAGAGCCGCTCAATTGC 1860  
DB |||||  
DB 1801 TGTAGATGACCAAAAGACGATATACGGGTAGAA CAGTAAAGAGAGCCGCTCAATTGC 1860  
QY 1861 GAGCGAGGCTTCAACACCTCCGTTCTACCGCTTCAACGACCAACAGTCTCATATGAGAC 1920  
DB |||||  
DB 1861 GAGCGAGGCTTCAACACCTCCGTTCTACCGCTTCAACGACCAACAGTCTCATATGAGAC 1920  
QY 1921 CGGCGGTTAGCCAAGTTGGTTAGAGAAATGAAAGAGGCAAAAATTA CATGGCGC 1980  
DB |||||  
DB 1921 CGGCGGTTAGCCAAGTTGGTTAGAGAAATGAAAGAGGCAAAAATTA CATGGCGC 1980  
QY 1981 TTGATATTCGGAATTTGCAATCTTATTTCTTAACAGTATGACCTTGGCTATCTGATGCC 2040  
DB |||||  
DB 1981 TTGATATTCGGAATTTGCAATCTTATTTCTTAACAGTATGACCTTGGCTATCTGATGCC 2040  
QY 2041 TCCCTTTATATAGACATGGGGGCTAGACACCTAGCGATCTTGTAGGCAATCCGACTAGG 2100  
DB |||||  
DB 2041 TCCCTTTATATAGACATGGGGGCTAGACACCTAGCGATCTTGTAGGCAATCCGACTAGG 2100  
QY 2101 AATTTCCAGGCAAGAAAGATTAATCTTACCTGGTTCCAAATCAAGATGTATGAT 2160  
DB |||||  
DB 2101 AATTTCCAGGCAAGAAAGATTAATCTTACCTGGTTCCAAATCAAGATGTATGAT 2160  
QY 2161 AGGATATATAGCAAGTGGCCTTGAAGTCTCCGTTGGCACTTGTAAATATGAGACACA 2220  
DB |||||  
DB 2161 AGGATATATAGCAAGTGGCCTTGAAGTCTCCGTTGGCACTTGTAAATATGAGACACA 2220  
QY 2221 AATTAAGACGCAATTAACATCTCTCTTATCAGATTAATGAGAGCTGCAAA CAACATGGG 2280  
DB |||||  
DB 2221 AATTAAGACGCAATTAACATCTCTCTTATCAGATTAATGAGAGCTGCAAA CAACATGGG 2280  
QY 2281 TGGGGGGCACTTATCCATGACCCAGATTAATATAGGGGGATTAAGCAAAAGAACTCATGTA 2340  
DB |||||  
DB 2281 TGGGGGGCACTTATCCATGACCCAGATTAATATAGGGGGATTAAGCAAAAGAACTCATGTA 2340  
QY 2341 GATGATCTAGTATGTCATCATCTATCTATCCCTGACATTTCAAGAAACATGTAATTTT 2400  
DB |||||  
DB 2341 GATGATCTAGTATGTCATCATCTATCTATCCCTGACATTTCAAGAAACATGTAATTTT 2400  
QY 2401 ATCCCGGCGCTTACTACAGGATCAGGTTGCACTGAAATCCCTCATTTGACATGAGTGT 2460  
DB |||||  
DB 2401 ATCCCGGCGCTTACTACAGGATCAGGTTGCACTGAAATCCCTCATTTGACATGAGTGT 2460  
QY 2461 ACCCATTACTGCTACACCCATTAATGTAAATTTGTCTGATGACAGATTCATCATTTCA 2520  
DB |||||

Db 2461 ACCATTACGCTACACCCATATGTATATGTCTGATGACAGATCACTCATTTCA 2520  
Qy 2521 TATCAGATTATTAAGCATTTGGTGTCTCCGACATCTGCAACAGGAGGATTTCTTTCT 2580  
Db 2521 TATCAGATTATTAAGCATTTGGTGTCTCCGACATCTGCAACAGGAGGATTTCTTTCT 2580  
Qy 2581 ACTCTGGCTTCCATCAACCTTGACGACACCCAAATGGAAGTCTTGACGTGTAGTCA 2640  
Db 2581 ACTCTGGCTTCCATCAACCTTGACGACACCCAAATGGAAGTCTTGACGTGTAGTCA 2640  
Qy 2641 ACTCCCGGGTGTGATGATGCTGCTCGAAGTCAACGAGACAGAGAGAGATTTAT 2700  
Db 2641 ACTCCCGGGTGTGATGATGCTGCTCGAAGTCAACGAGACAGAGAGAGATTTAT 2700  
Qy 2701 AACTCAGCTGTCTTCAACGCGATGTATATGAGGTTAGGTTGACGCGCAGTACCAC 2760  
Db 2701 AACTCAGCTGTCTTCAACGCGATGTATATGAGGTTAGGTTGACGCGCAGTACCAC 2760  
Qy 2761 GAAAGAGCCTAGATGTCACAACATTTTCGCGGACCTGGGTGCGCACTACCCAGAGTA 2820  
Db 2761 GAAAGAGCCTAGATGTCACAACATTTTCGCGGACCTGGGTGCGCACTACCCAGAGTA 2820  
Qy 2821 GGGGGTGGATCTTTTATTTGACAGCGGGTATGTTCTCAGTCTACGAGGGTTAAACCC 2880  
Db 2821 GGGGGTGGATCTTTTATTTGACAGCGGGTATGTTCTCAGTCTACGAGGGTTAAACCC 2880  
Qy 2881 AATTCAACCACTGACACTGTACAGAGAGGAAATATGATATACAGCGATACATGAC 2940  
Db 2881 AATTCAACCACTGACACTGTACAGAGAGGAAATATGATATACAGCGATACATGAC 2940  
Qy 2941 ACATGCCAGATGACAAAGATCAAGATTTGAAATGGCAAGTCTTGATTAAGCTTGA 3000  
Db 2941 ACATGCCAGATGACAAAGATCAAGATTTGAAATGGCAAGTCTTGATTAAGCTTGA 3000  
Qy 3001 CGGTTTGTGGGAAACCATATCAAGAGCTATCTTATCTACAGGTCAACCTCTTA 3060  
Db 3001 CGGTTTGTGGGAAACCATATCAAGAGCTATCTTATCTACAGGTCAACCTCTTA 3060  
Qy 3061 GGGCAAGCCCGTACTGACTGTACCGCCCAACAGTCACTCATGCGGCGGAGAGC 3120  
Db 3061 GGGCAAGCCCGTACTGACTGTACCGCCCAACAGTCACTCATGCGGCGGAGAGC 3120  
Qy 3121 AGAATTCACAGTAGGACATCTCATTTCTTGTATCAACAGGGTCACTACTCTCT 3180  
Db 3121 AGAATTCACAGTAGGACATCTCATTTCTTGTATCAACAGGGTCACTACTCTCT 3180  
Qy 3181 CCGCGCTTATTAATCTTATGACAGTCAAGCAAAACAGCACTCTTCAATAGTCTTAT 3240  
Db 3181 CCGCGCTTATTAATCTTATGACAGTCAAGCAAAACAGCACTCTTCAATAGTCTTAT 3240  
Qy 3241 ACATTCAGTCTTCACTCGGCGAGTATCTCCCTTGCGAGGCTTCAGAAAGTGGCC 3300  
Db 3241 ACATTCAGTCTTCACTCGGCGAGTATCTCCCTTGCGAGGCTTCAGAAAGTGGCC 3300  
Qy 3301 AACTCTGTGTACTGAGTCTATACATCATATCCCTTAATCTTATAGAAAC 3358  
Db 3301 AACTCTGTGTACTGAGTCTATACATCATATCCCTTAATCTTATAGAAAC 3358

RESULT 2  
US-09-741-744A-134  
; Sequence 134, Application US/09741744A  
; Publication No. US20030087417A1  
; GENERAL INFORMATION:  
; APPLICANT: Peeters, Bernadus  
; APPLICANT: de Leeuw, Olav  
; APPLICANT: Klaus, Guus  
; APPLICANT: Arnaud, Gielkens  
; TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnost  
; FILE REFERENCE: 2183-4646US  
; CURRENT APPLICATION NUMBER: US/09/741,744A  
; CURRENT FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: PCT/NL9/00377

;; PRIOR FILING DATE: 1999-06-17  
;; NUMBER OF SEQ ID NOS: 148  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO: 134  
;; LENGTH: 15186  
;; TYPE: DNA  
;; ORGANISM: Newcastle disease virus LaSota  
US-09-741-744A-134  
Query Match 99.9%; Score 3353.2; DB 3; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3353; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 ACGGTTGAAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCAAGCC 60  
Db 4498 ACGGTTGAAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCAAGCC 4557  
Qy 61 TTTCACCAAGAACCCAGACCTATGATGCTGACATTCGCGGTTGCGCTGGCAGTGTG 120  
Db 4558 TTTCACCAAGAACCCAGACCTATGATGCTGACATTCGCGGTTGCGCTGGCAGTGTG 4617  
Qy 121 CATCTGTCCGCAAACTCAATTGAGCAGGCTCTTGACAGCTGCAAGAAATGTGTATAC 180  
Db 4618 CATCTGTCCGCAAACTCAATTGAGCAGGCTCTTGACAGCTGCAAGAAATGTGTATAC 4677  
Qy 181 AGAGACAAAGCCGTCAACATATACCTCATCCCAAGCAGATCATATGTTAGCT 240  
Db 4678 AGAGACAAAGCCGTCAACATATACCTCATCCCAAGCAGATCATATGTTAGCT 4737  
Qy 241 CTTCCGAAATCTGCCAAGGTAAGAGGAGTGTGCGAAAGCCCTTGATGATACAA 300  
Db 4738 CTTCCGAAATCTGCCAAGGTAAGAGGAGTGTGCGAAAGCCCTTGATGATACAA 4797  
Qy 301 CAGGACATTTGACCACTTTGTCTCACCCCTTGATGATCTATCCGTAGATACAAAGT 360  
Db 4798 CAGGACATTTGACCACTTTGTCTCACCCCTTGATGATCTATCCGTAGATACAAAGT 4857  
Qy 361 TGTGACTACATCTGAGGAGGAGAGACAGGAGCGCTTATAGGCGCATTAATGGCGTGT 420  
Db 4858 TGTGACTACATCTGAGGAGGAGAGACAGGAGCGCTTATAGGCGCATTAATGGCGTGT 4917  
Qy 421 GGCCTTTGGGTTTCGACTGCGGCAAAATTAACGCGCGGCACTCTGATACAAAGCCAA 480  
Db 4918 GGCCTTTGGGTTTCGACTGCGGCAAAATTAACGCGCGGCACTCTGATACAAAGCCAA 4977  
Qy 481 ACAAATGCTGCAACATCTCCGACTTAAAGAGACATTCGCGCAACCAATGAGGCTGT 540  
Db 4978 ACAAATGCTGCAACATCTCCGACTTAAAGAGACATTCGCGCAACCAATGAGGCTGT 5037  
Qy 541 GCATGAGTCACTGACGATTTATGCACTAGCAGTGGCAATTGGGAATGACAGATT 600  
Db 5038 GCATGAGTCACTGACGATTTATGCACTAGCAGTGGCAATTGGGAATGACAGATT 5097  
Qy 601 TGTTAATGACCAATTTAATAAAGCTCAGGAATTAAGCTGCACTCAAAATTTGACAGCA 660  
Db 5098 TGTTAATGACCAATTTAATAAAGCTCAGGAATTAAGCTGCACTCAAAATTTGACAGCA 5157  
Qy 661 AGTTGTTGAGGTCAACCTGATCTTAACCGAATTAAGCTGAGATTTGAGACCAAT 720  
Db 5158 AGTTGTTGAGGTCAACCTGATCTTAACCGAATTAAGCTGAGATTTGAGACCAAT 5217  
Qy 721 CACTTCACTGCTTTAAACAAGCTGATATTCAGGCACTTTACATCTAGCTGTGAGAA 780  
Db 5218 CACTTCACTGCTTTAAACAAGCTGATATTCAGGCACTTTACATCTAGCTGTGAGAA 5277  
Qy 781 TATGATTAATCTTATTTGACTAAGTTAGGTGAGGAAACATTAATCTGAGCTATTAATGG 840  
Db 5278 TATGATTAATCTTATTTGACTAAGTTAGGTGAGGAAACATTAATCTGAGCTATTAATGG 5337  
Qy 841 TAGGCGCTTAATCAACCGGTAACCTATTTATGAGCTCAAGACTCAACTCTTGAGTAT 900  
Db 5338 TAGGCGCTTAATCAACCGGTAACCTATTTATGAGCTCAAGACTCAACTCTTGAGTAT 5397

QY 901 ACAGGTACTCTACCTTCAGTCGGGAACCTTAAATATGCGGCACTACTTGGAAAC 960  
DB 5398 ACAGGTAACTCTACCTTCAGTCGGGAACCTTAAATATGCGGCACTACTTGGAAAC 5457  
QY 961 CTTATCCGTAGCAACAACAGGGGATTGGCTCGGCACTTGCCCAAAAAGTGTGACACA 1020  
DB 5458 CTTATCCGTAGCAACAACAGGGGATTGGCTCGGCACTTGCCCAAAAAGTGTGACACA 5517  
QY 1021 GGTGCGTCTGTGTATAGAAAGCTTGAACCTCATCTGTATAGAAACTGACTTAGATT 1080  
DB 5518 GGTGCGTCTGTGTATAGAAAGCTTGAACCTCATCTGTATAGAAACTGACTTAGATT 5577  
QY 1081 ATATTGTACAAGATAGTAAGCTTCCCTATGTCCCTGTGTATTTATTCCTGTGAGCCG 1140  
DB 5578 ATATTGTACAAGATAGTAAGCTTCCCTATGTCCCTGTGTATTTATTCCTGTGAGCCG 5637  
QY 1141 CAATAGCTGGGCGGTATGTACTCAAAAGACCGAAGGGGCACTTACTACACATACATGAC 1200  
DB 5638 CAATAGCTGGGCGGTATGTACTCAAAAGACCGAAGGGGCACTTACTACACATACATGAC 5697  
QY 1201 TATCAAAAGTTCAGTCATCCGCAACTGCAAGATGACAACAATGTAGATGTGAAAACCCCC 1260  
DB 5698 TATCAAAAGTTCAGTCATCCGCAACTGCAAGATGACAACAATGTAGATGTGAAAACCCCC 5757  
QY 1261 GGGTATCATATCCGAAAACCTATGAGAGACCGGTCTCTTAATAGATTAACATCATGCAA 1320  
DB 5758 GGGTATCATATCCGAAAACCTATGAGAGACCGGTCTCTTAATAGATTAACATCATGCAA 5817  
QY 1321 TGTTTATCTTATGCGGGGATTACTTTAAGGCTCAGGCGGGAAATGCATGTAACTTATCA 1380  
DB 5818 TGTTTATCTTATGCGGGGATTACTTTAAGGCTCAGGCGGGAAATGCATGTAACTTATCA 5877  
QY 1381 GAAGAAATCTCAATATACAAGATTCCTCAAGTAAATATAACAAGGCAATCTTGATCTCAAC 1440  
DB 5878 GAAGAAATCTCAATATACAAGATTCCTCAAGTAAATATAACAAGGCAATCTTGATCTCAAC 5937  
QY 1441 TGAAGCTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAATATAGTTAAGAGAAACAA 1500  
DB 5938 TGAAGCTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAATATAGTTAAGAGAAACAA 5997  
QY 1501 CAGAAAACCTAGCAAAAGTCAATGTCAAACTGACATCTGCTCACTTACTTATAT 1560  
DB 5998 CAGAAAACCTAGCAAAAGTCAATGTCAAACTGACATCTGCTCACTTACTTATAT 6057  
QY 1561 CGTTTGACTATCATCTCTGTTTGTGTAATCTAGCTAGCTGATCTAGCATCTACT 1620  
DB 6058 CGTTTGACTATCATCTCTGTTTGTGTAATCTAGCTAGCTGATCTAGCATCTACT 6117  
QY 1621 AATGTACAGCAAAAGGCGCAACAAAACCTTATATGCTTGGAAATATACTCTAGA 1680  
DB 6118 AATGTACAGCAAAAGGCGCAACAAAACCTTATATGCTTGGAAATATACTCTAGA 6177  
QY 1681 TCGATGAGAGCCACTTACAAAATGTGAACACAGATGAGAACGAAAGTTTCCCTATAG 1740  
DB 6178 TCGATGAGAGCCACTTACAAAATGTGAACACAGATGAGAACGAAAGTTTCCCTATAG 6237  
QY 1741 TAATTTGTGGAAGTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAACTAACCGGT 1800  
DB 6238 TAATTTGTGGAAGTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAACTAACCGGT 6297  
QY 1801 TGTAGATGACCAAGAGAGATATACGGGTAGAACGTTAAGAGAGCCGCCCTCAATTTGC 1860  
DB 6298 TGTAGATGACCAAGAGAGATATACGGGTAGAACGTTAAGAGAGCCGCCCTCAATTTGC 6357  
QY 1861 GAGCCAGGCTTCAACAACCTCCGTTCTAACCGCTTCAACGACAACAGTCTCTCAATCATGAC 1920  
DB 6358 GAGCCAGGCTTCAACAACCTCCGTTCTAACCGCTTCAACGACAACAGTCTCTCAATCATGAC 6417  
QY 1921 CGGCGCGTTAGCAAGTTGGTTAGAGAAATGAGAAAGAGAGCAAAAATATCATGTGCGC 1980  
DB 6418 CGGCGCGTTAGCAAGTTGGTTAGAGAAATGAGAAAGAGAGCAAAAATATCATGTGCGC 6477  
QY 1981 TTGATATTCGGAGTGCATCTTATTTCTTAAACAGTAGTGAACCTTGCTATATCTGTAGCC 2040

DB 6478 TTGATATTCGGAGTGCATCTTATTTCTTAAACAGTAGTGAACCTTGCTATATCTGTAGCC 6537  
QY 2041 TCCCTTTTATATAGCATGCGGGGCTAGCACACTAGCCATCTTGTAGCATACCGACTAGG 2100  
DB 6538 TCCCTTTTATATAGCATGCGGGGCTAGCACACTAGCCATCTTGTAGCATACCGACTAGG 6597  
QY 2101 ATTTCCAGGGCAGAGAAAAGATTACATCTACACTTGGTCCCAATCAAGATGTAGTAT 2160  
DB 6598 ATTTCCAGGGCAGAGAAAAGATTACATCTACACTTGGTCCCAATCAAGATGTAGTAT 6657  
QY 2161 AGGATATATAGCAAGTGGCCCTTGAAGTCTCCGTTGGCATTGTAAATACAGAGACACA 2220  
DB 6658 AGGATATATAGCAAGTGGCCCTTGAAGTCTCCGTTGGCATTGTAAATACAGAGACACA 6717  
QY 2221 ATTTAGAACCCAAATTAACATCTCTCTTATCAGATTAATGAGCTGCAAAACAAGTGGG 2280  
DB 6718 ATTTAGAACCCAAATTAACATCTCTCTTATCAGATTAATGAGCTGCAAAACAAGTGGG 6777  
QY 2281 TGGGGGGCACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAAAGACTCATTTGTA 2340  
DB 6778 TGGGGGGCACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAAAGACTCATTTGTA 6837  
QY 2341 GATAGTCTATGATGTGCATCATCTATCCCTGTGCATTTGAAGAACATCTGAATTT 2400  
DB 6838 GATAGTCTATGATGTGCATCATCTATCCCTGTGCATTTGAAGAACATCTGAATTT 6897  
QY 2401 ATCCCGGCGCTTACTACAGGATCAGGTTGCACTGCAATACCTCATTTGACATGAGTGT 2460  
DB 6898 ATCCCGGCGCTTACTACAGGATCAGGTTGCACTGCAATACCTCATTTGACATGAGTGT 6957  
QY 2461 ACCCATTAAGTCTACACCCCAATATGTAAATGTCTGTGATGACAGAGATCACTCAATTCA 2520  
DB 6958 ACCCATTAAGTCTACACCCCAATATGTAAATGTCTGTGATGACAGAGATCACTCAATTCA 7017  
QY 2521 TATCAGATTTAGCACTTGTGTGCTCCGGAACATCTGCAACAGGAGGGATTTCTTTCT 2580  
DB 7018 TATCAGATTTAGCACTTGTGTGCTCCGGAACATCTGCAACAGGAGGGATTTCTTTCT 7077  
QY 2581 ACTCTGGGTTCCATCAACCTGAGACGACACCAAAATCGAAAGTCTTGCAGTGTGAGTGA 2640  
DB 7078 ACTCTGGGTTCCATCAACCTGAGACGACACCAAAATCGAAAGTCTTGCAGTGTGAGTGA 7137  
QY 2641 ACTCCCTGGGTTGTGATATGTCTGTGCTCGAAAGTCAACGAGACAGAGAAAGATTAT 2700  
DB 7138 ACTCCCTGGGTTGTGATATGTCTGTGCTCGAAAGTCAACGAGACAGAGAAAGATTAT 7197  
QY 2701 AACTCAGCTGTCCCTACGCGGATGTACATGAGGAGTTAGGTTCCAGCGGCCAGTACCAC 2760  
DB 7198 AACTCAGCTGTCCCTACGCGGATGTACATGAGGAGTTAGGTTCCAGCGGCCAGTACCAC 7257  
QY 2761 GAAAAGGACCTAGATGTCAACAACATTATGCGGGAATCGGGTGGCAACTACCCAGAGTA 2820  
DB 7258 GAAAAGGACCTAGATGTCAACAACATTATGCGGGAATCGGGTGGCAACTACCCAGAGTA 7317  
QY 2821 GGGGGTGTGATCTTTTATTTGACAGCCGCGTATGCTTCACTTACGAGGGTTAAAAACC 2880  
DB 7318 GGGGGTGTGATCTTTTATTTGACAGCCGCGTATGCTTCACTTACGAGGGTTAAAAACC 7377  
QY 2881 AATTTCACCCAGTACACTGTACAGAAAGGAAATATGTGATATACAGGATACATGAC 2940  
DB 7378 AATTTCACCCAGTACACTGTACAGAAAGGAAATATGTGATATACAGGATACATGAC 7437  
QY 2941 ACATGCCCAATAGAGCAAGACTACCGAGTTCGAATGGCCAAAGTCTTCGATTAAGCCGGA 3000  
DB 7438 ACATGCCCAATAGAGCAAGACTACCGAGTTCGAATGGCCAAAGTCTTCGATTAAGCCGGA 7497  
QY 3001 CGGTTTGTGGGAAACGATACAGAGGCTATCTTATCTTCAAGGTGTCAATCTCTTA 3060  
DB 7498 CGGTTTGTGGGAAACGATACAGAGGCTATCTTATCTTCAAGGTGTCAATCTCTTA 7557  
QY 3061 GGGGAAAGCCCGTACTGATCTGTACCGCCCAACAGTCACTCATGCGGGGCCGAAAGGC 3120



Dh 7558 GGGAGAACCCGGTACTGACTGTACCCGCCAACACAGTCACACTCATAGGGGCCGAAGGC 7617  
Qy 3121 AGAATTCACAGTAGGAGACATCTCATTTCTTGTATGACAGGGGTGATCATACTTCTCT 3180  
Dh 7618 AGAATTCACAGTAGGAGACATCTCATTTCTTGTATGACAGGGGTGATCATACTTCTCT 7677  
Qy 3181 CCGCGCTTATTTATCTTATGACAGTCAGCAACAAACAGCCACTCTTCATAGTCTTAT 3240  
Dh 7678 CCGCGCTTATTTATCTTATGACAGTCAGCAACAAACAGCCACTCTTCATAGTCTTAT 7737  
Qy 3241 ACAATTCAGTCTTACATCGCGCCAGGTAGTATCCCTTGCCAGAGCTTCAGCAAGATGCCCC 3300  
Dh 7738 ACAATTCAGTCTTACATCGCGCCAGGTAGTATCCCTTGCCAGAGCTTCAGCAAGATGCCCC 7797  
Qy 3301 AACTCGTGTGTATCTGAGAGTCTATACAGATCATATCCCTTAATCTTCTATAGAAACC 3358  
Dh 7798 AACTCGTGTGTATCTGAGAGTCTATACAGATCATATCCCTTAATCTTCTATAGAAACC 7855

## RESULT 3

US-10-377-718-3  
; Sequence 3, Application US/10377718  
; Publication No. US20030175291A1  
; GENERAL INFORMATION:  
; APPLICANT: KUD, Teun Yuang  
; TITLE OF INVENTION: MULTIPLE AND MULTIVALENT DNA VACCINES IN OVO  
; FILE REFERENCE: 39734-186920  
; CURRENT APPLICATION NUMBER: US/10/377, 718  
; CURRENT FILING DATE: 2003-03-04  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 15186  
; TYPE: DNA  
; ORGANISM: Newcastle disease virus (NDV)  
US-10-377-718-3

Query Match 99.9%; Score 3353.2; DB 6; Length 15186;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGGGTAGAAGATTCTGGATCCCGGTTGGCGCCCTTCACAGGTGCAAGATGGGCTCCAGACC 60  
Dh 4498 ACGGGTAGAAGATTCTGGATCCCGGTTGGCGCCCTTCACAGGTGCAAGATGGGCTCCAGACC 4557  
Qy 61 TTCTACCAAGAACCCAGACCTTATGATGCTGATCTATCCGGGTTGGCGCTGGCACTGAGTTG 120  
Dh 4558 TTCTACCAAGAACCCAGACCTTATGATGCTGATCTATCCGGGTTGGCGCTGGCACTGAGTTG 4617  
Qy 122 CATCTGCGCGCAAACTCCATGATGCGAGGCTCTTCAGAGCTGCAAGAAATTTGTGTTAC 180  
Dh 4618 CATCTGCGCGCAAACTCCATGATGCGAGGCTCTTCAGAGCTGCAAGAAATTTGTGTTAC 4677  
Qy 181 AGAGAACAAACCGGTCAACATATACCTCATCCAGACAGAGTCAATCATAGTTAAAGT 240  
Dh 4678 AGAGAACAAACCGGTCAACATATACCTCATCCAGACAGAGTCAATCATAGTTAAAGT 4737  
Qy 241 CTTCCGCAATCTGCGCAAGATTAAGAGCATGTGCGAAAGCCCTTGGATGCAATCAA 300  
Dh 4738 CTTCCGCAATCTGCGCAAGATTAAGAGCATGTGCGAAAGCCCTTGGATGCAATCAA 4797  
Qy 301 CAGAGCAATTGACCACTTTGCTCACCCCTTGTGACTCTTATCCGTAGATACAAAGATC 360  
Dh 4798 CAGAGCAATTGACCACTTTGCTCACCCCTTGTGACTCTTATCCGTAGATACAAAGATC 4857  
Qy 361 TGAGACTACACTTGAGAGGGGGAGACAGGGGCGCTTATAGCGCCATTATTTGGCGGTGT 420  
Dh 4858 TGAGACTACACTTGAGAGGGGGAGACAGGGGCGCTTATAGCGCCATTATTTGGCGGTGT 4917  
Qy 421 GGGCTTTGGGGTTGCACTGCGCGCAAAATACAGCGCGCGCAGCTCTGATACAGCCAA 480  
Dh 4918 GGGCTTTGGGGTTGCACTGCGCGCAAAATACAGCGCGCGCAGCTCTGATACAGCCAA 4977

Qy 481 ACAAATGCTGCCAATCTCTCCGACTTTAAAGAGACATGGCCGCAACCAATGAGGCTGT 540  
Dh 4978 ACAAATGCTGCCAATCTCTCCGACTTTAAAGAGATGGCCCAACCAATGAGGCTGT 5037  
Qy 541 GCATGAGGTCACTGACGGAATTAATGCAACTAGCAGTGGCAGTTGGGAAGATGACAGATT 600  
Dh 5038 GCATGAGGTCACTGACGGAATTAATGCAACTAGCAGTGGCAGTTGGGAAGATGACAGATT 5097  
Qy 601 TGTATGACCAATTTATATAAAACAGCTCAGAAATTAAGCTGATCAAAATTTGACAGCA 660  
Dh 5098 TGTATGACCAATTTATATAAAACAGCTCAGAAATTAAGCTGATCAAAATTTGACAGCA 5157  
Qy 661 AGTTGGTGTAGAGTCAACCTGTACTTAACCGAATTAACATACATATTTGCGAACCAAT 720  
Dh 5158 AGTTGGTGTAGAGTCAACCTGTACTTAACCGAATTAACATACATATTTGCGAACCAAT 5217  
Qy 721 CACTTCACTGCTTTAAACAAGCTGACTATTTAGGCACTTTACAAATGAGCTGTGAAA 780  
Dh 5218 CACTTCACTGCTTTAAACAAGCTGACTATTTAGGCACTTTACAAATGAGCTGTGAAA 5277  
Qy 781 TATGATTTACTTATTTGACTAAGTTAGGTAGGGAACAATCAACTCAGCTCATTAATCGG 840  
Dh 5278 TATGATTTACTTATTTGACTAAGTTAGGTAGGGAACAATCAACTCAGCTCATTAATCGG 5337  
Qy 841 TAGCGGCTTAATCAACCGGTAAACCTTATTTATACACTCACAGACTCAACTCTTGGGTAT 900  
Dh 5338 TAGCGGCTTAATCAACCGGTAAACCTTATTTATACACTCACAGACTCAACTCTTGGGTAT 5397  
Qy 901 ACAGGTAACTCTTACTTCACTGAGTGGGAACCTAAATTAATGCGGCACTTCTTGGAAAC 960  
Dh 5398 ACAGGTAACTCTTACTTCACTGAGTGGGAACCTAAATTAATGCGGCACTTCTTGGAAAC 5457  
Qy 961 CTTATCCGTAGACCAACCAAGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
Dh 5458 CTTATCCGTAGACCAACCAAGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 5517  
Qy 1021 GGTGCGTCTGTGTATAGAAAGAACTTGAACCTCTACTGTATAGAAACTGACTTAAGATT 1080  
Dh 5518 GGTGCGTCTGTGTATAGAAAGAACTTGAACCTCTACTGTATAGAAACTGACTTAAGATT 5577  
Qy 1081 ATATTTGACAAAGAAATGATTAAGTTCCCTTATGTCCCCGTGATTTATCTCGCTGAGCGG 1140  
Dh 5578 ATATTTGACAAAGAAATGATTAAGTTCCCTTATGTCCCCGTGATTTATCTCGCTGAGCGG 5637  
Qy 1141 CAATACGTCGCGCTGTATGTACTCAAGAAGGCGCACTTACTACACATCATGATGAC 1200  
Dh 5638 CAATACGTCGCGCTGTATGTACTCAAGAAGGCGCACTTACTACACATCATGATGAC 5697  
Qy 1201 TATCAAAAGTTCAAGTCACTGCGCAACTGCAAGATGACAAATGTAGATGTGTAAACCCGCC 1260  
Dh 5698 TATCAAAAGTTCAAGTCACTGCGCAACTGCAAGATGACAAATGTAGATGTGTAAACCCGCC 5757  
Qy 1261 GGGTATCATATCCGAAACCTATGAGAAAGCCGTCTCTTAATAGATTAACAAATGATGCA 1320  
Dh 5758 GGGTATCATATCCGAAACCTATGAGAAAGCCGTCTCTTAATAGATTAACAAATGATGCA 5817  
Qy 1321 TGTTTTATCCTTAGGCGGGAATTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 1380  
Dh 5818 TGTTTTATCCTTAGGCGGGAATTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 5877  
Qy 1381 GAAGAATATCTCAATACAAAGATTTCTCAAGTAAATTAACAGGCAATCTTATATCTCAAC 1440  
Dh 5878 GAAGAATATCTCAATACAAAGATTTCTCAAGTAAATTAACAGGCAATCTTATATCTCAAC 5937  
Qy 1441 TGAGCTTGGGAATGTCAACACTGATCAAGTATGCTTTGAATTAAGTTAGAGAAAGCAA 1500  
Dh 5938 TGAGCTTGGGAATGTCAACACTGATCAAGTATGCTTTGAATTAAGTTAGAGAAAGCAA 5997  
Qy 1501 CAGAAACTGACAAAGTCAATGCAACCTGATGACAGCAATGCTGCTCATTAATTAAT 1560  
Dh 5998 CAGAAACTGACAAAGTCAATGCAACCTGATGACAGCAATGCTGCTCATTAATTAAT 6057  
Qy 1561 CGTTTGACTATCATATCTCTGTTTGTGTATTAAGCTGATTAAGCTGATTAAGCTGAT 1620

```
Db 6058 CGTTTGACATACATCTCTGTTTGGATACCTGATTCAGATCTACCT 6117
Qy 1621 AATGTACAGCAAAAGGCGCAACAAAACCTTATTAATGCTTGGGAATATACCTAGA 1680
Db 6118 AATGTACAGCAAAAGGCGCAACAAAACCTTATTAATGCTTGGGAATATACCTAGA 6177
Qy 1681 TCAGATGAGAGCCCTACAAAATGTGAACAGATGAGAGAGCAAGGTTTCCCTAATAG 1740
Db 6178 TCAGATGAGAGCCCTACAAAATGTGAACAGATGAGAGAGCAAGGTTTCCCTAATAG 6237
Qy 1741 TAATTTGTGAAAGTCTGTGATCTGTGATCTGATCAGAGTTAAGAAAACTAACGGCT 1800
Db 6238 TAATTTGTGAAAGTCTGTGATCTGTGATCTGATCAGAGTTAAGAAAACTAACGGCT 6297
Qy 1801 TGTAGATGACCAAAAGAGAGATATACGGGTAGAACGGTAAGAGAGCCGCCCTCAATTGC 1860
Db 6298 TGTAGATGACCAAAAGAGAGATATACGGGTAGAACGGTAAGAGAGCCGCCCTCAATTGC 6357
Qy 1861 GAGCCAGGCTTCAACAACTCCGTTCTACCGCTTCAACGACAGTCTCTCAATGAGAC 1920
Db 6358 GAGCCAGGCTTCAACAACTCCGTTCTACCGCTTCAACGACAGTCTCTCAATGAGAC 6417
Qy 1921 CGGCGCGTTAGCCAAAGTTGGCTTGAAGATGATGAAAAGAGAGCAAAAAATACATGGCGC 1980
Db 6418 CGGCGCGTTAGCCAAAGTTGGCTTGAAGATGATGAAAAGAGAGCAAAAAATACATGGCGC 6477
Qy 1981 TTGATATTCGGAGTTGCAATCTTATCTTAAACAGTATGACCTTGGCTATCTGTAGCC 2040
Db 6478 TTGATATTCGGAGTTGCAATCTTATCTTAAACAGTATGACCTTGGCTATCTGTAGCC 6537
Qy 2041 TCCCTTTATATAGCATGAGGAGCTAGACACCTAGCGATCTTGAAGCATACCGATAGG 2100
Db 6538 TCCCTTTATATAGCATGAGGAGCTAGACACCTAGCGATCTTGAAGCATACCGATAGG 6597
Qy 2101 ATTTCCAGGGCAAGAAAAGATTACATCTACACTTGGCTTCAATCAAGATGATGAT 2160
Db 6598 ATTTCCAGGGCAAGAAAAGATTACATCTACACTTGGCTTCAATCAAGATGATGAT 6657
Qy 2161 AGGATATATAGCAAGTGGCCCTTGAAGTCCGTTGGCATTTGTAATACTGAGACCA 2220
Db 6658 AGGATATATAGCAAGTGGCCCTTGAAGTCCGTTGGCATTTGTAATACTGAGACCA 6717
Qy 2221 ATTATGACGCAATACATCTCTCTTATCAGATTAATGAGAGCTGCAACACAGTGG 2280
Db 6718 ATTATGACGCAATACATCTCTCTTATCAGATTAATGAGAGCTGCAACACAGTGG 6777
Qy 2281 TGGGGGACCTTATCCATGACCCAGATTATATAGGGGAGATGGCAAAAGACTATTGTA 2340
Db 6778 TGGGGGACCTTATCCATGACCCAGATTATATAGGGGAGATGGCAAAAGACTATTGTA 6837
Qy 2341 GATGATGCTAGTATGATCATATCTTATCCCTCTGCAATTTCAAGAACATCTGAATTTT 2400
Db 6838 GATGATGCTAGTATGATCATATCTTATCCCTCTGCAATTTCAAGAACATCTGAATTTT 6897
Qy 2401 ATCCCGGCGCTACTACAGATCAGGTGCACTCGAATACCTCATTTGACATGAGTCT 2460
Db 6898 ATCCCGGCGCTACTACAGATCAGGTGCACTCGAATACCTCATTTGACATGAGTCT 6957
Qy 2461 ACCCATTAATCTGCTACACCCATATGTAATTTGTTGATGAGAGATCACTCATTTCA 2520
Db 6958 ACCCATTAATCTGCTACACCCATATGTAATTTGTTGATGAGAGATCACTCATTTCA 7017
Qy 2521 TATCAGATTTAGACCTTGGTGTGCTCGGACATCTGCAACAGGGAAGGATCTTTTCT 2580
Db 7018 TATCAGATTTAGACCTTGGTGTGCTCGGACATCTGCAACAGGGAAGGATCTTTTCT 7077
Qy 2581 ACTCTGCTTCAATCAACTGAGACGACCCAAATGAGAAATGTTGACATGAGTGA 2640
Db 7078 ACTCTGCTTCAATCAACTGAGACGACCCAAATGAGAAATGTTGACATGAGTGA 7137
Qy 2641 ACTTCCCTGGGTTGTGATATGCTGTGCTCGAAATGTCAGGAGACAGAGAAATATAT 2700
```

```
Db 7138 ACTCCCTGGGTTGTGATATGCTGTGCTCGAAAGTCAACGAGACAGAGAAATATAT 7197
Qy 2701 AACTCAGCTGTCCCTACGCGGATGATCATGAGAGTTAGGTTTCAACGCGCATACAC 2760
Db 7198 AACTCAGCTGTCCCTACGCGGATGATCATGAGAGTTAGGTTTCAACGCGCATACAC 7257
Qy 2761 GAAAAGACCTTACATGATCACAATTTATGGGGAATGGGATGCGCACTACCCGAGATA 2820
Db 7258 GAAAAGACCTTACATGATCACAATTTATGGGGAATGGGATGCGCACTACCCGAGATA 7317
Qy 2821 GGGGGTGAATCTTTATTTGAACAGCGGATATGTTTCACTCATGAGGATTAAACC 2880
Db 7318 GGGGGTGAATCTTTATTTGAACAGCGGATATGTTTCACTCATGAGGATTAAACC 7377
Qy 2881 AATTTCACCAAGTACACTGTACAGAAAGGAAATATGTGATATCAACGATACATGAC 2940
Db 7378 AATTTCACCAAGTACACTGTACAGAAAGGAAATATGTGATATCAACGATACATGAC 7437
Qy 2941 ACATGCCAGATGACAAAGTACAGATTTGGAATGGCCAAAGTTTGTATTAAGCTTGA 3000
Db 7438 ACATGCCAGATGACAAAGTACAGATTTGGAATGGCCAAAGTTTGTATTAAGCTTGA 7497
Qy 3001 CGGTTTGTGGGAAAGCATACAGCAGAGCTATCTTATCTATCAAGTGTCAACATCTTA 3060
Db 7498 CGGTTTGTGGGAAAGCATACAGCAGAGCTATCTTATCTATCAAGTGTCAACATCTTA 7557
Qy 3061 GCGGAAAGCCGGTACTGATACCGCCCAACACTGACACTCATGAGGAGCGGAAAGC 3120
Db 7558 GCGGAAAGCCGGTACTGATACCGCCCAACACTGACACTCATGAGGAGCGGAAAGC 7617
Qy 3121 AGAATTTTCAAGTAAAGGACATCTCATTTTCTGTATTAAGAGGTCATATCTTCT 3180
Db 7618 AGAATTTTCAAGTAAAGGACATCTCATTTTCTGTATTAAGAGGTCATATCTTCT 7677
Qy 3181 CCGCGTTATATATCTTATGATGACAGTACAGCAACAAACAGCCACTCTTCAATGCTTAT 3240
Db 7678 CCGCGTTATATATCTTATGATGACAGTACAGCAACAAACAGCCACTCTTCAATGCTTAT 7737
Qy 3241 ACAATCAATCCTTCACTCGGCGAGATGATCCCTTGCAGAGCTTCAAGATGCGCC 3300
Db 7738 ACAATCAATCCTTCACTCGGCGAGATGATCCCTTGCAGAGCTTCAAGATGCGCC 7797
Qy 3301 AACTCGTGTACTGAGATCTATACATGATCCATATCCCTAATCTTATAGAAAC 3358
Db 7798 AACTCGTGTACTGAGATCTATACATGATCCATATCCCTAATCTTATAGAAAC 7855

RESULT 4
US-10-429-735-3
; Sequence 3, Application US/10429735
; Publication No. US20030207836A1
; GENERAL INFORMATION:
; APPLICANT: KDO, Teun Yuang
; TITLE OF INVENTION: VACCINE ACCELERATOR FACTOR (VAF) FOR IMPROVEMENT OF VACCINATIONS
; FILE REFERENCE: 39734-188449
; CURRENT APPLICATION NUMBER: US/10/429, 735
; CURRENT FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 15186
; TYPE: DNA
; ORGANISM: Newcastle disease virus (NDV)
US-10-429-735-3

Query Match 99.9%; Score 3353.2; DB 6; Length 15186;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3353; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGGATGAAGATTCGATCCCGGTTGGGCGCTCCAGGTGAAGAATGGGCTCCAGACC 60
Db 4498 ACGGATGAAGATTCGATCCCGGTTGGGCGCTCCAGGTGAAGAATGGGCTCCAGACC 4557
```

Qy 61 TTCTACCAAGAACCCAGACCTTATGATGCTGACTATCGGGTTGCGCTGACCTGAGTTG 120  
Db 4558 TTCTACCAAGAACCCAGACCTTATGATGCTGACTATCGGGTTGCGCTGACTGAGTTG 4617  
Qy 121 CATCTGTCCGGCAAACTTCATTTGATGCGAGCCCTTTGACAGCTGACGAAATTTGGTTAC 180  
Db 4618 CATCTGTCCGGCAAACTTCATTTGATGCGAGCCCTTTGACAGCTGACGAAATTTGGTTAC 4677  
Qy 181 AGGAGCAAAAGCCGTCAATATACCTCACTCCAGACAGATCAATCATAGTTAAAGCT 240  
Db 4678 AGGAGCAAAAGCCGTCAATATACCTCACTCCAGACAGATCAATCATAGTTAAAGCT 4737  
Qy 241 CCTCCCAATCTGCCCCAAGATTAAGSAGSCATGTGCGAAAGCCCCCTTGATGATACAA 300  
Db 4738 CCTCCCAATCTGCCCCAAGATTAAGSAGSCATGTGCGAAAGCCCCCTTGATGATACAA 4797  
Qy 301 CAGGACATTTGACCACTTTGCTCAACCCCTTTGATCTTATCCGTAGGATACAGAGTC 360  
Db 4798 CAGGACATTTGACCACTTTGCTCAACCCCTTTGATCTTATCCGTAGGATACAGAGTC 4857  
Qy 361 TGTGACTACATCTGAGAGGGGAGACAGGGGCGCTTATAG3CGCATTAATTTGGGGTGT 420  
Db 4858 TGTGACTACATCTGAGAGGGGAGACAGGGGCGCTTATAG3CGCATTAATTTGGGGTGT 4917  
Qy 421 GGCCTTTGGGGTTGCAACTGCGGCAAAATAACAGCGCGCAGCTCTGATACAAAGCCAA 480  
Db 4918 GGCCTTTGGGGTTGCAACTGCGGCAAAATAACAGCGCGCAGCTCTGATACAAAGCCAA 4977  
Qy 481 ACAAAATGCTGCCAATCATCTCCGACTTAAAGAGACATTCGCCAACAATGAGGCTGT 540  
Db 4978 ACAAAATGCTGCCAATCATCTCCGACTTAAAGAGACATTCGCCAACAATGAGGCTGT 5037  
Qy 541 GCATGAGGTCATGACGGATTATGCGCACTGACAGTGGCAATGGGAGATGACAGAGTT 600  
Db 5038 GCATGAGGTCATGACGGATTATGCGCACTGACAGTGGCAATGGGAGATGACAGAGTT 5097  
Qy 601 TGTTAATGACCAATTTAATAAAAGCTCAGGAAATTAAGCTGACATCAAAATTTGCACAGCA 660  
Db 5098 TGTTAATGACCAATTTAATAAAAGCTCAGGAAATTAAGCTGACATCAAAATTTGCACAGCA 5157  
Qy 661 AGTTGTGTAGAGCTCAACCTGTACCTTAACCGAATTTGACTACAGTATTCGACCACAAT 720  
Db 5158 AGTTGTGTAGAGCTCAACCTGTACCTTAACCGAATTTGACTACAGTATTCGACCACAAT 5217  
Qy 721 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTACAACTTAAGCTGGTGA 780  
Db 5218 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTACAACTTAAGCTGGTGA 5277  
Qy 781 TATGGAATTAATTAATGATTAAGTGTAGGTGAGGAAACAATCACTCAGCTCATTAATCGG 840  
Db 5278 TATGGAATTAATTAATGATTAAGTGTAGGTGAGGAAACAATCACTCAGCTCATTAATCGG 5337  
Qy 841 TAGCGGCTTAATCAACCGGTAAACCTTAATCTAATCGACTCAAGACTCAACTCTTGGGTAT 900  
Db 5338 TAGCGGCTTAATCAACCGGTAAACCTTAATCTAATCGACTCAAGACTCAACTCTTGGGTAT 5397  
Qy 901 ACAGGTAACTTAACCTTAAGTGGGAACTTAATTAATGCTGTGCACTTACTTGGAAAC 960  
Db 5398 ACAGGTAACTTAACCTTAAGTGGGAACTTAATTAATGCTGTGCACTTACTTGGAAAC 5457  
Qy 961 CTTATCCGTAGCAACACAGGGGATTTGGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
Db 5458 CTTATCCGTAGCAACACAGGGGATTTGGCTCGGCACTTGTCCCAAAAGTGTGACACA 5517  
Qy 1021 GGTGCGTTCTGTGATAGAGAACTTGACACCTCATACTGTATAGAACTGACTTATGATTT 1080  
Db 5518 GGTGCGTTCTGTGATAGAGAACTTGACACCTCATACTGTATAGAACTGACTTATGATTT 5577  
Qy 1081 ATATTGTACAAAGATAGTAAGTTTCCCTATGTCCTTGATTTATTTCTGTTTGAAGGG 1140  
Db 5578 ATATTGTACAAAGATAGTAAGTTTCCCTATGTCCTTGATTTATTTCTGTTTGAAGGG 5637

Qy 1141 CAATAGTCGGCCCTGTATGTACTCAAAAGCCGAGCCACTTATACACCATATGATAC 1200  
Db 5638 CAATAGTCGGCCCTGTATGTACTCAAAAGCCGAGCCACTTATACACCATATGATAC 5697  
Qy 1201 TATCAAAAGTTCACTCATCGCAACTGCAAGATGACAAATGTAGATGTGTAACCCCCC 1260  
Db 5698 TATCAAAAGTTCACTCATCGCAACTGCAAGATGACAAATGTAGATGTGTAACCCCCC 5757  
Qy 1261 GGTATCATATCGCAAACTATGAGAAAGCCGTCTCTTAATAGATAAACAATCATGCA 1320  
Db 5758 GGTATCATATCGCAAACTATGAGAAAGCCGTCTCTTAATAGATAAACAATCATGCA 5817  
Qy 1321 TGTTTATCTTACGCGGGAATTACTTTAAGCTCAGTGGGGAATTTGATGTAATCA 1380  
Db 5818 TGTTTATCTTACGCGGGAATTACTTTAAGCTCAGTGGGGAATTTGATGTAATCA 5877  
Qy 1381 GAAGAAATATCTCAATPACAAAGTCTCAAGTAATATAACAGCAATCTGATATCTCAAC 1440  
Db 5878 GAAGAAATATCTCAATPACAAAGTCTCAAGTAATATAACAGCAATCTGATATCTCAAC 5937  
Qy 1441 TGACCTTGGGAATGTCAACACTCGATCAGTAATGCTTTGAATAATTAGAGAAAGCAA 1500  
Db 5938 TGACCTTGGGAATGTCAACACTCGATCAGTAATGCTTTGAATAATTAGAGAAAGCAA 5997  
Qy 1501 CAGAAACTAGACAAAGTCAATGTCAAACTGACATGACATCTGCTCATTAATCTATAT 1560  
Db 5998 CAGAAACTAGACAAAGTCAATGTCAAACTGACATGACATCTGCTCATTAATCTATAT 6057  
Qy 1561 CGTTTGACTATCATATCTCTGTTTGTATATCTTACGCTGATTTACGATGCTACT 1620  
Db 6058 CGTTTGACTATCATATCTCTGTTTGTATATCTTACGCTGATTTACGATGCTACT 6117  
Qy 1621 AATGTACAAAGCAAAAGCGCAACAAACCTTATATAGGCTTGGGAATTAATCTTACA 1680  
Db 6118 AATGTACAAAGCAAAAGCGCAACAAACCTTATATAGGCTTGGGAATTAATCTTACA 6177  
Qy 1681 TCAATGAGAGCCACTACAAATAATGTGAACAAGTGAAGCAAGAGGTTTCCCTAATAG 1740  
Db 6178 TCAATGAGAGCCACTACAAATAATGTGAACAAGTGAAGCAAGAGGTTTCCCTAATAG 6237  
Qy 1741 TAAATTTGTGAAAGTTCTGTAGTGTGAGTTCAGTTCAAGAGTTAAGAAACCTACCGGT 1800  
Db 6238 TAAATTTGTGAAAGTTCTGTAGTGTGAGTTCAGTTCAAGAGTTAAGAAACCTACCGGT 6297  
Qy 1801 TGTAGATGACCAAAAGACATATACGGGTAGAACGGTAAAGAGAGCCGCCCTCAATTCG 1860  
Db 6298 TGTAGATGACCAAAAGACATATACGGGTAGAACGGTAAAGAGAGCCGCCCTCAATTCG 6357  
Qy 1861 GAGCCAGGCTTACAAACCTCGCTTACCGCTTACCGACAAACAGTCTCAATCATGAC 1920  
Db 6358 GAGCCAGGCTTACAAACCTCGCTTACCGCTTACCGACAAACAGTCTCAATCATGAC 6417  
Qy 1921 CGCCGCTTTAGCCAAAGTTGCTTGAAGAAATGATGAAAGAGGGCAAAATAACATGAGGGC 1980  
Db 6418 CGCCGCTTTAGCCAAAGTTGCTTGAAGAAATGATGAAAGAGGGCAAAATAACATGAGGGC 6477  
Qy 1981 TTGATATTCGGGATTTGCAATCTTATCTTAAACAAGTGTGACTTGTGGCTATATCTGTAGCC 2040  
Db 6478 TTGATATTCGGGATTTGCAATCTTATCTTAAACAAGTGTGACTTGTGGCTATATCTGTAGCC 6537  
Qy 2041 TCCCTTTATATATAGATGGGGCTAGACACACTAGCCGATCTTTAGGCAATACGACTAGG 2100  
Db 6538 TCCCTTTATATATAGATGGGGCTAGACACACTAGCCGATCTTTAGGCAATACGACTAGG 6597  
Qy 2101 ATTTCCAGGGCAAGAAAGAAATTAATCACTTACACTTGGTCCAAACAGATGTAGAT 2160  
Db 6598 ATTTCCAGGGCAAGAAAGAAATTAATCACTTACACTTGGTCCAAACAGATGTAGAT 6657  
Qy 2161 AGATATATTAAGCAAGTGGCCCTTGAAGTCTCGGTGTGCAATTTGTAATACTGAGACCA 2220  
Db 6658 AGATATATTAAGCAAGTGGCCCTTGAAGTCTCGGTGTGCAATTTGTAATACTGAGACCA 6717  
Qy 2221 ATTATGAACGAATPACATCTCTCTTATACAGATTAATGAGACTGCAAAACAAGTGGG 2280

Db	6718	ATTATGAACGGAAATACATCTCTCTCTTATACAGTTAATGAGCTGCAGAAACAAGTGGG	6777
Oy	2281	TGGGGGGCACCTATCCATGACCCAGATTATAATAGGGGGATAGCGAAAGAACTATTGTA	2340
Db	6778	TGGGGGGCACCTATCCATGACCCAGATTATAATAGGGGGGATAGCGAAAGAACTATTGTA	6837
Oy	2341	GATGATGCTAGTGAATGTACATCATCTCTATCCCTCTGATTTCAAGAACATCTGAATTTT	2400
Db	6838	GATGATGCTAGTGAATGTACATCATCTCTATCCCTCTGATTTCAAGAACATCTGAATTTT	6897
Oy	2401	ATCCCGGGCCCTACACAGAGATCAGGTTGCACTGGAATACCCTCATTTGACATGAGTCT	2460
Db	6898	ATCCCGGGCCCTACACAGAGATCAGGTTGCACTGGAATACCCTCATTTGACATGAGTCT	6957
Oy	2461	ACCATTACTGCTACACCCATATATGTAAATATGTCTGAGTGCAGAGATCACTCAATTCA	2520
Db	6958	ACCATTACTGCTACACCCATATATGTAAATATGTCTGAGTGCAGAGATCACTCAATTCA	7017
Oy	2521	TATCAGATTTTAGCATCTTGTTGTGTCTCCGGAACATCTGCAACAGGAGGGATATCTTTTCT	2580
Db	7018	TATCAGATTTTAGCATCTTGTTGTGTCTCCGGAACATCTGCAACAGGAGGGATATCTTTTCT	7077
Oy	2581	ACTCGCGTTCATCAACCTGGAAGCAACCCAAAATGGAAAGTCTGAGTGAATGCA	2640
Db	7078	ACTCGCGTTCATCAACCTGGAAGCAACCCAAAATGGAAAGTCTGAGTGAATGCA	7137
Oy	2641	ACTCCCCGGGTTGTGATATGCTGTGCTCGAAAGTCAGAGACAGAGAGAGAAAGATTAT	2700
Db	7138	ACTCCCCGGGTTGTGATATGCTGTGCTCGAAAGTCAGAGACAGAGAGAGAAAGATTAT	7197
Oy	2701	AACCTACGCTGTCCCTACCGGGATGGTACATGGAAGTTATAGGTTTGCAGCGCCAGTACAC	2760
Db	7198	AACCTACGCTGTCCCTACCGGGATGGTACATGGAAGTTATAGGTTTGCAGCGCCAGTACAC	7257
Oy	2761	GAAAAAGACCTAAGATGTACAAACATTATTCGGGGACTGGGTGGCCACTACCCAGAGATA	2820
Db	7258	GAAAAAGACCTAAGATGTACAAACATTATTCGGGGACTGGGTGGCCACTACCCAGAGATA	7317
Oy	2821	GGGGGTGGATCTTTTATTTGACAGCCGCGTATGTTCTCAGTCTACGAGGGTTAAAAACC	2880
Db	7318	GGGGGTGGATCTTTTATTTGACAGCCGCGTATGTTCTCAGTCTACGAGGGTTAAAAACC	7377
Oy	2881	AATTCAACCCAGTGAACCTGTAACGAAAGGAAATATGTATATACAAGCATACATATGAC	2940
Db	7378	AATTCAACCCAGTGAACCTGTAACGAAAGGAAATATGTATATACAAGCATACATATGAC	7437
Oy	2941	ACATGCCCAATGACAGACCTACCAATTTGGAATGGCAAGTCTTGATATACCTTGA	3000
Db	7438	ACATGCCCAATGACAGACCTACCAATTTGGAATGGCAAGTCTTGATATACCTTGA	7497
Oy	3001	CGGTTGGTGGGAAAACGATACAGAGGCTATCTTATCAAGAGGTCAACATCTTA	3060
Db	7498	CGGTTGGTGGGAAAACGATACAGAGGCTATCTTATCAAGAGGTCAACATCTTA	7557
Oy	3061	GGCGAAGACCGGATATGTAAGTGAACCGGCCAACAAGTCACTCATGAGGGCCGAAGGC	3120
Db	7558	GGCGAAGACCGGATATGTAAGTGAACCGGCCAACAAGTCACTCATGAGGGCCGAAGGC	7617
Oy	3121	AGAAATTCTCAGATAGGGACATCTCATTTCTTGTAATCAACAGAGGTCACTACTTCTCT	3180
Db	7618	AGAAATTCTCAGATAGGGACATCTCATTTCTTGTAATCAACAGAGGTCACTACTTCTCT	7677
Oy	3181	CCCGCGTTATATATATCTCTATGACAGTCAAGCAACAAAGCACTCTTCATATGCTTTAT	3240
Db	7678	CCCGCGTTATATATATCTCTATGACAGTCAAGCAACAAAGCACTCTTCATATGCTTTAT	7737
Oy	3241	ACATTCAATGCTCTTCACTCGGCGAGATATGATATCCCTTGCCAGGCTTCAAGCAAGTCCCC	3300
Db	7738	ACATTCAATGCTCTTCACTCGGCGAGATATGATATCCCTTGCCAGGCTTCAAGCAAGTCCCC	7797
Oy	3301	AACCTGTGTACTGAGTCACTATACAGATCAATCCCTTAATCTTATATAGAACCC	3358

```

Db      7798  AACTGCTGTGTTACTGAGGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 7855

RESULT 5
US-10-824-782-134
; Sequence 134, Application US/10824782
; Publication No. US20040234552A1
GENERAL INFORMATION:
; APPLICANT: Peeters, Bernadus; De Leeuw, Olav; Klaus, Guus; Gielkens, Arnold
; TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnostic
; FILE REFERENCE: 2183-4646US
; CURRENT APPLICATION NUMBER: US/10/824,782
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US/10/788,232
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/NL99/00377
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 134
; LENGTH: 15186
; TYPE: DNA
; ORGANISM: Newcastle disease virus strain LaSota
US-10-824-782-134

Query Match      99.9%; Score 3353.2; DB 8; Length 15186;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  ACGGTAAGAATTTCTGGATCCCGGTTGGCGCCCTCCAGATGCAAGATGGGCTCCAGACC 60
Db      4498  ACGGTAAGAATTTCTGGATCCCGGTTGGCGCCCTCCAGATGCAAGATGGGCTCCAGACC 4557
QY      61  TTCTACCAAGAACCCAGACACTATGATGCTGACTATCCGGGTTGCGCTGCACTGAGTTG 120
Db      4558  TTCTACCAAGAACCCAGACACTATGATGCTGACTATCCGGGTTGCGCTGCTGACTGAGTTG 4617
QY      121  CATCTGTCGGGCAATCTCCATTGATGCGAGGCGCTCTTGCACTGCGAGAAATTGTTGTTAC 180
Db      4618  CATCTGTCGGGCAATCTCCATTGATGCGAGGCGCTCTTGCACTGCGAGAAATTGTTGTTAC 4677
QY      181  AGGAGACAAGACCCGTCATATATACCTCATCCGACAGACAGATTCATATGTTAAAGT 240
Db      4678  AGGAGACAAGACCCGTCATATATACCTCATCCGACAGAGATTCATATGTTAAAGT 4737
QY      241  CCTCCCGAATCTGCCAAGATTAAGAGGCGATGTGCGAAGCCCTTGATGATCATCAAA 300
Db      4738  CCTCCCGAATCTGCCAAGATTAAGAGGCGATGTGCGAAGCCCTTGATGATCATCAAA 4797
QY      301  CAGACATTTGACCACTTTTGCTACCCCTTGTGTGACTTATCCGTAGATACAGAGTC 360
Db      4798  CAGACATTTGACCACTTTTGCTACCCCTTGTGTGACTTATCCGTAGATACAGAGTC 4857
QY      361  TGTGACTATCATCTGAGAGGGGGGAGACAGGGGGCGCTTATAGGGCCATTAATTGGCGTGT 420
Db      4858  TGTGACTATCATCTGAGAGGGGGGAGACAGGGGGCGCTTATAGGGCCATTAATTGGCGTGT 4917
QY      421  GGGCTCTGGGGGTTGGACCTGGCGCAAAATTAACGGGGCGGAGCTCTGATTAAGGCCAA 480
Db      4918  GGGCTCTGGGGGTTGGACCTGGCGCAAAATTAACGGGGCGGAGCTCTGATTAAGGCCAA 4977
QY      481  ACAAAATGCTGCCAATCTCTCCGACTTAAAGAGACATTTGGCGCAACCAATGAGGCTGT 540
Db      4978  ACAAAATGCTGCCAATCTCTCCGACTTAAAGAGACATTTGGCGCAACCAATGAGGCTGT 5037
QY      541  GCATGAGGTCACTGACGGATTATGCGCACTAGCAGTGGCAGTTGGGAAGATGACAGAGTT 600
Db      5038  GCATGAGGTCACTGACGGATTATGCGCACTAGCAGTGGCAGTTGGGAAGATGACAGAGTT 5097
QY      601  TGTTAATGACCAATTTAATAAAGCAGCTCAGGAATTAAGCTGCATCAAAATTGCCACAGCA 660
Db      5098  TGTTAATGACCAATTTAATAAAGCAGCTCAGGAATTAAGCTGCATCAAAATTGCCACAGCA 5157

```

QY 661 AGTTGGTGTAGAGCTCAACCTGTACTTACCGGAATTGACTACAGTATTCGAGCCACAAT 720  
DB 5158 AGTTGGTGTAGAGCTCAACCTGTACTTACCGGAATTGACTACAGTATTCGAGCCACAAT 5217  
QY 721 CACTTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCGGGGAAA 780  
DB 5218 CACTTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCGGGGAAA 5277  
QY 781 TATGATTAATCTTATTTGACTAAAGTATAGGTAGGGAACAATCACTCAGCTCATTAATCGG 840  
DB 5278 TATGATTAATCTTATTTGACTAAAGTATAGGTAGGGAACAATCACTCAGCTCATTAATCGG 5337  
QY 841 TAGCGGCTTAATCAACCGGTAAACCTATTCTATAGACTCAAGACTCAACTCTGGGTAT 900  
DB 5338 TAGCGGCTTAATCAACCGGTAAACCTATTCTATAGACTCAAGACTCAACTCTGGGTAT 5397  
QY 901 ACAGGTAACTTACTTCACTGCGGGAACCTAAATTAATATGCGTGCACCTTCTGGAAC 960  
DB 5398 ACAGGTAACTTACTTCACTGCGGGAACCTAAATTAATATGCGTGCACCTTCTGGAAC 5457  
QY 961 CTTATCCGTAGACAACAACGAGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
DB 5458 CTTATCCGTAGACAACAACGAGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 5517  
QY 1021 GGTCGGTTCTGTGTATGAGAAGACTTGACACCTCATACTGTATAGAAACTGACTTATGATT 1080  
DB 5518 GGTCGGTTCTGTGTATGAGAAGACTTGACACCTCATACTGTATAGAAACTGACTTATGATT 5577  
QY 1081 ATATTGTACAAAGATATGTAAGCTTCCCTATGTCCCTGTGTATTTATTCCTGCTTGAAGGG 1140  
DB 5578 ATATTGTACAAAGATATGTAAGCTTCCCTATGTCCCTGTGTATTTATTCCTGCTTGAAGGG 5637  
QY 1141 CAATAGCTCGGCTGTATGTACTCAAAAGACGAAAGGCACTTACTACACCATCATGAC 1200  
DB 5638 CAATAGCTCGGCTGTATGTACTCAAAAGACGAAAGGCACTTACTACACCATCATGAC 5697  
QY 1201 TATCAAGGTTCACTCATCGGCAACTGCAAGATGACAATGTAGATGTGTAAACCCCC 1260  
DB 5698 TATCAAGGTTCACTCATCGGCAACTGCAAGATGACAATGTAGATGTGTAAACCCCC 5757  
QY 1261 GGGTATCATATCGCAAACTATGAGAAAGCGGTGCTCTATATGATTAACAATCATGTGCA 1320  
DB 5758 GGGTATCATATCGCAAACTATGAGAAAGCGGTGCTCTATATGATTAACAATCATGTGCA 5817  
QY 1321 TGTTTATCCCTTAGCGGGAATPACTTTAAGGCTCAGTGGGGAATTCGATGATPACTTCA 1380  
DB 5818 TGTTTATCCCTTAGCGGGAATPACTTTAAGGCTCAGTGGGGAATTCGATGATPACTTCA 5877  
QY 1381 GAAGAAATATCTCAATACAAAGATTTCTCAAGTAAATATAACAGGCAATCTTGATATCTCAAC 1440  
DB 5878 GAAGAAATATCTCAATACAAAGATTTCTCAAGTAAATATAACAGGCAATCTTGATATCTCAAC 5937  
QY 1441 TGAAGTTGGGAATGTCAACAATCGATCAAGTATGCTTTGAATAAGTTAGAGAAAGCAA 1500  
DB 5938 TGAAGTTGGGAATGTCAACAATCGATCAAGTATGCTTTGAATAAGTTAGAGAAAGCAA 5997  
QY 1501 CAGAAACTAGCAAAAGTCAATGTCAAACTGATCAATGCTCTCTCATTAATTAAT 1560  
DB 5998 CAGAAACTAGCAAAAGTCAATGTCAAACTGATCAATGCTCTCTCATTAATTAAT 6057  
QY 1561 CGTTTGAATCATATCTCTGTTTGTGTATGATTAAGCTGATTCAGATGCTACT 1620  
DB 6058 CGTTTGAATCATATCTCTGTTTGTGTATGATTAAGCTGATTCAGATGCTACT 6117  
QY 1621 AATGTACAAGCAAAAGGCGCAAAACCTTATATGCTTGGGAATTAATCTTACA 1680  
DB 6118 AATGTACAAGCAAAAGGCGCAAAACCTTATATGCTTGGGAATTAATCTTACA 6177  
QY 1681 TCAGATGAGGCGCACTACAAAATGTGAAACAAGATGAGAACGAGGTTCCCTAATAG 1740  
DB 6178 TCAGATGAGGCGCACTACAAAATGTGAAACAAGATGAGAACGAGGTTCCCTAATAG 6237  
QY 1741 TAATTGTGTGAAGGTTCTGTAGTCTGTCAAGTTCAAGAGATTAAAGAAAACCTACCGGT 1800

DB 6238 TAATTGTGTGAAGGTTCTGTAGTCTGTCAAGTTCAAGAGATTAAAGAAAACCTACCGGT 6297  
QY 1801 TGTAGATGACCAAGAGAGATATACGGGTAGAACGTTAAGAGAGCCGCCCTCAATTGC 1860  
DB 6298 TGTAGATGACCAAGAGAGATATACGGGTAGAACGTTAAGAGAGCCGCCCTCAATTGC 6357  
QY 1861 GAGCCAGGCTTACACACTCGGTTCTACCGGTTCAACGACAACAGTCTCATATCGAC 1920  
DB 6358 GAGCCAGGCTTACACACTCGGTTCTACCGGTTCAACGACAACAGTCTCATATCGAC 6417  
QY 1921 CGGCGCGTTAGCCAAAGTTGGTTAGAAATGATGAAAGAGGCAAAAATACATGGCGC 1980  
DB 6418 CGGCGCGTTAGCCAAAGTTGGTTAGAAATGATGAAAGAGGCAAAAATACATGGCGC 6477  
QY 1981 TTGATATTCGGATTGCAATCTTATTTCTTAAACAGTATGACCTTGGCTATATCTAGCC 2040  
DB 6478 TTGATATTCGGATTGCAATCTTATTTCTTAAACAGTATGACCTTGGCTATATCTAGCC 6537  
QY 2041 TCCCTTTTATATAGCATGGGGCTAGACAACCTAGCCATCTTGTAGGCATACCGACTAGG 2100  
DB 6538 TCCCTTTTATATAGCATGGGGCTAGACAACCTAGCCATCTTGTAGGCATACCGACTAGG 6597  
QY 2101 ATTTCCAGGGGAGAAAGAAATTAACATCTACCTTGGTTCCATCAAGATGTAGTAT 2160  
DB 6598 ATTTCCAGGGGAGAAAGAAATTAACATCTACCTTGGTTCCATCAAGATGTAGTAT 6657  
QY 2161 AGGATATTAAGCAAGTGGCCCTGAGTCTCGGTTGGCATTTAAATACTGAGACACA 2220  
DB 6658 AGGATATTAAGCAAGTGGCCCTGAGTCTCGGTTGGCATTTAAATACTGAGACACA 6717  
QY 2221 ATTATGAACGCAATATACATCTCTCTTATAGATTAATGAGGCTGCAACAAGTGGG 2280  
DB 6718 ATTATGAACGCAATATACATCTCTCTTATAGATTAATGAGGCTGCAACAAGTGGG 6777  
QY 2281 TGGGGGGCACTTATCCATGACCCAGATTAATAGGGGGGATAGCCAAAGAACTGATGTA 2340  
DB 6778 TGGGGGGCACTTATCCATGACCCAGATTAATAGGGGGGATAGCCAAAGAACTGATGTA 6837  
QY 2341 GATGATCTAGTATGTCACATCATCTTATCCCTCTGCACTTTCAAGAACATCTGAATTT 2400  
DB 6838 GATGATCTAGTATGTCACATCATCTTATCCCTCTGCACTTTCAAGAACATCTGAATTT 6897  
QY 2401 ATCCCGGCGCTTACTACAGGATCAGTTGCACTCGAATACCTCATTTGACATGATGCT 2460  
DB 6898 ATCCCGGCGCTTACTACAGGATCAGTTGCACTCGAATACCTCATTTGACATGATGCT 6957  
QY 2461 ACCGATTACTGTACACCCCATATGTAAATTTGTCTGATGCAAGATCACTCAATTCA 2520  
DB 6958 ACCGATTACTGTACACCCCATATGTAAATTTGTCTGATGCAAGATCACTCAATTCA 7017  
QY 2521 TATCAGATTTTGAAGCTTGGTGTGCTCCGACATCTGCAACAGGAGGATTTCTTTTCT 2580  
DB 7018 TATCAGATTTTGAAGCTTGGTGTGCTCCGACATCTGCAACAGGAGGATTTCTTTTCT 7077  
QY 2581 ACTGTGGTTCCATCAACTGAGACACCCAAATGCGAAGTCTTGCAAGTGTAGTCA 2640  
DB 7078 ACTGTGGTTCCATCAACTGAGACACCCAAATGCGAAGTCTTGCAAGTGTAGTCA 7137  
QY 2641 ACTCCCTGGGTTGTGATATCTGTGCTCGAAGTCAACGAGACAGAGAAAGATTAAT 2700  
DB 7138 ACTCCCTGGGTTGTGATATCTGTGCTCGAAGTCAACGAGACAGAGAAAGATTAAT 7197  
QY 2701 AACTCAGCTGTCCCTACCGGATGTATCAATGGAGGTTAGGTTGACAGGCACTACAC 2760  
DB 7198 AACTCAGCTGTCCCTACCGGATGTATCAATGGAGGTTAGGTTGACAGGCACTACAC 7257  
QY 2761 GAAAGAGACCTAGATGTCAACAATTTATGCGGGAATGGGTGGCACTACCCAGAGTA 2820  
DB 7258 GAAAGAGACCTAGATGTCAACAATTTATGCGGGAATGGGTGGCACTACCCAGAGTA 7317  
QY 2821 GGGGGGTGATCTTTTATTTGACAGCGCGTATGTTCTCAGTCTACGAGGTTTAAACCC 2880



Db 7318 GGGGGTGGATCTTTATTTGAACGCGGTAATGTTCTCAGTCTACGAGGGTTAAAAACC 73177  
Qy 2881 AATTCAACCAAGTACACTGTATACAGGAAGGAATAATGTATATATCAAGCGATACATGAC 2940  
Db 7378 AATTCAACCAAGTACACTGTATACAGGAAGGAATAATGTATATATCAAGCGATACATGAC 7437  
Qy 2941 ACATGCCAGATGAGCAAGCACTACAGATTTGAAATGCGCAAGTCTTGATTAAGCTTGA 3000  
Db 7438 ACATGCCAGATGAGCAAGCACTACAGATTTGAAATGCGCAAGTCTTGATTAAGCTTGA 7497  
Qy 3001 CGATTTGGTGGGAAACGCAATACAGCAAGGCTATCTTATCTATCAAGGCTCAACATCTCTTA 3060  
Db 7498 CGATTTGGTGGGAAACGCAATACAGCAAGGCTATCTTATCTATCAAGGCTCAACATCTCTTA 7557  
Qy 3061 GGGGAAGACCCGGTACTGTACTGTACCGCCCAACAGTCACTCATGSGGGCCGAAGGC 3120  
Db 7558 GGGGAAGACCCGGTACTGTACTGTACCGCCCAACAGTCACTCATGSGGGCCGAAGGC 7617  
Qy 3121 AGAATTTCAACAGTACAGGACATCTCATTTCTTGATCAACGAGGGTCATCACTTCTCT 3180  
Db 7618 AGAATTTCAACAGTACAGGACATCTCATTTCTTGATCAACGAGGGTCATCACTTCTCT 7677  
Qy 3181 CCGGCGTATTAATATCTATGACAGTACAGCAACAAACAGCCACTCTTCAATAGTCTTAT 3240  
Db 7678 CCGGCGTATTAATATCTATGACAGTACAGCAACAAACAGCCACTCTTCAATAGTCTTAT 7737  
Qy 3241 ACATTCATGCTTCACTCGGCGAGTATGATCCCTTGCCAGGCTTCAGCAAGATGCCCC 3300  
Db 7738 ACATTCATGCTTCACTCGGCGAGTATGATCCCTTGCCAGGCTTCAGCAAGATGCCCC 7797  
Qy 3301 AACTCGTGTATCTGAGTCTATACAGATTCATATCCCTAATCTTCTATAGAAACC 3358  
Db 7798 AACTCGTGTATCTGAGTCTATACAGATTCATATCCCTAATCTTCTATAGAAACC 7855

RESULT 6  
US-10-788-232-134  
/ Sequence 134, Application US/10788232  
/ Publication No. US20040235134A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Peeters, Bernardus; de Leeuw, Olav; Klaus, Gius; Gielkens, Armond  
/ TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnosti  
/ FILE REFERENCE: 2183-4646US  
/ CURRENT APPLICATION NUMBER: US/10/788, 232  
/ CURRENT FILING DATE: 2004-02-26  
/ PRIOR APPLICATION NUMBER: PCT/NL99/00377  
/ PRIOR FILING DATE: 1999-06-17  
/ NUMBER OF SEQ ID NOS: 150  
/ SOFTWARE: Patent version 3.0  
/ SEQ ID NO 134  
/ LENGTH: 15186  
/ TYPE: DNA  
/ ORGANISM: Newcastle disease virus strain LaSota  
US-10-788-232-134

Query Match 99.9%; Score 3353.2; DB 8; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGGGTGAAGATTTGGATTCGGGTTGGCGCCCTTCAGGTGCAAGATGGGCTTCAGACC 60  
Db 4498 ACGGGTGAAGATTTGGATTCGGGTTGGCGCCCTTCAGGTGCAAGATGGGCTTCAGACC 4557  
Qy 61 TTCTACCAAGAACCCGACCTATGATGCTGACATCCGGGTTGGCGTGCACCTGAGTTG 120  
Db 4558 TTCTACCAAGAACCCGACCTATGATGCTGACATCCGGGTTGGCGTGCACCTGAGTTG 4617  
Qy 121 CATCTGCGGCAAACTCATTTGATGAGGAGGCTCTTGAGCTGACAGAAATTTGTGTTAC 180  
Db 4618 CATCTGCGGCAAACTCATTTGATGAGGAGGCTCTTGAGCTGACAGAAATTTGTGTTAC 4677  
Qy 181 AGGAGCAAAAGCGTCAACATATACACTCATCCAGACAGATCAATCAATAGTTAAGCT 240

Db 4678 AGGAGCAAAAGCGTCAACATATACACTCATCCAGACAGATCAATCAATAGTTAAGCT 4737  
Qy 241 CCTCCGAATCTGCCCAAGGATTAAGAGCATGTGCCAAAGCCCTTGGATGATACAA 300  
Db 4738 CCTCCGAATCTGCCCAAGGATTAAGAGCATGTGCCAAAGCCCTTGGATGATACAA 4797  
Qy 301 CAGGACATTGACCACTTGTCTACCCCCCTTGGTACTCTATCCGTATGATACAGAGTGC 360  
Db 4798 CAGGACATTGACCACTTGTCTACCCCCCTTGGTACTCTATCCGTATGATACAGAGTGC 4857  
Qy 361 TGTGACTACATCTGAGAGGGGGGAGACAGGGGGCCCTTAATGGGGCCATTATTTGGCGGTGT 420  
Db 4858 TGTGACTACATCTGAGAGGGGGGAGACAGGGGGCCCTTAATGGGGCCATTATTTGGCGGTGT 4917  
Qy 421 GGCCTTTGGGGTTGCAACTGCCCCCACAATAATACAGCGGCGGAGCTCTGATACAAAGCAA 480  
Db 4918 GGCCTTTGGGGTTGCAACTGCCCCCACAATAATACAGCGGCGGAGCTCTGATACAAAGCAA 4977  
Qy 481 ACAAAATGCTGCCAATCTCTCCGACTTAAGAAGAGCATTTGCCGAACCAATGAGCTGT 540  
Db 4978 ACAAAATGCTGCCAATCTCTCCGACTTAAGAAGAGCATTTGCCGAACCAATGAGCTGT 5037  
Qy 541 GCATGAGGTGACAGAGGATTTATCGCAACTAGAGAGTGGGAGTTGGGAGATGAGCAGTT 600  
Db 5038 GCATGAGGTGACAGAGGATTTATCGCAACTAGAGAGTGGGAGTTGGGAGATGAGCAGTT 5097  
Qy 601 TGTTAATGACCAATTTAATAAACAGCTCAGAAATTAAGCTGATCAAAATGACAGCA 660  
Db 5098 TGTTAATGACCAATTTAATAAACAGCTCAGAAATTAAGCTGATCAAAATGACAGCA 5157  
Qy 661 AGTTGGTGNAGCTCAACCTGTACTTAACCGAATTTGACTACAGTATTCGAGCACAAT 720  
Db 5158 AGTTGGTGNAGCTCAACCTGTACTTAACCGAATTTGACTACAGTATTCGAGCACAAT 7217  
Qy 721 CACTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACACTGATGAGAAA 780  
Db 5218 CACTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACACTGATGAGAAA 5277  
Qy 781 TATGATTAATTAATGACTAAGTATGATGAGGAAACAATCAACTCAGCTCATTAATCGG 840  
Db 5278 TATGATTAATTAATGACTAAGTATGATGAGGAAACAATCAACTCAGCTCATTAATCGG 5337  
Qy 841 TACCGGCTTAATCAACCGGTAACTCTTATTCATACGACTCAGACTCACTCTTGGGTAT 900  
Db 5338 TACCGGCTTAATCAACCGGTAACTCTTATTCATACGACTCAGACTCACTCTTGGGTAT 5397  
Qy 901 ACAGGTAACTCTACCTTCACTGCGGGAACCTAATTAATGCGGCCACTTCTTGAAC 960  
Db 5398 ACAGGTAACTCTACCTTCACTGCGGGAACCTAATTAATGCGGCCACTTCTTGAAC 5457  
Qy 961 CTATCCGTAAAGCAACAGGGGATTTGCTGCGCACTTGTCCCAAAAGTGTGACACA 1020  
Db 5458 CTATCCGTAAAGCAACAGGGGATTTGCTGCGCACTTGTGTCCCAAAAGTGTGACACA 5517  
Qy 1021 GGTGCGTTCTGTATTAAGAACTTGAACCTTGAACCTTATTAATTAATCCGCTTGAACGG 1080  
Db 5518 GGTGCGTTCTGTATTAAGAACTTGAACCTTGAACCTTATTAATTAATCCGCTTGAACGG 5577  
Qy 1081 ATAATTGACAAAGAAATGTAAGTTCCTTATGTCCTCCGATTAATTAATCCGCTTGAACGG 1140  
Db 5578 ATAATTGACAAAGAAATGTAAGTTCCTTATGTCCTCCGATTAATTAATCCGCTTGAACGG 5637  
Qy 1141 CAATACGTCGGCTGTATGTAATCAAGACGGAAGGCGCACTTATACACCATATCATGAC 1200  
Db 5638 CAATACGTCGGCTGTATGTAATCAAGACGGAAGGCGCACTTATACACCATATCATGAC 5697  
Qy 1201 TATCAAGGTTCACTGATGCGCAACTGCAAGATGACAACTGATGATGTTAAACCCCCC 1260  
Db 5698 TATCAAGGTTCACTGATGCGCAACTGCAAGATGACAACTGATGATGTTAAACCCCCC 5757  
Qy 1261 GGGTATCATATGCGCAAACTATGAGAGAGCGGTCTCTAATGATTAACATCATGCAA 1320  
Db 5758 GGGTATCATATGCGCAAACTATGAGAGAGCGGTCTCTAATGATTAACATCATGCAA 5817



QY 1321 TGTTCCTTACGCGGGAATACCTTTAAGGCTAGTGGGAATTCAGTGTACTTATCA 1380  
Db 5818 TGTTCCTTACGCGGGAATACCTTTAAGGCTAGTGGGAATTCAGTGTACTTATCA 5877  
QY 1381 GAAGAAATATCTCAATACAGATTCTCAATATATATAACAGCAATCTTGATATCTCAAC 1440  
Db 5878 GAAGAAATATCTCAATACAGATTCTCAATATATATAACAGCAATCTTGATATCTCAAC 5937  
QY 1441 TGAGCTTGGGAATTCACAACTGATCAGTAATGCTTTGAATTAAGTTAGGAAAGCA 1500  
Db 5938 TGAGCTTGGGAATTCACAACTGATCAGTAATGCTTTGAATTAAGTTAGGAAAGCA 5997  
QY 1501 CAGAAAACCTAGACAAAGTCAATGTCAAACTGACTAGCACTGCTCTCATTTACTATAT 1560  
Db 5998 CAGAAAACCTAGACAAAGTCAATGTCAAACTGACTAGCACTGCTCTCATTTACTATAT 6057  
QY 1561 CGTTTGACTATCATCATCTCTTGTGTTTGTGTATACTTACCTGATTTCTAGACTACT 1620  
Db 6058 CGTTTGACTATCATCATCTCTTGTGTTTGTGTATACTTACCTGATTTCTAGACTACT 6117  
QY 1621 AATGTACAGCAAAAGCGCAACAAAACCTTATATATGCTTGGGAATATCTTGA 1680  
Db 6118 AATGTACAGCAAAAGCGCAACAAAACCTTATATATGCTTGGGAATATCTTGA 6177  
QY 1681 TCAGATGAGGCCACTACAAAATGTGAACACAGTGAAGAAAGGTTCCCTAATAG 1740  
Db 6178 TCAGATGAGGCCACTACAAAATGTGAACACAGTGAAGAAAGGTTCCCTAATAG 6237  
QY 1741 TAAATTTGTGAAAAGTTCTGTAGTCTGTCTCAGTTCAAGAGTTAAGAAAACTACCGGT 1800  
Db 6238 TAAATTTGTGAAAAGTTCTGTAGTCTGTCTCAGTTCAAGAGTTAAGAAAACTACCGGT 6297  
QY 1801 TGTATGATGACCAAGAGAGATATACGGGTAGAAGGTGAAGAGCGCCCTCAATTGC 1860  
Db 6298 TGTATGATGACCAAGAGAGATATACGGGTAGAAGGTGAAGAGCGCCCTCAATTGC 6357  
QY 1861 GAGCAGAGCTTACAACTCCGTTCTACCGCTTACCGCAACAGTCTCTCATCTGAGAC 1920  
Db 6358 GAGCAGAGCTTACAACTCCGTTCTACCGCTTACCGCAACAGTCTCTCATCTGAGAC 6417  
QY 1921 CGCGCCGTTAGCCAAAGTTGCTTAGAGATGAGAAAGAGGCAAAAATACATGCGGC 1980  
Db 6418 CGCGCCGTTAGCCAAAGTTGCTTAGAGATGAGAAAGAGGCAAAAATACATGCGGC 6477  
QY 1981 TTGATATTCGGGATTGCAATCTTATTTTAAACAGTATGACCTTGCTATATCTGAGCC 2040  
Db 6478 TTGATATTCGGGATTGCAATCTTATTTTAAACAGTATGACCTTGCTATATCTGAGCC 6537  
QY 2041 TCCCTTTTATATACAGGGGGCTAGCAACCTAGCCGATCTTGTAGGATACCGACTAGG 2100  
Db 6538 TCCCTTTTATATACAGGGGGCTAGCAACCTAGCCGATCTTGTAGGATACCGACTAGG 6597  
QY 2101 ATTTCCAGGGGCAAGAAAAGATTACATCTACACTTGGTTCATCAAGATGATAGAT 2160  
Db 6598 ATTTCCAGGGGCAAGAAAAGATTACATCTACACTTGGTTCATCAAGATGATAGAT 6657  
QY 2161 AGATATATTAAGCAAGTGGCCCTTGAATCTCCGTTGGGATTTAATATCTGAGACCA 2220  
Db 6658 AGATATATTAAGCAAGTGGCCCTTGAATCTCCGTTGGGATTTAATATCTGAGACCA 6717  
QY 2221 ATTTAGAACGCAATTAACATCTCTCTCTTATACAGATTATAGAGCTGCAACAAAGTGGG 2280  
Db 6718 ATTTAGAACGCAATTAACATCTCTCTCTTATACAGATTATAGAGCTGCAACAAAGTGGG 6777  
QY 2281 TGGGGGCACTATTCATGACCAAGATTAATAGGGGGATAGGCAAAAGCTCATTTGA 2340  
Db 6778 TGGGGGCACTATTCATGACCAAGATTAATAGGGGGATAGGCAAAAGCTCATTTGA 6837  
QY 2341 GATGATGCTAGTATGATCAATCATTTCTTCTGCTTGCATTTCAAGAACATCTGAATTTT 2400  
Db 6838 GATGATGCTAGTATGATCAATCATTTCTTCTGCTTGCATTTCAAGAACATCTGAATTTT 6897

QY 2401 ATCCCGGCGCTTACTACAGATCAAGTTGCACTGGAATACCTCATTTGACATGAGTCT 2460  
Db 6898 ATCCCGGCGCTTACTACAGATCAAGTTGCACTGGAATACCTCATTTGACATGAGTCT 6957  
QY 2461 ACCCATTAAGCTACACCCAAATGTAATATGTCGGAATGACAGATCACTCATTTCA 2520  
Db 6958 ACCCATTAAGCTACACCCAAATGTAATATGTCGGAATGACAGATCACTCATTTCA 7017  
QY 2521 TATCAGATTTTGAAGCTTGTGTCTCCGACATCTGCAACAGGAGGATTTCTTTCT 2580  
Db 7018 TATCAGATTTTGAAGCTTGTGTCTCCGACATCTGCAACAGGAGGATTTCTTTCT 7077  
QY 2581 ACTCTGGTTTCATCAACTGAGACGACCCAAAATGGAAGTTCTTGACGTGTAGTCA 2640  
Db 7078 ACTCTGGTTTCATCAACTGAGACGACCCAAAATGGAAGTTCTTGACGTGTAGTCA 7137  
QY 2641 ACTCCCTGGTTGTGATATAGTCTGTCTCGAAATCTACCGGAGACAGAGAAAGATTAT 2700  
Db 7138 ACTCCCTGGTTGTGATATAGTCTGTCTCGAAAGTCAAGAGACAGAGAAAGATTAT 7197  
QY 2701 AACTCAGCTGCCCTACCGGATGATACATGAGGTTAGGGTTGACGCGCACTACAC 2760  
Db 7198 AACTCAGCTGCCCTACCGGATGATACATGAGGTTAGGGTTGACGCGCACTACAC 7257  
QY 2761 GAAAAGACCTAGATGTCAACAATTATCGGGAATGAGTGGCCCACTACCCAGAGTA 2820  
Db 7258 GAAAAGACCTAGATGTCAACAATTATCGGGAATGAGTGGCCCACTACCCAGAGTA 7317  
QY 2821 GGGGGTGAATTTTATTTATGACAGCCGCTATAGTTTCTCAGTCTACGAGGGTTTAAACCC 2880  
Db 7318 GGGGGTGAATTTTATTTATGACAGCCGCTATAGTTTCTCAGTCTACGAGGGTTTAAACCC 7377  
QY 2881 AATTCAACAGTGAACCTGTACAGAAAGGAAATATGATATACAAACGATACATAGAC 2940  
Db 7378 AATTCAACAGTGAACCTGTACAGAAAGGAAATATGATATACAAACGATACATAGAC 7437  
QY 2941 ACATGCCAGATGAGCAAGACTACCAATTGGAATGCGCAAGTCTTGTATAGCTTGA 3000  
Db 7438 ACATGCCAGATGAGCAAGACTACCAATTGGAATGCGCAAGTCTTGTATAGCTTGA 7497  
QY 3001 CGGTTTGGTGGGAAACGATACAGAGGCTATCTTATATCAAGGTGTCAACATCTTTA 3060  
Db 7498 CGGTTTGGTGGGAAACGATACAGAGGCTATCTTATATCAAGGTGTCAACATCTTTA 7557  
QY 3061 GGGCAAGCCGGTACTGATCCGCGCAACAGTCACTCATGSGGGGCGAAGGC 3120  
Db 7558 GGGCAAGCCGGTACTGATCCGCGCAACAGTCACTCATGSGGGGCGAAGGC 7617  
QY 3121 AGAATTCACAGTAGGACATCTCATTTCTTGTATCAACAGAGGTATCATTTCTCT 3180  
Db 7618 AGAATTCACAGTAGGACATCTCATTTCTTGTATCAACAGAGGTATCATTTCTCT 7677  
QY 3181 CCGCGTTTATATCTTATGACAGTCAAGCAACAAACAGGCACTTGTATAGTCTTAT 3240  
Db 7678 CCGCGTTTATATCTTATGACAGTCAAGCAACAAACAGGCACTTGTATAGTCTTAT 7737  
QY 3241 ACATTTCAATGCTTCACTCGGCGCAGTAGTATCCCTTGCGAGGCTTCAAGAAAGTCCC 3300  
Db 7738 ACATTTCAATGCTTCACTCGGCGCAGTAGTATCCCTTGCGAGGCTTCAAGAAAGTCCC 7797  
QY 3301 AACTGTGTGTACTGAGTCTATACAGATCCATATCCCTTATATGAAGCC 3358  
Db 7798 AACTGTGTGTACTGAGTCTATACAGATCCATATCCCTTATATGAAGCC 7855

RESULT 7  
US-10-440-419-55  
; Sequence 55, Application US/10440419  
; Publication No US20030224017A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMBL, SIBA K.  
; APPLICANT: HUANG, ZHOUJI  
; TITLE OF INVENTION: RECOMBINANT NEWCASTLE DISEASE VIRUSES USEFUL AS

TITLE OF INVENTION: VACCINES OR VACCINE VECTORS  
FILE REFERENCE: 108172-00096  
CURRENT APPLICATION NUMBER: US/10/440,419  
CURRENT FILING DATE: 2003-05-19  
PRIOR APPLICATION NUMBER: 09/926,431  
PRIOR FILING DATE: 2002-03-06  
PRIOR APPLICATION NUMBER: PCT/US00/06700  
PRIOR FILING DATE: 2000-05-05  
PRIOR APPLICATION NUMBER: 60/381,462  
PRIOR FILING DATE: 2002-05-17  
PRIOR APPLICATION NUMBER: 60/171,072  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: 60/132,597  
PRIOR FILING DATE: 1999-05-05  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 55  
LENGTH: 15900  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Recombinant cDNA for NDV  
US-10-440-419-55

Query Match 99.7%; Score 3346.8; DB 6; Length 15900;  
Best Local Similarly 99.8%; Pred. No. 0;  
Matches 3351; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ACGGGTGAAGATCTGGATCCGGCTTGGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60  
DB 5212 ACGGGTGAAGATCTGGATCCGGCTTGGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 5271  
QY 61 TTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTTGCGCTGGCAGCTGAGTTG 120  
DB 5272 TTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTTGCGCTGGCAGCTGAGTTG 5331  
QY 121 CATCTGTCGGGCAAACTTCATGTATGGCAGGCTCTTGGCAAGTGGCTTAC 180  
DB 5332 CATCTGTCGGGCAAACTTCATGTATGGCAGGCTCTTGGCAAGTGGCTTAC 5391  
QY 181 AGGAGCAAAAGCGGTCAACATATACACTCATCCAGACAGGATCATCATAGTTAAGCT 240  
DB 5392 AGGAGCAAAAGCGGTCAACATATACACTCATCCAGACAGGATCATCATAGTTAAGCT 5451  
QY 241 CCTCCGCAATCTGCGCCAGGATTAAGAGCATGTGCGAAGAGCCCTTGGATGATCAAA 300  
DB 5452 CCTCCGCAATCTGCGCCAGGATTAAGAGCATGTGCGAAGAGCCCTTGGATGATCAAA 5511  
QY 301 CAGGACATTTGACCATTTTGTCTCAACCCCTTGGTGAATCTTATCGGTAGATCAAGAGTC 360  
DB 5512 CAGGACATTTGACCATTTTGTCTCAACCCCTTGGTGAATCTTATCGGTAGATCAAGAGTC 5571  
QY 361 TTGATCATCATCTGGAGGGGGGAGACAGGGGGCGCTTATAGGGGCTTATTTGGCGGTGT 420  
DB 5572 TTGATCATCATCTGGAGGGGGGAGACAGGGGGCGCTTATAGGGGCTTATTTGGCGGTGT 5631  
QY 421 GGCTCTTGGGGTTGCAACTGCGGCAAAATTAACAGCGCGCAGCTCTGATTAAGCCAA 480  
DB 5632 GGCTCTTGGGGTTGCAACTGCGGCAAAATTAACAGCGCGCAGCTCTGATTAAGCCAA 5691  
QY 481 ACAAAATGCTGCCAACATCTCCGACCTTAAAGAGAGCATTTGCCGAACCAATGAGGCTGT 540  
DB 5692 ACAAAATGCTGCCAACATCTCCGACCTTAAAGAGAGCATTTGCCGAACCAATGAGGCTGT 5751  
QY 541 GCATGAGCTCATGACGATTTATGCAACTAGCAGTGGCAGTTGGGAAGATGACGAGTT 600  
DB 5752 GCATGAGCTCATGACGATTTATGCAACTAGCAGTGGCAGTTGGGAAGATGACGAGTT 5811  
QY 601 TGTAAATGACCAATTTTATATAAAGAGCTCAGAAATTAAGATGATCAAAATTTGACAGCA 660  
DB 5812 TGTAAATGACCAATTTTATATAAAGAGCTCAGAAATTAAGATGATCAAAATTTGACAGCA 5871  
QY 661 AGTTGTGATGAGCTCAACCTGTATCTTAACCGAATTGACTACAGTATTGGACCACAAAAT 720

DB 5872 AGTTGTGATGAGCTCAACCTGTATCTTAACCGAATTGACTACAGTATTGGACCACAAAAT 5931  
QY 721 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGA 780  
DB 5932 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGA 5991  
QY 781 TATGATTAATCTTATGACTAAGTATGATGAGGAAACAATCAACTGAGCTCATTAATCGG 840  
DB 5992 TATGATTAATCTTATGACTAAGTATGATGAGGAAACAATCAACTGAGCTCATTAATCGG 6051  
QY 841 TAGCGCTTATATACCGGTAACCTTATCTATAGACTCAAGACTCACTTGGGTAT 900  
DB 6052 TAGCGCTTATATACCGGTAACCTTATCTATAGACTCAAGACTCACTTGGGTAT 6111  
QY 901 ACAGTAATCTTACCTTCACTGAGTGGAACTTAATATATGTCGACCACTTGGAAAC 960  
DB 6112 ACAGTAATCTTACCTTCACTGAGTGGAACTTAATATATGTCGACCACTTGGAAAC 6171  
QY 961 CTTATCCGTAAAGCAACAAGGGGATTTGCTGGCACTTGTCCCAAAAGTGTGACACA 1020  
DB 6172 CTTATCCGTAAAGCAACAAGGGGATTTGCTGGCACTTGTCCCAAAAGTGTGACACA 6231  
QY 1021 GGTCGGTCTGTATGAGAAAGCTTGACACCTCATCTGATATAGAACTGACTAGATT 1080  
DB 6232 GGTCGGTCTGTATGAGAAAGCTTGACACCTCATCTGATATAGAACTGACTAGATT 6291  
QY 1081 ATATTGACAAAGATATGATTAAGTTCCCTATGTCCTCTGATTTATTCCTGCTTGAACGG 1140  
DB 6292 ATATTGACAAAGATATGATTAAGTTCCCTATGTCCTCTGATTTATTCCTGCTTGAACGG 6351  
QY 1141 CAATACGCGCTGTATGATCTAAGAACCCGAAGGGGCACTTATCAGCATATGATGAC 1200  
DB 6352 CAATACGCGCTGTATGATCTAAGAACCCGAAGGGGCACTTATCAGCATATGATGAC 6411  
QY 1201 TATCAAAAGTTCACTGATCCGCAACCTGCAAGATGACAAACATGATGATGATTAACCCGCC 1260  
DB 6412 TATCAAAAGTTCACTGATCCGCAACCTGCAAGATGACAAACATGATGATGATTAACCCGCC 6471  
QY 1261 GGGTATCATATCGCAAAACTATGAGAGAGCGGTGTCTCTAATGATTAACAATGATGACAA 1320  
DB 6472 GGGTATCATATCGCAAAACTATGAGAGAGCGGTGTCTCTAATGATTAACAATGATGACAA 6531  
QY 1321 TGTATTATCTTAAAGCGGATTAACCTTAAAGCTCAGTGGGAAATTCATGATTAATCA 1380  
DB 6532 TGTATTATCTTAAAGCGGATTAACCTTAAAGCTCAGTGGGAAATTCATGATTAATCA 6591  
QY 1381 GAGGAATATCTCAATTAAGAAATCTCAAGTAATTAATTAACAGGCAATCTGTATCTCAAC 1440  
DB 6592 GAGGAATATCTCAATTAAGAAATCTCAAGTAATTAATTAACAGGCAATCTGTATCTCAAC 6651  
QY 1441 TGAGCTTGGGATGTCAACAACCTGATCAGTAAATGCTTTGAATTAAGTAAAGAAACAA 1500  
DB 6652 TGAGCTTGGGATGTCAACAACCTGATCAGTAAATGCTTTGAATTAAGTAAAGAAACAA 6711  
QY 1501 CAGAAAACTAGCAAAAGTCAATGCAACTGACTAGACATCTGCTCTCATTAATCTATAT 1560  
DB 6712 CAGAAAACTAGCAAAAGTCAATGCAACTGACTAGACATCTGCTCTCATTAATCTATAT 6771  
QY 1561 CGTTTGAATCATATCTCTGTTTGGTATTAATTAAGCTGATTAAGCTGATTAAGCTGAT 1620  
DB 6772 CGTTTGAATCATATCTCTGTTTGGTATTAATTAAGCTGATTAAGCTGATTAAGCTGAT 6831  
QY 1621 AATGTACAAGCAAAAGCGGCAACAAACCTTATTAATGCTTGGAAATATATCTTGA 1680  
DB 6832 AATGTACAAGCAAAAGCGGCAACAAACCTTATTAATGCTTGGAAATATATCTTGA 6891  
QY 1681 TCAGATGAGGCACTTACAATAATTTGTAACACAGATGAGGACGAAGGTTTCCCTAATAG 1740  
DB 6892 TCAGATGAGGCACTTACAATAATTTGTAACACAGATGAGGACGAAGGTTTCCCTAATAG 6951  
QY 1741 TAATTTGTGAAAGTTCTGTAGTCTGTCAAGTTCAAGAGTTTAAGAAAACTACCGGT 1800

Db 6952 TAATTTGTGAAAGTTCTGTAGTCTGTCACTTCAAGAGTTAAAGAAAACTACGGCT 7011  
Qy 1801 TGTAGATGACCAAGAGAGATATACGGGTAGAACGTTAAGAGAGCCGCCCTCAATTC 1860  
Db 7012 TGTAGATGACCAAGAGAGATATACGGGTAGAACGTTAAGAGAGCCGCCCTCAATTC 7071  
Qy 1861 GAGCCAGGCTTACACACTCCGTTCTACCGCTTACCGGACCAAGCTCTCAATCAGTGAAC 1920  
Db 7072 GAGCCAGGCTTACACACTCCGTTCTACCGCTTACCGGACCAAGCTCTCAATCAGTGAAC 7131  
Qy 1921 CGGCGCGTTAGCCAAAGTTGCGTTAGAGATGAAAGAGAGGAAAAAATACATGGGCG 1980  
Db 7132 CGGCGCGTTAGCCAAAGTTGCGTTAGAGATGAAAGAGAGGAAAAAATACATGGGCG 7191  
Qy 1981 TTGATATTCGGATTTGCAATCTTATTTCTTAAACAGTAGTACCTTGGCTATATCTGAGCC 2040  
Db 7192 TTGATATTCGGATTTGCAATCTTATTTCTTAAACAGTAGTACCTTGGCTATATCTGAGCC 7251  
Qy 2041 TCCCTTTTATATAGCATGGGGGCTAGCACACTAGCCGCTTGTAGGCAATCCGACTAGG 2100  
Db 7252 TCCCTTTTATATAGCATGGGGGCTAGCACACTAGCCGCTTGTAGGCAATCCGACTAGG 7311  
Qy 2101 ATTTCCAGGGAGAGAAAGAAATTAACATCTCACTTGGCTTCAATCAAGATGTAGTAT 2160  
Db 7312 ATTTCCAGGGAGAGAAAGAAATTAACATCTCACTTGGCTTCAATCAAGATGTAGTAT 7371  
Qy 2161 AGGATATATAGCAAGTGGCCCTTGAAGTCTCGTTGGCAATGTAAATATCTGAGACCA 2220  
Db 7372 AGGATATATAGCAAGTGGCCCTTGAAGTCTCGTTGGCAATGTAAATATCTGAGACCA 7431  
Qy 2221 ATTAATGAAAGCAATMACATCTCTCTTATCAGATTAATGAGAGCTGCAACACAGTGGG 2280  
Db 7432 ATTAATGAAAGCAATMACATCTCTCTTATCAGATTAATGAGAGCTGCAACACAGTGGG 7491  
Qy 2281 TGGGGGGACCTATCCATGACCCGATTAATATAGGGGGGATAGGCAAGAACTCATTTGA 2340  
Db 7492 TGGGGGGACCTATCCATGACCCGATTAATATAGGGGGGATAGGCAAGAACTCATTTGA 7551  
Qy 2341 GATGATGCTATGATGTCATCATTCATTCCTCTGATTTCAAGAACATCTGAATTTT 2400  
Db 7552 GATGATGCTATGATGTCATCATTCATTCCTCTGATTTCAAGAACATCTGAATTTT 7611  
Qy 2401 ATCCGGCGGCTTACAGATCAGATTCAGTTCACCTGCAATACCTCATTTGACATGAGTCT 2460  
Db 7612 ATCCGGCGGCTTACAGATCAGATTCAGTTCACCTGCAATACCTCATTTGACATGAGTCT 7671  
Qy 2461 ACCCATTAAGTCTACACCCATATGTAAATTTGTCTGATGACAGATCATCTCATTTCA 2520  
Db 7672 ACCCATTAAGTCTACACCCATATGTAAATTTGTCTGATGACAGATCATCTCATTTCA 7731  
Qy 2521 TATCAGATTTAGCATTTGGTGTCTCGGACATCTGCAACAGGAGGATTTCTTTTCT 2580  
Db 7732 TATCAGATTTAGCATTTGGTGTCTCGGACATCTGCAACAGGAGGATTTCTTTTCT 7791  
Qy 2581 ACTCTGCGTTCACTCAACCTGAGACAGACCCAAAATCGAAGTCTTGTGACGTGAGTGA 2640  
Db 7792 ACTCTGCGTTCACTCAACCTGAGACAGACCCAAAATCGAAGTCTTGTGACGTGAGTGA 7851  
Qy 2641 ACTCTCTGCGTTGTGATGTCTGTCTCGAAAGTCAACGAGACAGAGAAAGATTTAT 2700  
Db 7852 ACTCTCTGCGTTGTGATGTCTGTCTCGAAAGTCAACGAGACAGAGAAAGATTTAT 7911  
Qy 2701 AACTCAGCTGTCTTACGCGGATGTATCATGAGGAGTTTACGGGTTTCGACGCGCAATACAC 2760  
Db 7912 AACTCAGCTGTCTTACGCGGATGTATCATGAGGAGTTTACGGGTTTCGACGCGCAATACAC 7971  
Qy 2761 GAAAAGACCTAGATGTCACAACTTATTCGGGAGCTGGGTGCGCAACTACCCAGAGATA 2820  
Db 7972 GAAAAGACCTAGATGTCACAACTTATTCGGGAGCTGGGTGCGCAACTACCCAGAGATA 8031  
Qy 2821 GGGGGGTGAATCTTTTATTTAGACGCGCGGTATGATTTCTCACTACGAGAGGTTAAAAACC 2880  
Db 8032 GGGGGGTGAATCTTTTATTTAGACGCGCGGTATGATTTCTCACTACGAGAGGTTAAAAACC 8091

Qy 2881 AATTACCCAGTGAACCTGTACAGAGAAAGGAAATATGTGATATACAGCGATACATGAC 2940  
Db 8092 AATTACCCAGTGAACCTGTACAGAGAAAGGAAATATGTGATATACAGCGATACATGAC 8151  
Qy 2941 ACATGCCCAATGAGCAAGATATACAGATTTGGAATGGCAGTCTTGTATTAAGCTTGA 3000  
Db 8152 ACATGCCCAATGAGCAAGATATACAGATTTGGAATGGCAGTCTTGTATTAAGCTTGA 8211  
Qy 3001 CGGTTTGTGGGAAAGCAATACAGAGCTATCTTATCTATCAAGTGTCAACATCTTTA 3060  
Db 8212 CGGTTTGTGGGAAAGCAATACAGAGCTATCTTATCTATCAAGTGTCAACATCTTTA 8271  
Qy 3061 GGGGAGAACCCGTAAGTACTGTACCGGCCAACACAGTCACTCATAGGGGGCGAAGGC 3120  
Db 8272 GGGGAGAACCCGTAAGTACTGTACCGGCCAACACAGTCACTCATAGGGGGCGAAGGC 8331  
Qy 3121 AGAATTTCTACAGTAGGAGCATCTCATTTCTTTGTATCAAGAGGGGTATCATCTTCT 3180  
Db 8332 AGAATTTCTACAGTAGGAGCATCTCATTTCTTTGTATCAAGAGGGGTATCATCTTCT 8391  
Qy 3181 CCGCGTTATTAATATCTCATAGCAGTACAGCAAAACAGGCACTTTCATAGTCTTAT 3240  
Db 8392 CCGCGTTATTAATATCTCATAGCAGTACAGCAAAACAGGCACTTTCATAGTCTTAT 8451  
Qy 3241 ACATTCATGCTTCACTCGGCCAGTAGTATCCCTTGCCAGGCTTACAGAAATGCCCC 3300  
Db 8452 ACATTCATGCTTCACTCGGCCAGTAGTATCCCTTGCCAGGCTTACAGAAATGCCCC 8511  
Qy 3301 AACTGTGTGTACTGAGATCTATACAGATTCATATCCCTTAATCTTATTAAGAAC 3358  
Db 8512 AACTGTGTGTACTGAGATCTATACAGATTCATATCCCTTAATCTTATTAAGAAC 8569

RESULT 8  
US-10-440-419-56  
; Sequence 56, Application US/10440419  
; Publication No. US20030224017A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMAL, SIBA K.  
; TITLE OF INVENTION: RECOMBINANT NEWCASTLE DISEASE VIRUSES USERFUL AS  
; FILE REFERENCE: 108172-00096  
; CURRENT APPLICATION NUMBER: US/10/440, 419  
; PRIOR FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: 09/926, 431  
; PRIOR FILING DATE: 2002-03-06  
; PRIOR APPLICATION NUMBER: PCT/US00/06700  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 60/381, 462  
; PRIOR FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: 60/171, 072  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: 60/132, 597  
; PRIOR FILING DATE: 1999-05-05  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 56  
; LENGTH: 15882  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant cDNA for NDV  
US-10-440-419-56  
Query Match 95.2%; Score 3198; DB 6; Length 15882;  
Best Local Similarity 97.0%; Pred. No. 0;  
Matches 3258; Conservative 0; Mismatches 100; Indels 0; Gaps 0;  
Qy 1 ACGGGTAGAAGATTCTGATTCGCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60  
Db 4498 ACGGGTAGAAGATTCTGATTCGCGGTTGGCGCCCTTCTAGGTGCAAGATGGGCCCCAGACC 4557

QY 61 TTCTACCAAGAACCCAGACCTTATGATGCTGACTATTCGGGGTTCGGTGCATCGAGTTG 120  
DB 4558 TTCTACCAAGAACCCAGACTTACTATGATGCTGACTGCTCGAGTCCGGCTGGTACTGAGTTG 4617  
QY 121 CATCTGTCGGGCAAACTCCATTTGATGTCAGGGCTCTTGTCAGCTGCAGGAATTTGGTTAC 180  
DB 4618 CATCTGTCGGGCAAACTCCATTTGATGTCAGGGCTCTTGTCAGCTGCAGGAATTTGGTTAC 4677  
QY 181 AGGAGACAAAGCCGTCAACATATACCTCATCCAGACAGATCAATCATAGTTAAGCT 240  
DB 4678 AGGAGACAAAGCACTCAACATATACCTCATCCAGACAGATCAATCATAGTTAAGCT 4737  
QY 241 CTTCCCGAATCTGCCCCAAGATTAAGAGCATGTGCGAAAGCCCCCTTGATGATCAAA 300  
DB 4738 CTTCCCGAATCTGCCCCAAGATTAAGAGCATGTGCGAAAGCCCCCTTGATGATCAAA 4797  
QY 301 CAGGACCTTGAACCACTTTGCTCAACCCCTTGTTGATCTCTATCCGTAGATTAAGAGTGC 360  
DB 4798 CAGGACCTTGAACCACTTTGCTCAACCCCTTGTTGATCTCTATCCGTAGATTAAGAGTGC 4857  
QY 361 TGTGACTACATCTGAGGGGAGACAGGGGCGCTTATAGGCGCCATTTATTTGGCGGTGT 420  
DB 4858 TGTGACTACATCTGAGGGGAGACAGGAAAGCTTTTATAGGCGCCATTTATTTGGCGGTGT 4917  
QY 421 GGGCTTTGGGGTTGCAACTGCGCGCAAAATTAACGCGCGCAGCTCTGATACAAAGCAA 480  
DB 4918 GGGCTTTGGGGTTGCAACTGCGCGCAAAATTAACGCGCGCAGCTCTGATACAAAGCAA 4977  
QY 481 ACAAAATGCTGCCCAACATCTCTCCGACTTTAAAGAGATGTCGCCCAACCAATGAGGTGT 540  
DB 4978 ACAAAATGCTGCCCAACATCTCTCCGACTTTAAAGAGATGTCGCCCAACCAATGAGGTGT 5037  
QY 541 GCATGAGGTGACTGACGGATTTATCGCAACTAGCAGTGGAGTTGGGAAGATGCAGAGTT 600  
DB 5038 GCATGAGGTGACTGACGGATTTATCGCAACTAGCAGTGGAGTTGGGAAGATGCAGAGTT 5097  
QY 601 TGTTAATGACCAATTTAATAAACAAGCTCAGGAATTGACTGATCAAAATTTGCACAGCA 660  
DB 5098 TGTTAATGACCAATTTAATAAACAAGCTCAGGAATTGACTGATCAAAATTTGCACAGCA 5157  
QY 661 AGTTGGTGTAGAGTCAACCTGTATCTTAACCGAATTTGACTACAGTATTTGGACCAAAAT 720  
DB 5158 AGTTGGTGTAGAGTCAACCTGTATCTTAACCGAATTTGACTACAGTATTTGGACCAAAAT 5217  
QY 721 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTCAATCAATGCTGATGGAAA 780  
DB 5218 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTCAATCAATGCTGATGGAAA 5277  
QY 781 TATGATTAATCTTATTTGACTAAGTTAGGTAGGGAAACAATCAACTGACTATTAATCGG 840  
DB 5278 TATGATTAATCTTATTTGACTAAGTTAGGTAGGGAAACAATCAACTGACTATTAATCGG 5337  
QY 841 TAGCGGCTTATATCCGGTAAACCTTATTCATAGACTCACAGACTCAACTCTTGGGTAT 900  
DB 841 TAGCGGCTTATATCCGGTAAACCTTATTCATAGACTCACAGACTCAACTCTTGGGTAT 5338  
QY 901 ACAGGTAACTCTACCTTCAAGCGGGAACCTTAATATATGCGTGCACCTACTTGGAAAC 960  
DB 5398 ACAGGTAACTCTACCTTCAAGCGGGAACCTTAATATATGCGTGCACCTACTTGGAAAC 5457  
QY 961 CTTATCCGTAAAGCAACAAGGGGATTTGGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
DB 5458 CTTATCCGTAAAGCAACAAGGGGATTTGGCTCGGCACTTGTCCCAAAAGTGTGACACA 5517  
QY 1021 GGTGCGTTCTGTGATAGAGAACTTGAACCTCTACTGTATAGAAACTGACTTAAATTT 1080  
DB 5518 GGTGCGTTCTGTGATAGAGAACTTGAACCTCTACTGTATAGAAACTGACTTAAATTT 5577  
QY 1081 AATATTGACAAAGATAGTAAGTTCCTATGTCCTGCTGATTTATTCCTGCTTGAGCGG 1140  
DB 5578 AATATTGACAAAGATAGTAAGTTCCTATGTCCTGCTGATTTATTCCTGCTTGAGCGG 5637

QY 1141 CAATACGTGGGCTGTGATTTGATCTCAAGACCGAAGGGCACTTACTACACATACATGAC 1200  
DB 5638 CAATACATCGGCTGTGATTTGATCTCAAGACCGAAGGGCACTTACTACACATACATGAC 5697  
QY 1201 TATCAAGGTTCACTCATCCGCAACTGCAAGATGACAAACATGTGATGTGTTAAACCCCC 1260  
DB 5698 TATCAAGGCTCACTCATCCGCAACTGCAAGATGACAAACATGTGATGTGTTAAACCCCC 5757  
QY 1261 GGGTATCATATCGCAAAACTATGAGAGACCGTGTCTTAATAGATTAACAATCATGACAA 1320  
DB 5758 GGGTATCATATCGCAAAACTATGAGAGACCGTGTCTTAATAGATTAACAATCATGACAA 5817  
QY 1321 TGTTTTATCTTATAGCGGGATTAACCTTTAAGGCTCAGTGGGGAAATTCAGTAACTTATCA 1380  
DB 5818 TGTTTTATCTTATAGCGGGATTAACCTTTAAGGCTCAGTGGGGAAATTCAGTAACTTATCA 5877  
QY 1381 GAAGAAATATCTCAATACAAAGATTTCTAAGTAAATTAACAAGGCAATCTTGATATCTCAAC 1440  
DB 5878 GAAGAAATATCTCAATACAAAGATTTCTAAGTAAATTAACAAGGCAATCTTGATATCTCAAC 5937  
QY 1441 TGAGCTTGGGAATGTCAAACAATCGATCAGTAATGCTTTGAATTAAGTAAAGAAACAA 1500  
DB 5938 TGAGCTTGGGAATGTCAAACAATCGATCAGTAATGCTTTGAATTAAGTAAAGAAACAA 5997  
QY 1501 CAGAAAATTAAGCAAAATGATCAATGCAAACTGACTAGACATCTGCTCTCAATTAATAT 1560  
DB 5998 CAGAAAATTAAGCAAAATGATCAATGCAAACTGACTAGACATCTGCTCTCAATTAATAT 6057  
QY 1561 GGTTTGACTATCATCTCTGTTGTTTGGTATTAAGTAAAGCTAATTTAGACATGCTACT 1620  
DB 6058 GGTTTGACTATCATCTCTGTTGTTTGGTATTAAGTAAAGCTAATTTAGACATGCTACT 6117  
QY 1621 AATGTACAAACAAAGGCGCAACAAAAACCTTATATGCTTGGGAATTAATCTTGA 1680  
DB 6118 AATGTATTAACAAAGGCGCAACAAAGGCTTATATGCTTGGGAATTAATCTTGA 6177  
QY 1681 TCAATGATAGGCCATCTCAAAAAATGTGAACAACAGATAGAGAAAGAAAGTTCCCTAATAG 1740  
DB 6178 TCAATGATAGGCCATCTCAAAAAATGTGAACAACAGATAGAGAAAGAAAGTTCCCTAATAG 6237  
QY 1741 TAAATTTGTGAAGGTTCTGAGTGTCTGAGTTCAGAGTTAAGAAATAAATCTACCGGT 1800  
DB 6238 TAAATTTGTGAAGGTTCTGAGTGTCTGAGTTCAGAGTTAAGAAATAAATCTACCGGT 6237  
QY 1801 TGTAGATGACCAAAAGACGATATACGGGTAGAAACGGTAAAGAGGCCGCCCTCAATTGC 1860  
DB 6298 TGTAGATGACCAAAAGACGATATACGGGTAGAAACGGTAAAGAGGCCGCCCTCAATTGC 6357  
QY 1861 GAGCCAGGCTTCAACAACCTTCCTTCTACCGCTTACCGCAACAAGTCTCAATATATGAC 1920  
DB 6358 GAGCCAGGCTTCAACAACCTTCCTTCTACCGCTTACCGCAACAAGTCTCAATATATGAC 6417  
QY 1921 CGGCGGTTAGGCAAGTTGGTTAGAGAAATGATGAAGAAAGAGGCAAAAATPACATGCGC 1980  
DB 6418 CGGCGGTTAGGCAAGTTGGTTAGAGAAATGATGAAGAAAGAGGCAAAAATPACATGCGC 6477  
QY 1981 TTGATATTCGGATTGCAATCTTATTTAAAGATGAGCTTGGCTATATCTGTAGCC 2040  
DB 6478 TTGATATTCGGATTGCAATCTTATTTAAAGATGAGCTTGGCTATATCTGTAGCC 6537  
QY 2041 TCCCTTTATATAGCATGGGGGCTAGACACCTTAGCGATTTGTAGGCATACCGACTAGG 2100  
DB 6538 TCCCTTTATATAGCATGGGGGCTAGACACCTTAGCGATTTGTAGGCATACCGACTAGG 6597  
QY 2101 AATTTCCAGGCAAGAAAGATTAACATCTCACTTGGTTCCATCAATCAAGATAGTAGAT 2160  
DB 6598 AATTTCCAGGCAAGAAAGATTAACATCTCACTTGGTTCCATCAATCAAGATAGTAGAT 6657  
QY 2161 AGGATATTAAGCAAGTGGCTTGAAGTCTCCGTTGGCAATTTGTTAAATCTGAGACACA 2220  
DB 6658 AGGATATTAAGCAAGTGGCTTGAAGTCTCCGTTGGCAATTTGTTAAATCTGAGACACA 6717  
QY 2221 AATATGAACGCAATTAACATCTCTCTTATCAAGATTAATGAGCTGCAAAACAAGTGGG 2280

Db 6718 ATTATGAACGCAATPAACATCTCTCTATAGATTAATGAGCTGCGCAACACGCGGG 6777  
Qy 2281 TGGGGGGGCACTTATCCATGACCCAGATTAATATAGGGGGGATAGGCAAGAACTCATTTGA 2340  
Db 6778 TGGGGGGGCACTTATCCATGACCCAGATTTTATCGGGGGGATAGGCAAGAACTCATTTGA 6837  
Qy 2341 GATGATGTAGTGAATGTCACATCATATTCCTCTGCAATTCAGAAATCTGAATTTT 2400  
Db 6838 GATGATGTAGTGAATGTCACATCATATTCCTCTGCAATTCAGAAATCTGAATTTT 6897  
Qy 2401 ATCCCGGCGCTTACTACAGATCAGGTGCACTGCAATACCTCATTTGACATGAGTCT 2460  
Db 6898 ATCCCGGCGCTTACTACAGATCAGGTGCACTGCAATACCTCATTTGACATGAGTCT 6957  
Qy 2461 ACCCATTAATGCTCAACCATTAATGTAATTTGTCGATGAGATCACTACATTTCA 2520  
Db 6958 ACCCATTAATGCTCAACCATTAATGTAATTTGTCGATGAGATCACTACATTTCA 7017  
Qy 2521 TATCAGTATTTAGCACTTGCTGCTCCGCAATCTGCAAGAGGGATTTCTTTTCT 2580  
Db 7018 CATCAGTATTTAGCACTTGCTGCTCCGCAATCTGCAAGAGGGATTTCTTTTCT 7077  
Qy 2581 ACTCTGCGTTCCATCAACCTGAGCAACCCAAATCGAAAGTCTTGCACTGTGAGTCA 2640  
Db 7078 ACTCTGCGTTCCATCAACCTGAGTGAACCCAAATCGAAAGTCTTGCACTGTGAGTCA 7137  
Qy 2641 ACTCCCGGCTTGAATGATGCTGCTCGAAAGTCAAGGAGACAGAGAGAAAGATTTAT 2700  
Db 7138 ACTCCCTTAAGTGTGATGATGCTGCTCGAAAGTCAAGGAGACAGAGAGAAATTTAT 7197  
Qy 2701 AACTCAGCTGTCCTTACCGGATGGTATAGGGAGTTAGGGTTTGAAGGCGCATGACAC 2760  
Db 7198 AACTCAGCTGTCCTTACCGGATGGTATAGGGAGTTAGGGTTTGAAGGCGCATGACAC 7257  
Qy 2761 GAAAGAGACTAGATGTCACAACTTATTCGGGAGCTGGGTGGCCACTACCCAGAGATA 2820  
Db 7258 GAAAGAGACTAGATGTCACAACTTATTCGGGAGCTGGGTGGCCACTACCCAGAGATA 7317  
Qy 2821 GGGGGTGAATCTTTTATGACAGCGCGCTATGTTCTCAAGTCTAGGGGGTTAAACCC 2880  
Db 7318 GGGGGTGAATCTTTTATGACAGCGCGCTATGTTCTCAAGTCTAGGGGGTTAAACCC 7377  
Qy 2881 AATTCAACCCAGTGAACCTGTACAGAGAGGAAATATGATATATACAGCATATCATGAC 2940  
Db 7378 AATTCAACCCAGTGAACCTGTACAGAGAGGAAATATGATATATACAGCATATCATGAC 7437  
Qy 2941 ACATGCCAGATGACAGCAAGACTACAGATTCGAATGGCCAAGTCTTCGTATTAAGCTTGA 3000  
Db 7438 ACATGCCAGATGACAGCAAGACTACAGATTCGAATGGCCAAGTCTTCGTATTAAGCTTGA 7497  
Qy 3001 CGGTTTGGTGGGAAAGCATACAGAGGCTATCTTATCTATCAAGGTCTCAACATCTTGG 3060  
Db 7498 CGGTTTGGTGGGAAAGCATACAGAGGCTATCTTATCTATCAAGGTCTCAACATCTTGG 7557  
Qy 3061 GGGCAAGACCGGATCTGATCTACCGCCCAACAGTCACTGATGGGGGCGAAGGC 3120  
Db 7558 GGGCAAGACCGGATCTGATCTACCGCCCAACAGTCACTGATGGGGGCGAAGGC 7617  
Qy 3121 AGAATTTCTCAAGTAGGACATCTCATTTCTTGTATCAACGAGGCTCATCATCTTCTCT 3180  
Db 7618 AGAATTTCTCAAGTAGGACATCTCATTTCTTGTATCAACGAGGCTCATCATCTTCTCT 7677  
Qy 3181 CCGCGGTTATATATCTATGACAGTCAAGCAAGAAACAGCCATCTTCATAGTCTTAT 3240  
Db 7678 CCGCGGTTATATATCTATGACAGTCAAGCAAGAAACAGCCATCTTCATAGTCTTAT 7737  
Qy 3241 ACATTCATGCTTCACTCGGCAAGTAGTATCCCTGCGAGGCTTCAGCAAGATGCCCC 3300  
Db 7738 ACATTCATGCTTCACTCGGCAAGTAGTATCCCTGCGAGGCTTCAGCAAGATGCCCC 7797  
Qy 3301 AACTCGTGTCTTACTGAGTCTATACAGATCCATATCCCTATCTTCTATGAAGCC 3358  
|||||

Db 7798 AACTCGTGTCTTACTGAGTCTATACAGATCCATATCCCTAATCTTCTATGAAGCC 7855  
RESULT 9  
US-09-881-457A-1  
; Sequence 1, Application US/09881457A  
; Patent No. US20020081316A1  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D  
; APPLICANT: Cook, Stephanie M  
; APPLICANT: Mild, Marsha A  
; TITLE OF INVENTION: No. US20020081316A1el Avian Herpes Virus and Uses Thereof  
; FILE REFERENCE: ST0105K10KOK  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US/09/881,457A  
; PRIOR FILING DATE: 1999-10-25  
; PRIOR APPLICATION NUMBER: 08/426,352  
; PRIOR FILING DATE: 1999-10-25  
; PRIOR APPLICATION NUMBER: 08/804,372  
; PRIOR FILING DATE: 1997-02-21  
; PRIOR APPLICATION NUMBER: PCT/US95/10245  
; PRIOR FILING DATE: 1995-08-09  
; PRIOR APPLICATION NUMBER: 08/663,566  
; PRIOR FILING DATE: 1996-06-13  
; PRIOR APPLICATION NUMBER: 08/288,065  
; PRIOR FILING DATE: 1994-08-09  
; PRIOR APPLICATION NUMBER: PCT/US93/05681  
; PRIOR FILING DATE: 1993-06-14  
; PRIOR APPLICATION NUMBER: 08/023,610  
; PRIOR FILING DATE: 1993-02-26  
; PRIOR APPLICATION NUMBER: 07/898,087  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 3570  
; TYPE: DNA  
; ORGANISM: Newcastle disease virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1194)..(2888)  
; OTHER INFORMATION: NDV Fusion Protein  
; NAME/KEY: misc\_feature  
; LOCATION: (1355)  
; OTHER INFORMATION: n = any nucleotide  
US-09-881-457A-1  
Query Match 50.7%; Score 1701.6; DB 3; Length 3570;  
Beat Local Similarity 98.4%; Fred. No. 0;  
Matches 1749; Conservative 0; Mismatches 25; Indels 3; Gaps 3;  
Qy 16 TGGATCCGGGTTGGGCGCCTCAGGTGCAAGTGGGCTCCAGACCTTCTACCAAGAACCC 75  
Db 1199 TGGATCCGGGTTGGGCGCCTCAGGTGCAAGTGGGCTCCAGACCTTCTACCAAGAACCC 1258  
Qy 76 AGACCTATGATGCTGATATCCGGGTTGCGCTGGCACTGAGTTGATCTGTCCGGCAAA 135  
Db 1259 AGACCTATGATGCTGATATCCGGGTTGCGCTGGCACTGAGTTGATCTGTCCGGCAAA 1318  
Qy 136 CTCATTTGATGCGAGGCTCTTTGCAAGCTGCAAGAAATGTTGTTTAAAGAGACAAAGCCGT 195  
Db 1319 CTCATTTGATGCGAGGCTCTTTGCAAGCTGCAAGAAATGTTGTTTAAAGAGACAAAGCAAT 1377  
Qy 196 CAACATATACCTCATCCAGACAGATCATCATAGTTAAGTCTCTCCGAATCTGCC 255  
Db 1378 CAACATATACCTCATCCAGACAGG-TCAATCAT-TTAAAGTCTCTCCGAATCTGCC 1435  
Qy 256 CAAGATTAAGAGGCGATGCGAAAGCCCTTGTATGATCAACAGAGCAATTGACAC 315  
Db 1436 AAAGATTAAGAGGCGATGCGAAAGCCCTTGTATGATCAACAGAGCAATTGACAC 1495  
Qy 316 TTTGCTCACCCCTCTGTTGACTCTATCCGTATAGATTAAGAGTGTGACTACATCTGG 375  
Db 1496 TTTGCTCACCCCTCTGTTGACTCTATCCGTATAGATTAAGAGTGTGACTACATCTGG 1555



QY 376 AGGGGGAGACAGGGGGCCTTATAGCGCCATATTGGCGGTGTGCTTTGGGGTTGC 435  
DB 1556 AGGGGGAGACAGGGGGCCTTATAGCGCCATATTGGCGGTGTGCTTTGGGGTTGC 1615  
QY 436 AACTGCCGCAAAATTAACAGGGGGCGGAGCTGTATCAACGCCAAACAAATGCTGCCAA 495  
DB 1616 AACTGCCGCAAAATTAACAGGGGGCGGAGCTGTATCAACGCCAAACAAATGCTGCCAA 1675  
QY 496 CATCTCCGACTTAAAGAGACATTTGCGCAACCAATGAGCTGTGCATGAGTCACTGA 555  
DB 1676 CATCTCCGACTTAAAGAGACATTTGCGCAACCAATGAGCTGTGCATGAGTCACTGA 1735  
QY 556 CGGATTTCCGACATGAGGAGTTGGGAAAGATGACAGATTTGTTAAATGACCAATT 615  
DB 1736 CGGATTTCCGACATGAGGAGTTGGGAAAGATGACAGATTTGTTAAATGACCAATT 1795  
QY 616 TAATTAACAGCTCAGAAATTAGACTGCATCAAAATTGCAAGAAAGTGTGTAAGACT 675  
DB 1796 TAATTAACAGCTCAGAAATTAGACTGCATCAAAATTGCAAGAAAGTGTGTAAGACT 1855  
QY 676 CAACCTTACCTTAACCGAATTTGATGATGCGACCAAAATCACTTACCTGCTT 735  
DB 1856 CAACCTTACCTTAACCGAATTTGATGATGCGACCAAAATCACTTACCTGCTT 1915  
QY 736 AAACAAGCTGATTTAGGACCTTTTCAATCTAGCTGTGGAATAATGATTAATT 795  
DB 1916 AAACAAGCTGATTTAGGACCTTTTCAATCTAGCTGTGGAATAATGATTAATT 1975  
QY 796 GACTTAATTTAGTGTAGGAAACATCAACTGACTCATTAATCGGTAGCGCTTAATCAC 855  
DB 1976 GACTTAATTTAGTGTAGGAAACATCAACTGACTCATTAATCGGTAGCGCTTAATCAC 2035  
QY 856 CGGTAAACCTATTCTATACGACTCAGACACTCACTCTGGGTATACAGTAACTTACC 915  
DB 2036 CGGTAAACCTATTCTATACGACTCAGACACTCACTCTGGGTATACAGTAACTTACC 2095  
QY 916 TTCACTGGGAACTTAATAATATATGCGTCCACTTCTTGAAACCTTATCCGTAGCAC 975  
DB 2096 TTCACTGGGAACTTAATAATATATGCGTCCACTTCTTGAAACCTTATCCGTAGCAC 2155  
QY 976 AACCAAGGGAATTTGCTCGGACCTTGTCCCAAAAGTGTGACACAGGTCTGTGAT 1035  
DB 2156 AACCAAGGGAATTTGCTCGGACCTTGTGTCCCAAAAGTGTGACACAGGTCTGTGAT 2215  
QY 1036 AGAAGAACTTGAACCTCATCTGTATAGAAAGTGAATTTATTTATGTAACAAGAT 1095  
DB 2216 AGAAGAACTTGAACCTCATCTGTATAGAAAGTGAATTTATTTATGTAACAAGAT 2275  
QY 1096 AGTAAAGTTCCCTATGTCCCTGTGTATTTATCTGTCTTGAGCGGCAATAGTGGGCTG 1155  
DB 2276 AGTAAAGTTCCCTATGTCCCTGTGTATTTACTCTGTCTTGAGCGGCAATAGTGGGCTG 2335  
QY 1156 TATGTACTCAAAAGCCGAGGCGGACTTATCAACATATGCTATCAAAAGTTCACT 1215  
DB 2336 TATGTACTCAAAAGCCGAGGCGGACTTATCAACATATGCTATCAAAAGTTCACT 2395  
QY 1216 CATGCGCAACTGCAAGATGACCAATGTATGTATTAACCCCGGGGATCATATGCA 1275  
DB 2396 CATGCGCAACTGCAAGATGACCAATGTATGTATTAACCCCGGGGATCATATGCA 2455  
QY 1276 AAATATAGAGAAAGCCGTGTCTTAATAGATTAACCAATCATGCAATGTTTATCTTAA 1335  
DB 2456 AAATATAGAGAAAGCCGTGTCTTAATAGATTAACCAATCATGCAATGTTTATCTTAA 2515  
QY 1336 CGGGATTAATTTAAAGGCTCAGTGGGAAATTCATGATTAATCAAGAAATATCTCAAT 1395  
DB 2516 CGGGATTAATTTAAAGGCTCAGTGGGAAATTCATGATTAATCAAGAAATATCTCAAT 2575  
QY 1396 ACAAGATTCATAGTATTAATTAACAGCAATCTTGATATCTCACTAGCTGGGAATGT 1455  
DB 2576 ACAAGATTCATAGTATTAATTAACAGCAATCTTGATATCTCACTAGCTGGGAATGT 2635

QY 1456 CAACAATCCATCATGATATGCTTTGAATTAAGTAAAGAGAAAGCAAGAAATCTAGACA 1515  
DB 2636 CAACAATCCATCATGATATGCTTTGAATTAAGTAAAGAGAAAGCAAGAAATCTAGACA 2695  
QY 1516 AGTCAATGTCAAACTGACATGACATCTGCTCTCATTAATCTATATGTTTGAATCAT 1575  
DB 2696 AGTCAATGTCAAACTGACATGACATCTGCTCTCATTAATCTATATGTTTGAATCAT 2755  
QY 1576 ATCTTTGTTTTGTTGTTACTTACCTGATTTCTAGCATGTACTTAAATGTAACAA 1635  
DB 2756 ATCTTTGTTTTGTTGTTACTTACCTGATTTCTAGCATGTACTTAAATGTAACAA 2815  
QY 1636 GGGCCAAACAAAACCTTATTTATGCTTTGGAAATTAATCTTAATCAGATGAGACAC 1695  
DB 2816 GGGCCAAACAAAACCTTATTTATGCTTTGGAAATTAATCTTAATCAGATGAGACAC 2875  
QY 1696 TACAAAATGTGAACACAGATGAGAAAGAGTTTCCCTATATGATTTGTGAAAG 1755  
DB 2876 TACAAAATGTGAACACAGATGAGAAAGAGTTTCCCTATATGATTTGTGAAAG 2935  
QY 1756 TTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAAA 1792  
DB 2936 TTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAAA 2972

RESULT 10  
US-11-126-465-1  
: Sequence 1, Application US/11126465  
: Publication No. US20050202045A1  
: GENERAL INFORMATION:  
: APPLICANT: Cochran, Mark D  
: APPLICANT: Cook, Stephanie M  
: APPLICANT: Wild, Martha A  
: TITLE OF INVENTION: Novel Avian Herpes Virus and Uses Thereof  
: FILE REFERENCE: SY01105K10KOK  
: CURRENT APPLICATION NUMBER: US/11/126,465  
: PRIOR FILING DATE: 2005-05-11  
: PRIOR APPLICATION NUMBER: US/09/881,457  
: PRIOR FILING DATE: 2001-06-14  
: PRIOR APPLICATION NUMBER: 09/426,352  
: PRIOR FILING DATE: 1999-10-25  
: PRIOR APPLICATION NUMBER: 08/804,372  
: PRIOR FILING DATE: 1997-02-21  
: PRIOR APPLICATION NUMBER: PCT/US95/10245  
: PRIOR FILING DATE: 1995-08-09  
: PRIOR APPLICATION NUMBER: 08/663,566  
: PRIOR FILING DATE: 1996-06-13  
: PRIOR APPLICATION NUMBER: 08/288,065  
: PRIOR FILING DATE: 1994-08-09  
: PRIOR APPLICATION NUMBER: PCT/US93/05681  
: PRIOR FILING DATE: 1993-06-14  
: PRIOR APPLICATION NUMBER: 08/023,610  
: PRIOR FILING DATE: 1993-02-26  
: PRIOR APPLICATION NUMBER: 07/898,087  
: PRIOR FILING DATE: 1992-06-12  
: NUMBER OF SEQ ID NOS: 5  
: SOFTWARE: PatentIn Ver. 2.1  
: SEQ ID NO 1  
: LENGTH: 3570  
: TYPE: DNA  
: ORGANISM: Newcastle disease virus  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: (1194)..(2888)  
: OTHER INFORMATION: NDV Fusion Protein  
: FEATURE:  
: NAME/KEY: misc feature  
: LOCATION: (1355)  
: OTHER INFORMATION: n = any nucleotide  
US-11-126-465-1  
Query Match 50.7%; Score 1701.6; DB 10; Length 3570;  
Best local Similarity 98.4%; Pred. No. 0;



Matches 1749; Conservative 0; Mismatches 25; Indels 3; Gaps 3;			
Qy	16	TGATCCCGATTGCGCCCTCCAGGTGCAAGATGGCTCCAGACCTTCAACAAAGACC	75
Db	1199	TCGATCCCGATTGCGCCCTCCAGGTGCAAGATGGCTCCAGACCTTCAACAAAGACC	1258
Qy	76	AGCACTATGATGCTGACTATCCGGGTTGCGTGGCACTGAGTTGCATCTGTCCGGCAA	135
Db	1259	AGCACTATGATGCTGACTATCCGGGTTGCGTGGCACTGAGTTGCATCTGTCCGGCAA	1318
Qy	136	CTCATTTGATGGCAGGCGCTCTTGACGTGCAAGAAATGTTGTTTCAGAGACAAGACCGT	195
Db	1319	CTCATTTGATGGCAGGCGCTCTTGACGTGCAAGAAATGTTGTTTCAGAGACAAGACCAT	1377
Qy	196	CAACATATACACTCATCCAGACAGATCAATCATAGTTAAGCTCTCCGAAATCTGCC	255
Db	1378	CAACATATACACTCATCCAGACAGATCAATCATAGTTAAGCTCTCCGAAATCTGCC	1435
Qy	256	CAAGATTAAGAGGAGCATGTGCGAAAGCCCTTGAGTCAATCAACAGAGCATTGACAC	315
Db	1436	AAAGATTAAGAGGAGCATGTGCGAAAGCCCTTGAGTCAATCAACAGAGCATTGACAC	1495
Qy	316	TTTGTCTACCCCTTGTGTACTCTATCCGTAGATACAAAGTCTGTGACTACATCTGG	375
Db	1496	TTTGTCTACCCCTTGTGTACTCTATCCGTAGATACAAAGTCTGTGACTACATCTGG	1555
Qy	376	AGGGGGGAGACAGGGGCGCTTTATAGGCGCATTAATGGCGGTGTGCTTGGGGTTGC	435
Db	1556	AGGGGGGAGACAGGGGCGCTTTATAGGCGCATTAATGGCGGTGTGCTTGGGGTTGC	1615
Qy	436	AACTGCGGCACAAATTAACAGCGCGCGACCTCTGTATCAAGCCAAACAAATGTCTGCCA	495
Db	1616	AACTGCGGCACAAATTAACAGCGCGCGACCTCTGTATCAAGCCAAACAAATGTCTGCCA	1675
Qy	496	CATCTCTCGACTTAAAGAGACATTTGCCGCAACCAATGAGGCTGTGCACTGAGTCACTGA	555
Db	1676	CATCTCTCGACTTAAAGAGACATTTGCCGCAACCAATGAGGCTGTGCACTGAGTCACTGA	1735
Qy	556	CGGATTTTGGCACTAGAGTGGGAGTTGGGAGATGCGAGTTTGTATATGACCAAT	615
Db	1736	CGGATTTTGGCACTAGAGTGGGAGTTGGGAGATGCGAGTTTGTATATGACCAAT	1795
Qy	616	TATATAAAACAGCTGAGAAATTAGACTGATCAAAATTGCAACAGCAAGTTGGTGAAGCT	675
Db	1796	TATATAAAACAGCTGAGAAATTAGACTGATCAAAATTGCAACAGCAAGTTGGTGAAGCT	1855
Qy	676	CAACTGTACTTAACCGAATTGACTACAGTATTTGGACCAACAAATCACTTCACTGCTTT	735
Db	1856	CAACTGTACTTAACCGAATTGACTACAGTATTTGGACCAACAAATCACTTCACTGCTTT	1915
Qy	736	AAAAGACTGACTATTTGAGGACCTTTTCAATCTAGCTGGTGGAAATATGATTACTTAT	795
Db	1916	AAAAGACTGACTATTTGAGGACCTTTTCAATCTAGCTGGTGGAAATATGATTACTTAT	1975
Qy	796	GACTAAGTTAGTGTAGGAAACAATCAACTCAGCTCATTAATCGGTAGCGGCTTAATCAC	855
Db	1976	GACTAAGTTAGTGTAGGAAACAATCAACTCAGCTCATTAATCGGTAGCGGCTTAATCAC	2035
Qy	856	CGGTAACTTATTTCTATACAGCTCAAGACTCAACTTTGGGTATACAGSTAACTTAC	915
Db	2036	CGGTAACTTATTTCTATACAGCTCAAGACTCAACTTTGGGTATACAGSTAACTTAC	2095
Qy	916	TTTCAGTGGGAACTTAATAATATGCGGCACTACTTGGAAACCTTAATCCGTAAGAC	975
Db	2096	TTTCAGTGGGAACTTAATAATATGCGGCACTACTTGGAAACCTTAATCCGTAAGAC	2155
Qy	976	AACGAGGAGATTTGCTCGGCACTTGTCCAAAGATGTGACACAGGTCCGTTCTGTAT	1035
Db	2156	AACGAGGAGATTTGCTCGGCACTTGTCCAAAGATGTGACACAGGTCCGTTCTGTAT	2215
Qy	1036	AGAGAACTTGACACTTCATATCTGTATGAAGAACTGACTTAAGATTATATTTGACAGAT	1095
Db	2216	AGAGAACTTGACACTTCATATCTGTATGAAGAACTGACTTAAGATTATATTTGACAGAT	2275

Qy	1096	AGTAACTTCCCTATGTCCCTGGTATTTATTTCTGTGATGCGGCAATACGTCCGCTG	1155
Db	2276	AGTAACTTCCCTATGTCCCTGGTATTTATTTCTGTGATGCGGCAATACGTCCGCTG	2335
Qy	1156	TATGTACTCAAAAGCCGAGGCGCACTTACACACCAATACATACATCAAAAGTTCACT	1215
Db	2336	TATGTACTCAAAAGCCGAGGCGCACTTACACACCAATACATACATCAAAAGTTCACT	2395
Qy	1216	CATGCGCACTGCAAGATGACATGATGATGTGTAAACCCCGGGTATCATATGCA	1275
Db	2396	CATGCGCACTGCAAGATGACATGATGATGTGTAAACCCCGGGTATCATATGCA	2455
Qy	1276	AACTATGAGAGACCGTGTCTTATATGATTAACATCATGCAATGTTTATCTTAGG	1335
Db	2456	AACTATGAGAGACCGTGTCTTATATGATTAACATCATGCAATGTTTATCTTAGG	2515
Qy	1336	CGGATTAACCTTTAAGGCTCAATGGGGAATTTGATGTAACTTATCAAGAAATATCTCAT	1395
Db	2516	CGGATTAACCTTTAAGGCTCAATGGGGAATTTGATGTAACTTATCAAGAAATATCTCAT	2575
Qy	1396	ACAAATTTCTCAAGTAAATTAATACAGGCACTTGAATATCTCAACTGAGCTTGGGAATGT	1455
Db	2576	ACAAATTTCTCAAGTAAATTAATACAGGCACTTGAATATCTCAACTGAGCTTGGGAATGT	2635
Qy	1456	CAACAACCTCGATCAGTAAATGCTTTGAATTAAGTTAGAGAAACAAACAGAAACTAGACAA	1515
Db	2636	CAACAACCTCGATCAGTAAATGCTTTGAATTAAGTTAGAGAAACAAACAGAAACTAGACAA	2695
Qy	1516	AGTCAATGTCAACTGACTGACACATCTGCTCTCATTAATCTATATCTTTGAGTATAT	1575
Db	2696	AGTCAATGTCAACTGACTGACACATCTGCTCTCATTAATCTATATCTTTGAGTATAT	2755
Qy	1576	ATCTCTGTTTGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1635
Db	2756	ATCTCTGTTTGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2815
Qy	1636	GGCGCAACAAAACCTTATTAATGCTTGGGAATTAATCTAGATCAGATGAGAGCCAC	1695
Db	2816	GGCGCAACAAAACCTTATTAATGCTTGGGAATTAATCTAGATCAGATGAGAGCCAC	2875
Qy	1696	TACAAAATTTGGAACACAGATGAGAAACGAAGTTTCCCTAATATGATTTGTGGAAG	1755
Db	2876	TACAAAATTTGGAACACAGATGAGAAACGAAGTTTCCCTAATATGATTTGTGGAAG	2935
Qy	1756	TTCTGTAGTGTGTCAGTTGAGAGATTAAGAAAAA	1792
Db	2936	TTCTGTAGTGTGTCAGTTGAGAGATTAAGAAAAA	2972

RESULT 11  
US-10-838-834-19  
; Sequence 19, Application US/10838834  
; Publication No. US20050048074A1  
; GENERAL INFORMATION:  
; APPLICANT: Cardineau, et al.  
; TITLE OF INVENTION: Vectors and Cells for Preparing Immunoprotective Compositions  
; FILE REFERENCE: 3121/2022  
; CURRENT FILING DATE: 2004-05-04  
; PRIOR APPLICATION NUMBER: US 60/467,998  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 1734  
; TYPE: DNA  
; ORGANISM: Newcastle disease virus  
US-10-838-834-19

Query Match 42.7%; Score 1434.4; DB 8; Length 1734;  
Best Local Similarity 99.6%; Pred. No. 0;

Matches 1438; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1915 ATGACCGCGCCGTTAGCCAGATTGCGTTAGAGATGATGAAAGAGAGCAAAAAATACA 1974

DB 1 ATGGACGCGCGCGTTAGCCAGATTGCGTTAGAGATGATGAAAGAGAGCAAAAAATACA 60

QY 1975 TGGGCGCTTGATATTTCCGGAATTGCAATCTTATTTCTTAACAGTAGAGACTTGGCTATATCT 2034

DB 61 TGGGCGCTTGATATTTCCGGAATTGCAATCTTATTTCTTAACAGTAGAGACTTGGCTATATCT 120

QY 2035 GTAGCCCTCCCTTTATATAGCATGGGGGCTAGACACCTAGCGATCTTGTAGGATACCG 2094

DB 121 GTAGCCCTCCCTTTATATAGCATGGGGGCTAGACACCTAGCGATCTTGTAGGATACCG 180

QY 2095 ACTAGAGATTTCCAGGGGAGAAAGAAATTAATCATCTACCTTGGTTCCAAATCAAGATGTA 2154

DB 181 ACTAGAGATTTCCAGGGGAGAAAGAAATTAATCATCTACCTTGGTTCCAAATCAAGATGTA 240

QY 2155 GTAGATAGGATATATATAGCAAGTGGCCCTTGAATCTCTTATGAGATTATAGAGTCAAAAC 2214

DB 241 GTAGATAGGATATATATAGCAAGTGGCCCTTGAATCTCTTATGAGATTATAGAGTCAAAAC 300

QY 2215 ACACAAATTTATGAAACGCAATTAATCATCTCTTATGAGATTATAGAGTCAAAAC 2274

DB 301 ACACAAATTTATGAAACGCAATTAATCATCTCTTATGAGATTATAGAGTCAAAAC 360

QY 2275 AGTGGGTGGGGGACCTATTCATGACCCAGATTATATAGGGGGATAGGCAAAACCTC 2334

DB 361 AGGGGGTGGGGGACCTATTCATGACCCAGATTATATAGGGGGATAGGCAAAACCTC 420

QY 2335 ATTTGATGATGATGCTAGTATGTCATCATCTTATCTCTCTGATTTCAAGAACATCTG 2394

DB 421 ATTTGATGATGATGCTAGTATGTCATCATCTTATCTCTCTGATTTCAAGAACATCTG 480

QY 2395 AATTTATCCGGGGGCTACTACAGATCAGTTGCACTGGAATTAACCTCATTTGATGATG 2454

DB 481 AATTTATCCGGGGGCTACTACAGATCAGTTGCACTGGAATTAACCTCATTTGATGATG 540

QY 2455 AGTGTACATCCATTAAGTCTACACCCATATATATATTTGTCTGATGACAGATCACTCA 2514

DB 541 AGTGTACATCCATTAAGTCTACACCCATATATATATTTGTCTGATGACAGATCACTCA 600

QY 2515 CATTCATATCAGATTTTGAACATCTGTGTCTCCGACATCTGCAACAGGGAGGTTTTC 2574

DB 601 CATTCATATCAGATTTTGAACATCTGTGTCTCCGACATCTGCAACAGGGAGGTTTTC 660

QY 2575 TTTTCTACTGCGTTCCATCAACCTGAGACACCCAAATGCGAAGTCTGTGACGTG 2634

DB 661 TTTTCTACTGCGTTCCATCAACCTGAGACACCCAAATGCGAAGTCTGTGACGTG 720

QY 2635 AGTGTACATCCCTGAGTGTGATGATGCTGTCTGAAAGTCAAGAGACAGAGAGAA 2694

DB 721 AGTGTACATCCCTGAGTGTGATGATGCTGTCTGAAAGTCAAGAGACAGAGAGAA 780

QY 2695 GATTATTAATCACTGCTGTCCCTACGCGGATGATGATGAGGTTAGGTTTCAAGGCTG 2754

DB 781 GATTATTAATCACTGCTGTCCCTACGCGGATGATGATGAGGTTTCAAGGCTG 840

QY 2755 TACCAAGAAAGAACCTAGATGTCACAACTTATTTGGGGACCTGGGTGGCAACTACCA 2814

DB 841 TACCAAGAAAGAACCTAGATGTCACAACTTATTTGGGGACCTGGGTGGCAACTACCA 900

QY 2815 GAGATAGGGGGTGGATCTTTTATTTGACAGCGCGATGATGCTTCTAGCTTCAAGAGGTTT 2874

DB 901 GAGATAGGGGGTGGATCTTTTATTTGACAGCGCGATGATGCTTCTAGCTTCAAGAGGTTT 960

QY 2875 AAAACCAATTTACCAAGTGAACCTGTAACAGAAAGAAATATGATATACAGCGATAC 2934

DB 961 AAAACCAATTTACCAAGTGAACCTGTAACAGAAAGAAATATGATATACAGCGATAC 1020

QY 2935 AATGACATATGCCCAATGAGCAAGATCACTACATTTGGAATGGCAAGTCTTGTATAG 2994

DB 1021 AATGACATATGCCCAATGAGCAAGATCACTACATTTGGAATGGCAAGTCTTGTATAG 1080

QY 2995 CTTGACGCTTTGGTGGGAAACGATACAGCAGGCTATCTTATTTATCAAGGTGTCAACA 3054

DB 1081 CTTGACGCTTTGGTGGGAAACGATACAGCAGGCTATCTTATTTATCAAGGTGTCAACA 1140

QY 3055 TCCTTAGGCGAAGACCCGGTATGACTGTACCGGCCAACAAGTCACTCATGAGGGGCC 3114

DB 1141 TCCTTAGGCGAAGACCCGGTATGACTGTACCGGCCAACAAGTCACTCATGAGGGGCC 1200

QY 3115 GAAAGCAGAAATTTCTACAGTAGGAGCATCTCATTTCTTGTATCAACAGAGGTATCATAC 3174

DB 1201 GAAAGCAGAAATTTCTACAGTAGGAGCATCTCATTTCTTGTATCAACAGAGGTATCATAC 1260

QY 3175 TTCTCTCCGCGTTATATATCTTATGACGTGACGACAAACAGCCACTTTCATAGT 3234

DB 1261 TTCTCTCCGCGTTATATATCTTATGACGTGACGACAAACAGCCACTTTCATAGT 1320

QY 3235 CTTTATCATTTCAATGCTTCACTGCGGCGAGGTAGTATCCCTTGCAGGCTTCAGCAAGA 3294

DB 1321 CTTTATCATTTCAATGCTTCACTGCGGCGAGGTAGTATCCCTTGCAGGCTTCAGCAAGA 1380

QY 3295 TGCCCAACTCGTGTGTTACTGAGAGTCTATACAGATCCATATCCCTATCTATAGA 3354

DB 1381 TGCCCAACTCGTGTGTTACTGAGAGTCTATACAGATCCATATCCCTATCTATAGA 1440

QY 3355 AACCC 3358

DB 1441 AACCC 1444

RESULT 12

US-10-725-841-1

/ Sequence 1, Application US/10725841

/ Publication No. US20040131640A1

/ GENERAL INFORMATION:

/ APPLICANT: Geerligns, Harmen J.

/ APPLICANT: Brown, Ian H.

/ APPLICANT: Alexander, Dennis J.

/ APPLICANT: Collins, Michael S.

/ TITLE OF INVENTION: Escape Mutants of Newcastle Disease Virus as Marker Vaccines

/ FILE REFERENCE: AM100044

/ CURRENT APPLICATION NUMBER: US/10/725, 841

/ NUMBER OF SEQ ID NOS: 2

/ SOFTWARE: PatentIn version 3.2

/ SEQ ID NO 1

/ LENGTH: 1662

/ TYPE: DNA

/ ORGANISM: Paramyxovirus/Newcastle Disease Virus

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: (1)..(1662)

US-10-725-841-1

Query Match 42.1%; Score 1414; DB 7; Length 1662;

Best Local Similarity 90.7%; Pred. No. 0;

Matches 1507; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 47 ATGGGCTCCAGACCTTCTAACAGAAACCCAGACCTATGATGCTGACTATCCGGGTTGCG 106

DB 1 ATGGGCTCCAGACCTTCTAACAGAAACCCAGACCTTCTGATGCTGACCGGCTGCGG 60

QY 107 CTGGCACTGAGTTGATCTGTCCGGCAAACTCATTTGATGAGAGGCTCTTGGAGCTGCA 166

DB 61 CTGGCACTGAGTTGATCTGTCTGCGAAGTCTCTTGTATGAGAGGCTCTTGGAGCTGCA 120

QY 167 GGAATTTGTGTTTACAGAGACAAAGCGCTCAATATACCTTCATCTCCAGACAGATCA 226

DB 121 GGAATTTGTGTTTACAGAGACAAAGCGCTCAATATACCTTCATCTCCAGAGAGGTCA 180

QY 227 ATCATATGTTAAGTCTCTCCCGAATCTGCCCAAGATTAAGAGGCAATGGCAAGCCGCC 286

DB 181 ATCATATGTTAAGTCTCTCCCAATATATGCCCAAGATTAAGAGGCGTGTGCAAAAGCCCG 240

```

Qy 287 TTGATGATACAAACAGGACATTTGACCTTGTGACCCCCCTTGTGACTTATCCGT 346
Db 241 TTGGAGCGTACAAACAGGACATTTGCTGACCCCCCTTGTGATTTATTCGT 300
Qy 347 AGATATCAAGATGTGTGACATCTGTGAGGGGGGAGACAGGGGCCCTTTATGGGGCC 406
Db 301 AGATATCAAGATGTGTGACATCTGTGAGGGGAGAACGGGACCCCTTTATGGGGCC 360
Qy 407 ATTAATGGGGGTGTGGCTTGTGGGGTTGCACTGCGGCAAAATATACAGCGGCGGAGCT 466
Db 361 ATTAATGGGGGTGTGGCTTGTGGGGTTGCACTGCGGCAAAATATACAGCGGCGGAGCT 420
Qy 467 CTGATACAGGACAAACAAATGTGCGCAACATCTCCGACTTAAAGAGAGATTCGCGCA 526
Db 421 CTGATACAGGACAAACAAATGTGCGCAACATCTCCGCGCTTAAAGAGAGATTCGCGCA 480
Qy 527 ACCAATGAGGTGTGCACTGAGGTCACTGACGATTTATGCAACTAGACGTGGCTGGG 586
Db 481 ACCAATGAGGTGTGCACTGAGGTCACTGATGATTAATCAAACTAGACAGTGGCGTGGG 540
Qy 587 AAGATGAGAGATTTGTTAATGACCAATTTAATAAAGCTCAGGAAATTAAGATTCGATC 646
Db 541 AAGATGAGAGATTTGTTAATGACCAATTTAATAAAGCTCAGGAAATTAAGATTCGATC 600
Qy 647 AAAATTCACAGCAAGTTGGTGTAGAGCTCAACCTGTACTTAAACGAAATTAAGTACAGTA 706
Db 601 AAAATTCACAGCAAGTTGGTGTAGAGCTCAACCTGTACTTAAATTAAGTACAGTA 660
Qy 707 TTGGGACCAAGATCTTCACTGTCTTTAAACAGGTGACTTATTCAGGCACTTTACAT 766
Db 661 TTGGGACCAAGATCTTCACTGTCTTTAAACAGGTGACTTATTCAGGCGCTTTACAT 720
Qy 767 CTAGCTGTGTGAAATATGATTAATTAATGACTAAGTATGAGTATGGGAAATCAATC 826
Db 721 CTAGCTGTGTGAAATATGATTAATTAATGACTAAGTATGAGTATGGGAAATCAATC 780
Qy 827 AGGCTATTAATCGGTAGCGGCTTATCAACGGTAAACCTTATCTAATGACTCAGACT 886
Db 781 AGGCTATTAATGATGAGCGGCTTATCAACGGGAAACCTTATCTAATGACTCAGACT 840
Qy 887 CAATCTTGGGTATACAGTAACTCTACTTCACTGCGGAACTTAATATATGCTGCC 946
Db 841 CAGCTCTTGGGTATACAGTAACTCTACTTCACTGCGGAACTTAATATATGCTGCC 900
Qy 947 ACTTACTTGGAACTTATCCGTAAACCAACAGGGGATTTGCTGCGGCACTTGTCCA 1006
Db 901 ACTTACTTGGAACTTGTCTGTAAATCAACAGGATTTGCTGCGGCACTGCTCCA 960
Qy 1007 AAAATGAGTACACAGGTCGGTCTGTGATTAAGAACTTGAACCTCATCTGATATAGA 1066
Db 961 AAAATGAGTACACAGGTCGGTCTGTGATTAAGAACTTGAACCTCATCTGATATAGA 1020
Qy 1067 ACTGACTTAAGATTTATATTTGTAACAAGATTAAGTAACTTCCCTATGTCCCTGTATAT 1126
Db 1021 ACCGATTTGATCTAATTTGTAACAAGATTAAGTAACTTCCCTATGTCTCCTGTATAT 1080
Qy 1127 TCTGCTTGAAGCGGCAATGCTCGGCTGTATGTAATCAAAAGACGGAAGCGGCACTTACT 1186
Db 1081 TCTGCTTGAAGCGGCAATGCTCGGCTGTATGTAATCAAAAGACGGAAGCGGCACTACT 1140
Qy 1187 ACACATATACATATATTAAGTTCACTGCACTGCACTGCAAGATGACAAACATGTTGA 1246
Db 1141 ACAGCGTACATGACTCTCAAGGCTCAATGTTATGCACTGTAAGATGACAAACATGTTGA 1200
Qy 1247 TGTGTAAACCCCGGGTATCATATCGCAAACTATGAGAGAGCCGTCTCTATATAGAT 1306
Db 1201 TGTGTAAACCCCGGGTATCATATCGCAAACTATGAGAGAGCGTCTCTATATAGAT 1260
Qy 1307 AAACATATCATATGTTTATCTTATGCTTGAAGCGGATTAATTTAAGGCTCAGTGGGAAATTC 1366
Db 1261 AGGCAATCATGCAATGTCTATCTTATGACGGAATTAATCTTGAAGGCTCAGTGGGAAATTC 1320

```

```

Qy 1367 GATGTACTTATGAGAGAAATATCTCAATACAGATTTCTCAAGTATATATACAGGCAT 1426
Db 1321 GATGTACTTATGAGAGAAATATCTCAATACAGATTTCTCAAGTATATATACAGGCAT 1380
Qy 1427 CTGATATCTCAACTGAGCTTGGGAATGTCAACAACCTGATACGTAATGCTTTGAATAG 1486
Db 1381 CTGATATCTGACTGAGCTTGGGAATGTCAACAACCTGATACGTAATGCTTTGAATAG 1440
Qy 1487 TTAGAGAAAGCAACAGAAAACTAGCAAAAGTCAATGTCAACTGACTAGCAATCTGCT 1546
Db 1441 TTAGAGAAAGCAACAGAAAACTAGCAAAAGTCAATGTCAACTGACTAGCAATCTGCT 1500
Qy 1547 CTGATATCTTATCTTTTGGTGTGATCTTCTGTTTGGTATTAAGCTGAT 1606
Db 1501 CTGATATCTTATCTTTTGGTGTGATCTTCTGTTTGGTATTAAGCTGAT 1560
Qy 1607 CTGACATGCTACCTATGATCAAGCAAAAGCGGCAACAAACCTTATTAATGCTTGGG 1666
Db 1561 CTGACATGCTACCTATGATCAAGCAAAAGCGGCAACAAAGCGGCAACCTTATTAATGCTTGGG 1620
Qy 1667 AATATATCTTATGATCAAGTCAAGGCACTACAAAAATGTGA 1708
Db 1621 AATATATCTTATGATCAAGTCAAGGCACTACAAAAATGTGA 1662

```

```

RESULT 13
US-10-990-204-1
; Sequence 1, Application US/10990204
; Publication No. US2005069561A1
; GENERAL INFORMATION:
; APPLICANT: Geerlign, Harmen J.
; APPLICANT: Brown, Ian H.
; APPLICANT: Alexander, Dennis J.
; APPLICANT: Collins, Michael S.
; TITLE OF INVENTION: Escape Mutants of Newcastle Disease Virus as Marker Vaccines
; FILE REFERENCE: AM100044
; CURRENT APPLICATION NUMBER: US/10/990,204
; NUMBER OF FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Paramyxovirus/Newcastle Disease Virus
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)..(1662)
US-10-990-204-1

```

```

Query Match 42.1%; Score 1414; DB 9; Length 1662;
Best Local Similarity 90.7%; Pred. No. 0;
Matches 1507; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Qy 47 ATGAGCTTCAGACCTTTTACCAAGAACCCAGACCTATGATGCTGATCTATCCGGTTGCG 106
Db 1 ATGAGCTTCAGACCTTTTACCAAGAACCCAGACCTATGATGCTGATCTATCCGGTTGCG 60
Qy 107 CTGGCACTGAGTTCATCTGTCGGGCAAACTCCATTTGATGAGGAGGCTCTTGGAGCTGCA 166
Db 61 CTGGCACTGAGTTCATCTGTCGGGCAAACTCCATTTGATGAGGAGGCTCTTGGAGCTGCA 120
Qy 167 GGAATTTGTTTAAAGAGAGCAAAAGCGGTCAACATATATCACTCATCCAGACAGATCA 226
Db 121 GGAATTTGTTTAAAGAGAGCAAAAGCGGTCAACATATATCACTCATCCAGACAGGTCA 180
Qy 227 ATCATATGTTAAGCTCTCTCCGAATCTGCTCCAAAGATTAAGAGGCAATGTCGAAAGCCCC 286
Db 181 ATCATATGTTAAGCTCTCTCCGAATCTGCTCCAAAGATTAAGAGGCGGTGCAAAAGCCCCG 240
Qy 287 TTGATGATATCATACAGGACATTTGACCACTTGTGCTACCCCCCTTGTGATCTTATCCGT 346
Db 241 TTGAGGCGTACAAACAGGACATTTGATCTTGTCTACCCCCCTTGTGATCTTATTCGT 300

```

QY 347 AGATACAAAGTCTGTGACTACATCTGAGGGGAGACAGGGGCGCTTATATAGCGCC 406  
DB 301 AGGATCAAGAGTCTGTGACTACATCTGAGAGAGGAAACGGGACGCTTATAGCGCC 360  
QY 407 ATTATGGCGGTGTGGCTCTTGGGGTTGCACTGCGGCAAAATTAACAGCGGCGCGAGCT 466  
DB 361 ATTATCGCGGTGTGAGCTCTGCGGGTTGCAACGCTGACAGATTAACAGAGCTTCGCT 420  
QY 467 CTGATCAAGGCAAAACAAATGTGCGCAACCTCCGACTTAAAGAGAGATTTGCGCA 526  
DB 421 CTGATCAAGGCAAAACAAATGTGCGCAACCTCCGACTTAAAGAGAGATTTGCGCA 480  
QY 527 ACCAATGAGGCTGTGATGAGAGTCACTGACGGAATTAATGCAATGAGTGGCGATTGG 586  
DB 481 ACCAATGAGGCTGTGACAGAGTCACTGATGATTAATCAAACTAGCGTGGCGATTGG 540  
QY 587 AAGATGAGAGGTTGTTAATGACCAATTTAATAAACAGCTCAGGAATTGACCTGATC 646  
DB 541 AAGATGAGAGGTTGTTAATGACCAATTTAATAAACAGCTCAGGAATTGACCTGAT 600  
QY 647 AAAATTGACAGCAAGTTGTGTAGAGCTCAACCTGTACTTAACGAAATTTGACTACAGTA 706  
DB 601 AAAATTGACAGCAAGTTGTGTAGAGCTCAACCTGTACTTAACGAAATTTGACTACAGTA 660  
QY 707 TTGCGACCAAGAACTTCACTGCTTTAAACAGCTGACTATTGAGGCACTTTACAT 766  
DB 661 TTGCGGCGACAAATCACTTCCCTGCGCTTAAACCAAGCTGACTACAGGCGCTTTACAT 720  
QY 767 CTAGCTGTGAAATATGATGATTAATTAATGACTAGTTAGGTAAGGAACAACATC 826  
DB 721 CTAGCTGTGAAATATGATGATTAATTAATGACTAGTTAGGTAAGGAACAACATC 780  
QY 827 AGCTATTAATCGGTAGCGGCTTATCAACGGTAACTTATCTATACAGCTCAAGACT 886  
DB 781 AGCTATTAATGATGAGGCTTATCAACGGTAACTTATCTATACAGCTCAAGACT 840  
QY 887 CAACCTTGGGATATACAGTAACCTCACTTCACTGCGGAACTTAAATATATGCGTGC 946  
DB 841 CAAGCTTGGGATATACAGTAACCTCACTTCACTGCGGAACTTAAATATATGCGTGC 900  
QY 947 ACCTACTTGGAAACCTTATCGGTAAAGCAACAGGGGATTTGGCTGCGGCACTTGTCCA 1006  
DB 901 ACCTACTTGGAAACCTTATCGGTAAAGCAACAGGGGATTTGGCTGCGGCACTTGTCCA 960  
QY 1007 AAAGTGTGACACAGTCTGTGATAGAGAACTTGAACCTCATCTGATAGAA 1066  
DB 961 AAAGTGTGATAGAGTCTGTGATAGAGAACTTGAACCTCATCTGATAGAA 1020  
QY 1067 ACTGACTTGAATTTATATTTGTAAGAAATGTAACGTTCCCTATGTCCCTGATATTTAT 1126  
DB 1021 ACCGATTTGATCTATATTTGTAAGAAATGTAACGTTCCCTATGTCCCTGATATTTAT 1080  
QY 1127 TCTGTCTTGAAGGCGCAATAGTGGGCTGTATGTATCTCAAAAGACCGAAGGCGCACTTACT 1186  
DB 1081 TCTGTCTTGAAGGCGCAATAGTGGGCTGTATGTATCTCAAAAGACCGAAGGCGCACTTACT 1140  
QY 1187 ACACATATATGACTATCAAAAGTTGAGTCACTGCGCACTGCAAGATGACAAATGTAGA 1246  
DB 1141 ACAGCGGATATGACTCTCAAAAGGCTCAAGTTATGCGCACTGTAAGATGACAAATGTAGA 1200  
QY 1247 TGTGTAAACCCCGGGTATCATATGCAAAATATGAGAGAGCGGTCTCTATATAGAT 1306  
DB 1201 TGTGTAAACCCCGGGTATCATATGCAAAATATGAGAGAGCGGTCTCTATATAGAT 1260  
QY 1307 AAACATATATGCAATGTTTATCTTGTGGGCGGATTAATTTAGGCTCAAGTGGGAAATTC 1366  
DB 1261 AAGCAATATATGCAATGTTTATCTTGTGTGAGCGGAATTAATTTAGGCGGGAATTT 1320  
QY 1367 GATGTAACTTATGAGAGAAATATCTCAATCAAGATTTCTCAAGTAATATTAACAGGAAT 1426  
DB 1321 GATGTAACTTATGAGAGAAATATCTCAATCAAGATTTCTCAAGTAATATTAACAGGAAT 1380  
QY 1427 CTGTATATCTCAACTGAGCTTGGGAATGTCAACAACTGATCAGTAATGCTTTGAAATAG 1486

DB 1381 CTGATATCTTCGACTGTGACTTGGAAATGTCAACAACTCGATTAATATGCTTTGATAG 1440  
QY 1487 TTAGAGAAAGCAACAGAAAATAGCAAAAGTCAATGTCAAACTGATAGACATCTGCT 1546  
DB 1441 TTAGAGAAAGCAACAGAAAATAGCAAAAGTCAATGTCAAACTGATAGACATCTGCT 1500  
QY 1547 CTGATATCTTCGACTGTGACTTGGAAATGTCAACAACTCGATTAATATGCTTTGATAG 1606  
DB 1501 CTGATATCTTCGACTGTGACTTGGAAATGTCAACAACTCGATTAATATGCTTTGATAG 1560  
QY 1607 CTGATATCTTCGACTGTGACTTGGAAATGTCAACAACTCGATTAATATGCTTTGATAG 1666  
DB 1561 CTGATATCTTCGACTGTGACTTGGAAATGTCAACAACTCGATTAATATGCTTTGATAG 1620  
QY 1667 AATATATCTTCGACTGTGACTTGGAAATGTCAACAACTCGATTAATATGCTTTGATAG 1708  
DB 1621 AATATATCTTCGACTGTGACTTGGAAATGTCAACAACTCGATTAATATGCTTTGATAG 1662

RESULT 14  
US-09-784-990-10  
; Sequence 10. Application US/09784990  
; Patent No. US20020037292A1  
; GENERAL INFORMATION:  
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE  
; APPLICANT: BOUCHARDON, ANNABELLE  
; APPLICANT: RIVIERE, MICHEL  
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA  
; FILE REFERENCE: 454313-2260  
; CURRENT APPLICATION NUMBER: US/09/784,990  
; PRIOR FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: 96/09339  
; PRIOR FILING DATE: 1996-07-19  
; PRIOR APPLICATION NUMBER: PCT/FR97/01326  
; PRIOR FILING DATE: 1997-07-16  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 1662  
; TYPE: DNA  
; ORGANISM: Newcastle disease virus  
US-09-784-990-10

Query Match 40.6%; Score 1362.8; DB 3; Length 1662;  
Best Local Similarity 88.7%; Pred. No. 0;  
Matches 1475; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

QY 47 ATGGGCTCCAGACCTTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTGCG 106  
DB 1 ATGGGCTCCAGACCTTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTGCG 60  
QY 107 CTGCACTGAGTGTGATCTGTGTGCGGCAAACTCCATTTGATGAGGCGCTTTGAGGCTGCA 166  
DB 61 CTGCACTGAGTGTGATCTGTGTGCGGCAAACTCCATTTGATGAGGCGCTTTGAGGCTGCA 120  
QY 167 GGAATGTGATTCAGAGACAAAGCGGTCAACATATACCTCATCTCCAGACAGATCA 226  
DB 121 GGAATGTGATTCAGAGACAAAGCGGTCAACATATACCTCATCTCCAGACAGGCTCA 180  
QY 227 ATCATATTAAGTCTCTCCGAAATCTGCGCAAGATTAAGAGGCAATGTGCAAAAGCCCC 286  
DB 181 ATCATATTAAGTCTCTCCGAAATTAAGAGGCAATGTGCAAAAGCCCC 240  
QY 287 TTGATGATATCAACAGGACATTTGACATCTTTGCTCAACCCCTTGGTACTCTATTCGT 346  
DB 241 TTGATGATATCAACAGGACATTTGACATCTTTGCTCAACCCCTTGGTACTCTATTCGT 300  
QY 347 AGATCAAGAGTCTGTGACTATCATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 406  
DB 301 AGATCAAGAGTCTGTGACTATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
QY 407 ATTATTTGGCGGTGTGCTTTGGGGTTGCAACTGCGCAAAATTAACAGGCGCGGAGCT 466

```
Db 361 ATATCGGAGTGTAGCTCTTGGGGTTGCGACAGCTGACAGATTAACAGCAGCTTCGGCC 420
Qy 467 CTGATACAGGCAAAACAAATGTCCCAACATCTCCGACTTAAGAGAGATTGCCGA 526
Db 421 CTGATACAGGCAAAACAAATGTCCCAACATCTCCGACTTAAGAGAGATTGCCGA 480
Qy 527 ACCAATGAGGCTGTGCAAGAGTCACTGACGATTAATGCAATGACAGTGGCAGTTGG 586
Db 481 ACCAATGAGGCTGTGCAAGAGTCACTGACGATTAATGCAATGACAGTGGCAGTTGG 540
Qy 587 AAGATGACGAGTGTGTTAATGACCAATTTAATAAAGCTGAGGATTTGACTGCATC 646
Db 541 AAGATGACGAGTGTGTTAATGACCAATTTAATAAAGCTGAGGATTTGACTGCATC 600
Qy 647 AAATGTCACAGCAAGTTGGTGTAGAGTCAACCTGTACCTAACCGAATTGACTACAGTA 706
Db 601 AAATGTCACAGCAAGTTGGTGTAGAGTCAACCTGTACCTAACCTGATTTGACTACAGTA 660
Qy 707 TTGCGACCAAAATCACTTCACTGTCTTAAACAAGCTGACTATTCAAGCAGCTTAAAGT 766
Db 661 TTGGGCGCAAAATCACTTCCCTGCTTAACTGAGGACTATCCAGGCGCTTTACAT 720
Qy 767 CTAGCTGTGGAATATGATTAATCTTATGACTAATGAGTGTAGGGAACATCAACTC 826
Db 721 CTAGCTGTGATATGATTAATCTTATGACTAATGAGTGTAGGGAACATCAACTC 780
Qy 827 AGCTCATTAATCGGTAGCGGCTTAAATGACCGGTAACTCTTATGACTACAGACT 886
Db 781 AGCTCATTAATGATAGCGGCTTAAATGACCGGTAACTCTTATGACTACAGACT 840
Qy 887 CAATCTTGGGATATACAGTAACTCTTCACTTCACTGCGGAACTTAATATATATGCTGCC 946
Db 841 CAATCTTGGGATATACAGTAACTCTTCACTTCACTGCGGAACTTAATATATGCTGCC 900
Qy 947 ACTTACTTGAACCTTATCTGTAAGCAACAAGGAGATTTGCTCGGCACTTGTCCCA 1006
Db 901 ACTTACTTGAACCTTATCTGTAAGCAACAAGGAGATTTGCTCGGCACTTGTCCCA 960
Qy 1007 AAGTGTGTGACAGGTCGGTCTGTGATGAGAAACCTTGAACCTTATGATGATGAA 1066
Db 961 AAGTGTGTGACAGGTCGGTCTGTGATGAGAAACCTTGAACCTTATGATGATGAA 1020
Qy 1067 ACTGACTTAATTAATGATGACAGAAATGATTAAGTTCCTATGTCCTCGATATTAT 1126
Db 1021 ACCGACTTGAATTAATGATGACAGAAATGATTAAGTTCCTATGTCCTCGATATTAT 1080
Qy 1127 TCTGTGTTAGCGGCAATAGCTCGGCTGTATGTACTCAAGACGAAAGCGCACTTACT 1186
Db 1081 TCTGTGTTAGCGGCAATAGCTCGGCTGTATGTACTCAAGACGAAAGCGCACTTACT 1140
Qy 1187 ACACCATATGACTATCAAAAGTTCACTGATCGGCACTGCAAGATGACAACTGTAGA 1246
Db 1141 ACACCATATGACTATCAAAAGTTCACTGATCGGCACTGCAAGATGACAACTGTAGA 1200
Qy 1247 TGTGTAAACCCCGGGTATCATATCGCAAAACTATGAGAGAGCGTGTCTTAATGAT 1306
Db 1201 TGTGTAAACCCCGGGTATCATATCGCAAAACTATGAGAGAGCGTGTCTTAATGAT 1260
Qy 1307 AAACATCATGCAATGTTTATCTTATAGCGGGAATTAATTTAGGCTCAAGTGGGAAATTC 1366
Db 1261 AAGGACTCATGCAAGCTTATCTTATAGCGGGAATTAATTTAGGCTCAAGTGGGAAATTC 1320
Qy 1367 GATGTAACTTATGCAAGAAATATCTCAATACAGATTTCAAGTAATTAATACAGGCAAT 1426
Db 1321 GATGTAACTTATGCAAGAAATATCTCAATACAGATTTCAAGTAATTAATACAGGCAAT 1380
Qy 1427 CTGATATCTCAATGAGTGTGGAATGTCAACAATCGATCAGTAATGCTTTGATTAAG 1486
Db 1381 CTGATATATCACTGAGCTTTGGAAATGTCAACAATCAATTAATGCTTTGATTAAG 1440
Qy 1487 TTAGGAAAGCAACAGAAATCTAGACAAAGTCAATGTCAAACTGACTAGACATCTGCT 1546
```

```
Db 1441 TTAGGAAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACCAGCAATCTGCT 1500
Qy 1547 CTATTAATCTATATGTTTGTACTATCATATCTTGTGTTTGTGTATTAAGCTGATTT 1606
Db 1501 CTATTAATCTATATGTTTGTACTATCATATCTTGTGTTTGTGTATTAAGCTGATTT 1560
Qy 1607 CTAGATGCTTACTTAATGTACAGCAAAAGCGCAACAAAACCTTATTTGCTTGGG 1666
Db 1561 CTAGATGCTTACTTAATGTACAGCAAAAGCGCAACAAAACCTTATTTGCTTGGG 1620
Qy 1667 AATAATCTCTAGATGAGAGGCGCACTACAAAATGTGA 1708
Db 1621 AATAATCTCTGATGATGAGAGGCGCACTACAAAATGTGA 1662
```

## RESULT 15

```
US-10-229-412-10
; Sequence 10, Application US/10229412
; Publication No. US20030124145A1
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE
; APPLICANT: BOUCHARDON, ANNABELLE
; APPLICANT: RIVIERE, MICHEL
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA
; FILE REFERENCE: 454313-2260
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US/09/232,479
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: 96/09339
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: PCT/FR97/01326
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Newcastle disease virus
US-10-229-412-10
```

```
Query Match 40.6%; Score 1362.8; DB 6; Length 1662;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 1475; Conservative 0; Mismatches 187; Indels 0; Gaps 0;
```

```
Qy 47 ATGGGCTCCGAGCTTCTTACAGAAACCCAGACCTTATGATGCGATTCGGGTTGGC 106
Db 1 ATGGGCTCCGAGCTTCTTACAGAGATCCGGTACCTTAATGCTGATCATCCGAACCGC 60
Qy 107 CTGGCACTGAGTTGCTATCTGTCCGCAAACTCAATGATGAGGCGCTTGGCAGCTGCA 166
Db 61 CTGACATGAGCTGTATTCGGTCTGACAAAGCTCTTGTATGAGGAGGCGCTTGGCAGCTGCA 120
Qy 167 GGAATGTGTATACAGGAGCAAAAGCGGTCAACATATACACTTCATCCAGACAGATCA 226
Db 121 GGAATGTGTATACAGGAGCAAAAGCGGTCAACATATACACTTCATCCAGACAGGCTCA 180
Qy 227 ATCATATTAAGCTCTCCCGGAATTCGCGCAAGGATTAAGAGGAGTGTGGAAGCGCCC 286
Db 181 ATCATATTAAGTAACTCCCGGAATTCGCGCAAGGATTAAGAGGAGTGTGGAAGCGCCA 240
Qy 287 TTGATGATATCAACAGAGCAATTTGACCACTTTGCTCAACCCCTTGGTGAATCTATCCGT 346
Db 241 TTGAGGCAATCAACAGAGCACTGATCTTATCTTACTCAACCCCTTGGTGAATCTATCCGT 300
Qy 347 AGATTAACAAGTCTGTGACTTCACTTGAAGGGGGAGACAAGGCGCTTATTAAGCGCC 406
Db 301 AGATTAACAAGTCTGTGACTTCACTTGAAGGGGGAGACAAGGCGCTTATTAAGCGCC 360
Qy 407 ATTAATGCGGCTGTGCTCTTGGGTTGCAATGCGCGCAAAATTAAGGGGCGCGAGCT 466
Db 361 ATTAATGCGGCTGTGCTCTTGGGTTGCAAGCTGCAAGATTAAGGAGGCTTTCGGCC 420
```

QY 467 CTGATACAGCCAAACAAATGCTGCCAACATCTCCGACTTAAAGAGAGATTGCCCA 526  
DB 421 CTGATACAGCCAAACGAATGCTGCCAACATCTCCGCTTAAAGAGACATTTGCTGCA 480  
QY 527 ACCAAGAGGCTGCAAGAGTCACTGACGGAATTATGCAACCTAGACAGTGGCAGTTGGG 586  
DB 481 ACCAAGAGGCTGCAAGAGTCACTGACGGAATTATGCAACCTAGACAGTGGCAGTTGGG 540  
QY 587 AAGATGAGCAGTGTGTAATGACCAATTTAAATTTAAAACAGTCAGAAATTAGACTGCATC 646  
DB 541 AAGATGAGCAGTGTGTAATGACCAATTTAAATTTAAAACAGTCAGAAATTAGACTGCATC 600  
QY 647 AAAATTGCAAGCAGTGGTGTAGACTCAACTGTACCTAACCGAATTGACTACAGTA 706  
DB 601 AAAATTGCAAGCAGTGGTGTAGAACTCAACTGTACCTAACCTGAATTGACTACAGTA 660  
QY 707 TTGGGACCAAAATCACTTCACTGCTTTAAACAAGTGAATACTTCAAGGCACTTACAAT 766  
DB 661 TTGGGACCAAAATCACTTCCCTGCTTAACTCAGCTGACTATCCAAAGCGCTTTACAT 720  
QY 767 CTAGCTGTGGAATAATGATTAATTATGACTAAAGTTAGGTGAGGAACAATCAATC 826  
DB 721 CTAGCTGTGTATATGATTAATTGCTGACTAATTAAGTTAGGGAACAACCAATC 780  
QY 827 AGCTCAATTAATGAGTACGGCTTATCAACGGTAACTCTATTTCTATACACTCAGACT 886  
DB 781 AGCTCAATTAATGAGTACGGCTTATCAACGGTAACTCTATTTCTATACACTCAGACT 840  
QY 887 CAACCTGTGGTATACAGTAACTCTACCTTCACTGGGAACTTAATTAATGCGTGGC 946  
DB 841 CAACCTGTGGTATACAGTAACTTTCCTTCACTGGGAACTTAATTAATGCGTGGC 900  
QY 947 ACCTACTTGGAAACTTATCCGTAAAGCACAACAGGGGAATTGCTCGGCACTTGTCCA 1006  
DB 901 ACCTACTTGGAAACTTATCTGTAAAGCACAACAGGGGAATTGCTCGGCACTTGTCCA 960  
QY 1007 AAAGTGTGACACAGTGGTCTGTGTATGAAAGAACTTGACACTCATCTGTATGAA 1066  
DB 961 AAAGTGTGACACAGTGGTCTGTGTATGAAAGAACTTGACACTCATCTGTATGAGG 1020  
QY 1067 ACTGACTTAATTTATTTGTAAAGAAATGTAAGTTCCCTATGTCCTCGTATTTAT 1126  
DB 1021 ACCGACTTGAATTATCTGTAAAGAAATGTAAGTTCCCTATGTCCTCGTATTTAT 1080  
QY 1127 TCTGCTTGGAGCGCAATAGTGGCTGTATGTACTCAAGACGGAAGCGCACTTACT 1186  
DB 1081 TCTGCTGAGCGGTATATACGGCTTGATGATTCAAAGACTGAAGCGCACTTACT 1140  
QY 1187 ACAACATACATGACTATCAAGGTTCAATGCGCACTGCAAGATGACACATGTAGA 1246  
DB 1141 ACCGCAATATGCTCTCAAGGCTCAGTTATGSCAATTGCAAGCTGACACATGTAGA 1200  
QY 1247 TGTGTAAACCCCGGGTATCATGCGAAACATATGGAAGAAGCGGTCTCTAATGAT 1306  
DB 1201 TGTGTAAACCCCGGGTATCATATGCGAAATATGGAAGAAGCTGTCTTAAATGAT 1260  
QY 1307 AAACAATCATGACATGTTTTATCTTATGCGGGAATACTTTAAGGCTCAGTGGGAATTC 1366  
DB 1261 AAGCACTCATGCAAGCTTATCTTATGAGGGAATACTTGAAGCTCAGTGGGAATTT 1320  
QY 1367 GATGTAACTTATGAGAAATATCTCAATACAAGATTCTCAAGTAAATTAACAGGCAAT 1426  
DB 1321 GATGTAACTTATGAGAAATATCTTATCTAATACTCAAGTAAATTAACAGGCAAT 1380  
QY 1427 CTTGATATCTCAACTGAGCTTGGGAATGTCAACAACCTGATCAGTATGCTTTGAATAG 1486  
DB 1381 CTTGATATATCAACTGAGCTTGGGAATGTCAACAACCTGATCAGTATGCTTTGAATAG 1440  
QY 1487 TTAGAGGAAGCAACAGAAACTAGACAAAGTCAATGCAAACTGACTAGACATCTGCT 1546  
DB 1441 TTAGAGGAAGCAACAGAAACTAGACAAAGTCAATGCAAACTGACTAGACATCTGCT 1500  
QY 1547 CTCATTACCTATATCGTTTGTGACTATCATATCTTGTGTTTGTATATCTTACCTGATT 1606

DB 1501 CTGATTAACCTACATCGTTTAACTGTCATATCTCTGTTTGTGTACTTAAGCTTGCTT 1560  
QY 1607 CTAGCATGTACTTAATGTAACAAGCAAAAGCGCAACAAAACCTTATTTAGCTTGGG 1666  
DB 1561 CTAGCATGTACTTAATGTAACAAGCAAAAGCGCAACAAAACCTTATTTAGCTTGGG 1620  
QY 1667 AATTAATCTTGAATCAGATGAGAGCCACTACAAAATGTGA 1708  
DB 1621 AATTAATCCTTGTATCAGATGAGAGCCACTACAAAATATAGA 1662

Search completed: February 5, 2006, 07:03:34  
Job time : 2559 secs



November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

This Page Blank (uspic)

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: February 4, 2006, 22:04:33 ; Search time 538 Seconds  
(without alignments)  
5230.949 Million cell updates/sec

Title: US-10-800-256-1  
Perfect score: 3358  
Sequence: 1 acgggtagaagatctcgtgac.....cctaactctatagaacc 3358

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6068529 seqs, 41903697 residues

Total number of hits satisfying chosen parameters: 12137058

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA\_New:  
1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. *	Score	Query Match	Length	ID	Description
1	85	2.5	18967	US-11-014-842A-16	Sequence 16, Appl
2	43	1.3	759	US-11-155-478A-50	Sequence 50, Appl
3	43	1.3	13280	US-11-155-478A-174	Sequence 174, App
4	41.4	1.2	759	US-11-155-478A-26	Sequence 26, Appl
5	41.4	1.2	759	US-11-155-478A-49	Sequence 49, Appl
6	41.4	1.2	759	US-11-155-478A-51	Sequence 51, Appl
7	41.4	1.2	759	US-11-155-478A-52	Sequence 52, Appl
8	41.4	1.2	759	US-11-155-478A-53	Sequence 53, Appl
9	41.4	1.2	759	US-11-155-478A-54	Sequence 54, Appl
10	41.2	1.2	759	US-11-155-478A-27	Sequence 27, Appl
11	41.2	1.2	759	US-11-155-478A-28	Sequence 28, Appl
12	41.2	1.2	759	US-11-155-478A-31	Sequence 31, Appl
13	41.2	1.2	759	US-11-155-478A-32	Sequence 32, Appl
14	41.2	1.2	13335	US-11-155-478A-173	Sequence 173, App
15	39.8	1.2	759	US-11-155-478A-57	Sequence 57, Appl
16	39.8	1.2	759	US-11-155-478A-58	Sequence 58, Appl
17	38.8	1.2	759	US-11-155-478A-59	Sequence 59, Appl
18	38.4	1.1	13350	US-11-155-478A-1	Sequence 1, Appl
19	38	1.1	759	US-11-155-478A-29	Sequence 29, Appl
20	38	1.1	759	US-11-155-478A-34	Sequence 34, Appl
21	38	1.1	759	US-11-155-478A-44	Sequence 44, Appl
22	37.8	1.1	1125000	US-10-995-561-13286	Sequence 13286, A

23	37.6	1.1	394468	7	US-10-995-561-13473	Sequence 13473, A
24	37	1.1	600	7	US-10-750-185-1899	Sequence 1899, Ap
C 25	37	1.1	600	7	US-10-750-623-1899	Sequence 30, Appl
26	36.4	1.1	759	8	US-11-155-478A-30	Sequence 33, Appl
27	36.4	1.1	759	8	US-11-155-478A-33	Sequence 35, Appl
28	36.4	1.1	759	8	US-11-155-478A-35	Sequence 36, Appl
29	36.4	1.1	759	8	US-11-155-478A-36	Sequence 37, Appl
30	36.4	1.1	759	8	US-11-155-478A-37	Sequence 38, Appl
31	36.4	1.1	759	8	US-11-155-478A-38	Sequence 39, Appl
32	36.4	1.1	759	8	US-11-155-478A-39	Sequence 40, Appl
33	36.4	1.1	759	8	US-11-155-478A-40	Sequence 41, Appl
34	36.4	1.1	759	8	US-11-155-478A-41	Sequence 42, Appl
35	36.4	1.1	759	8	US-11-155-478A-42	Sequence 43, Appl
36	36.4	1.1	759	8	US-11-155-478A-43	Sequence 44, Appl
37	36.4	1.1	759	8	US-11-155-478A-44	Sequence 45, Appl
38	36.4	1.1	759	8	US-11-155-478A-46	Sequence 46, Appl
39	36.4	1.1	759	8	US-11-155-478A-47	Sequence 47, Appl
40	36.4	1.1	759	8	US-11-155-478A-48	Sequence 48, Appl
41	36.4	1.1	1060	7	US-10-750-185-40078	Sequence 40078, A
42	36.4	1.1	1060	7	US-10-750-623-40078	Sequence 40078, A
C 43	35.6	1.1	2261	7	US-10-750-185-47092	Sequence 47092, A
C 44	35.6	1.1	2261	7	US-10-750-623-47092	Sequence 47092, A
C 45	35.2	1.0	1193	7	US-10-750-185-61030	Sequence 61030, A

#### ALIGNMENTS

RESULT 1  
US-11-014-842A-16  
; Sequence 16, Application US/11014842A  
; Publication No. US20060013826A1  
; GENERAL INFORMATION:  
; APPLICANT: TANGY, FREDERIC  
; APPLICANT: LORIN, CLARISSE  
; APPLICANT: MOLETT, LUCIE  
; APPLICANT: DEBEBOQUE, FREDERIC  
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF  
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF  
; TITLE OF INVENTION: VACCINE COMPOSITIONS  
; FILE REFERENCE: 2356.0093  
; CURRENT APPLICATION NUMBER: US/11/014, 842A  
; CURRENT FILING DATE: 2004-12-20  
; PRIOR APPLICATION NUMBER: PCT/EP03/07146  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: EP 02291550.8  
; PRIOR FILING DATE: 2002-06-20  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 16  
; LENGTH: 18967  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Complete  
; OTHER INFORMATION: nucleotide sequence of the pTM-WVSchw plasmid  
; OTHER INFORMATION: (CNCM I-2889)  
US-11-014-842A-16  
Query Match 2.5%; Score 85; DB 8; Length 18967;  
Best Local Similarity 43.1%; Pred. No. 3e-15;  
Matches 412; Conservative 0; Mismatches 545; Indels 0; Gaps 0;  
QY CCCTTGGGACTCTATCGCTGAGTACAAAGTCTGTACTACATCTGGAGGGGAGAC 386  
DB 5808 CACTTAATGCAATACCCAGATATPAGACCGCTTACAGTGTACCTTCAAGTAGAGAC 5867  
QY 387 AGGGCGCCTTATAGGCGCCATTATTGGCGGTGTGCTTGGGGTTGCCAATCGCGAC 446  
DB 5868 ACAAGAGTTTGGGGGATATCTCGGAGGTGGCGCCCTTAGCGGTTCACAGCTGCTC 5927  
QY 447 AATATACGCGCGCGACGCTTGATACAGGCCAACAATGCTGCCAATCTCTCCGAC 506  
|||||

```
Db 5928 AGATAACACCCGCGATTGCACTTACCAAGTCATGCTGAACTCTCAACCCATCGACATC 5987
Qy 507 TTAAGAGAGCATTCGCCCAACCAATGAGGCTGTGCATGAGTCACTGACGATTTATCGC 566
Db 5988 TGAGAGGAGCGCTGGAACCTCTAATCAGGCAATTTGAGCAATCAGAACAGGAGGCG 6047
Qy 567 AACTAGACGTGGCAGTTGGGAAGATGACGAGTTTGTATATGACCAATTTATATAACAG 626
Db 6048 AGATGATATTGGCTGTTCAAGGCTGCCAAGCTACATCAATTAAGAGCTGTATCCGCTCA 6107
Qy 627 CTCGGAATTAGACTGCATCAAAATTTGACAGCAAGTTGGTGTAGAGCTCAACCTGTACC 686
Db 6108 TGAACCACTATCTTGTGATTTAATCGGCCAAAGCTCGGCTCAAAATGCTCGATATCT 6167
Qy 687 TAAACGAATTGACTACAGTATTCGACCAAAATCACTTCACTGCTTTAAACAAGCTGA 746
Db 6168 ATACAGAAATCCTCTCAATTAATTTGGCCCAATTTACGGGACCCTATCTCGGAGATAT 6227
Qy 747 CTATTCAGGCACTTTACATCTAGCTGTGGAAATATGATTAATCTTATGACTAAGTTAG 806
Db 6228 CTATCCAGGCTTTAGCTATCCGTTGGAGGAGACATCAATAGGTGTAGAAAAAGCTCG 6287
Qy 807 GTGTAGGGAACAATCAATCACTCATTTAATCGGAGGCTTATATCAACCGGTAAACCTTA 866
Db 6288 GATACATGAGGATGATTTTATTCGGGCATCTTAGAGAGCGGAAATTAAGGCCCGGATTA 6347
Qy 867 TTCTATACGACTCAACAGCTCACTTGGGTATACAGGTAACTTCACTTCACTGCGGGA 926
Db 6348 CTCACGTGACAGAGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCCG 6407
Qy 927 AACTAAATATATCGGTGCCACCTTACCTTGAACCTTATCCGTAAAGCAACCGAGGAT 986
Db 6408 AGATTAAGGGGTATTTGTCACCGGCTAGAGGGGGTCTCTTACAACTATAGCTCTGAAG 6467
Qy 987 TTGCTGCGGCACTTGTCCAAAGGTGACACAGGTGCTGTGTATAGTAAGAAGCTTG 1046
Db 6468 AGTGATATACCTGCTGCTCCAAAGTATGTGCAACCCAAAGGATCTTATCTGAAATTTTG 6527
Qy 1047 ACACCTCATCTGTATAGAACTGACTTATATATTTATATGTAAGAATATAGTCTCC 1106
Db 6528 ATGAGTATGCTGTATCTTATTCAGCAAGGAGGAGCTGTGAGCCAAATATCTTGTATCC 6587
Qy 1107 CTATGCTCCCTGTATTTATTTCTGCTTGAAGGCAATATCGGCTGTATGTCTCAA 1166
Db 6588 CGATGATGCTCTCTCCAAAGATGCTCCGGGGGTACACAAATCTGCTGCTGACAC 6647
Qy 1167 AGACCGAAGGCGCTTACATACATACATACATACATACATACATACATACATACAT 1226
Db 6648 TCGTATCCGGGTCTTTTGGGAACCGGTTCAATTTATATCAAAAGGAACTTATAGCCAAAT 6707
Qy 1227 GCAAGATGACAAATGTATGATGTATAAAGGCGGATATCATATCGCAAAATATATG 1283
Db 6708 GTGATCAATCTTGTGCAAGTGTATACACAGAGATCATTTATCAAGACCTTG 6764

RESULT 2
US-11-155-478A-50
; Sequence 50, Application US/11155478A
; Publication NO. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
```

```
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 759
; TYPE: DNA
; ORGANISM: human metapneumovirus
; NAME/KEY: gene
; LOCATION: (1)...(759)
; OTHER INFORMATION: human metapneumovirus, strain Quebec Isolate No
; OTHER INFORMATION: C-64199
US-11-155-478A-50

Query Match 1.3%; Score 43; DB 8; Length 759;
Best Local Similarity 47.3%; Pred. No. 0.0072;
Matches 130; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

Qy 411 TTGGCGGTGTGGCTCTTGGGTTGCACTCCGCAAAATTAAGAGGCGCGGAGCTGCA 470
Db 314 TAGGTGAATAGCTCTTGTGTGTCACAGACAGCAAGTCACAGGCAATTTGCGATAG 373
Qy 471 TACAAGCCAAACAAATGCTGCCAATCTCTCGACTTAAAGAGCATTTGCCGCAACA 530
Db 374 CCAAAACATPAAGGCTTGAGAGTAAGTAATGCAATCAAAAGATGCTCAAAACACCA 433
Qy 531 ATGAGCTGTGACAGCTGACGATATGCACTAGCACTGAGCTGGCGAGTTGGGAAGA 590
Db 434 ACAGGCGATATCCACACTAGAAATGAGTGCAGTCTAGCCACCGCATAGAGAGC 493
Qy 591 TGCAGCAGTTGTTAATAGCAATTTAATAAAGCTCAGTCAAGATTAGCTGATCAAAA 650
Db 494 TGAAGATTTGTAGCAAAACCTGACTAGTGAATTAACAAACAAATGTGACATTG 553
Qy 651 TTGCACAGCAAGTTGTGTAGAGCTCAACTGTAC 685
Db 554 CTGATCGAAGATGCTGTGACGCTTCACTCAATTTC 588

RESULT 3
US-11-155-478A-174
; Sequence 174, Application US/11155478A
; Publication NO. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 13280
; TYPE: DNA
; ORGANISM: Viruses
; FEATURE:
; OTHER INFORMATION: CAN9875 genomic DNA
US-11-155-478A-174

Query Match 1.3%; Score 43; DB 8; Length 13280;
Best Local Similarity 47.3%; Pred. No. 0.051;
Matches 130; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

Qy 411 TTGGCGGTGTGGCTCTTGGGTTGCACTCCGCAAAATTAAGAGGCGCGGAGCTGCA 470
Db 3377 TAGGTGAATAGCTCTTGTGTGTCACAGACAGCAAGTCACAGGCAATTTGCGATAG 3436
```

Oy	471	TACAGCCAAACAAATGCTGCCACATCTCCGACTTTAAAGAGACATTCGCCGAACA	530
Db	3437	CCAAACCATTAAGGCTTGAAGTGAATGCATCAAAAGTGCTTCAAAACCA	3496
Oy	531	ATGAGGCTGTGCATAGGCTCACTGACGGATTATTCGCAACTAGCAGTGCAGTTGGGAAGA	590
Db	3497	ATGAGGCAGTATCCACACTAGAGAAATGGAAGTCCGAGTCTTACCAACCGCAGTAAAGAGGC	3556
Oy	591	TGCACGAGTTGTTAATGACCAATTTAATAAACAAGCTCAGGAATTGACTGCATCAAAA	650
Db	3557	TGAAAGAAATTTGTGAGCAAAAACCTGCATAGTGCATTTAAACAAGAACAAATGTGACATTG	3616
Oy	651	TTGCACAGCAAGTTGCTGAGAGCTCAACCTGTAC	685
Db	3617	CTGATCTGAAGTGGCTGTCAGCTTCAGTCAATTC	3651

```

RESULT 4
US-11-155-478A-26
; Sequence 26, Application US/11155478A
; Publication No. US20060014140A1
GENERAL INFORMATION:
APPLICANT: Boivin, Guy
APPLICANT: UNIVERSITE LAVAIL
TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
TITLE OF INVENTION: RESPIRATORY VIRUSES
FILE REFERENCE: 6013-1480S
CURRENT APPLICATION NUMBER: US/11/155,478A
CURRENT FILING DATE: 2005-06-20
PRIOR APPLICATION NUMBER: CA 2,411,264
PRIOR FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: CA 2,418,004
PRIOR FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: PCT/CA2003/001994
PRIOR FILING DATE: 2003-12-19
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 759
TYPE: DNA
ORGANISM: human metapneumovirus
FEATURE:
NAME/KEY: gene
LOCATION: (1) ..(759)
OTHER INFORMATION: human metapneumovirus, strain Can 98-75
US-11-155-478A-26

```

Query	Match	Similarity	1.2%	Score	41.4	DB	8	Length	759
Beet	Local	Similarity	46.9%	Pred.	No.	0.023			
Matches	129	Conservative	0	Mismatches	146	Indels	0	Gaps	0
Qy	411	TTGGGGGTGTGGCTCTTGGGGGTGGCAATGCCGCA	CAAAATTA	CAGCGCCGCA	GCTCTGA	470			
Db	314	TAGGTGCAATATACCTCTGGTGTGGCCACAGCAG	CAGCAATGCA	CAGGACGATTCG	CATATG	373			
Qy	471	TACAGGCCAAACAAATGCTGCCAATCTCCGATTA	AAAGAGCAT	TTGCCCGACCA		530			
Db	374	CCAAATCCATTAGGCTTGAGAGTGAATGAATGCAT	CAAAAGTGTCT	CAAAACACCA		433			
Qy	531	ATGAGGCTGTGCATAGTAGGTCAC	TGCGAATTCGCA	CTAGCAAGTGGCAG	TTGGGAGA	590			
Db	434	ACGAGGCGATATCCACACTAGGAAATGGAGTCG	AGTCTTACGCA	CCGCGATGAAGAGC		493			
Qy	591	TGCACAGTTTGTATATGACCAATTTAATAAAC	AGCTCAGGAAT	TAGATGCATCAAA		650			
Db	494	TGAAGAAATTTGTGACCAAAACCTGACTAGTG	CAATTTAA	CAAGAACAAATG	GACATTG	553			
Qy	651	TTGCACAGCAAGTTGGTGTAGAGCTCA	CCTGTAC		685				
Db	554	CTGACCTGAAGATGGCTGTCAAGCTTCAGTCA	ATTC		588				

```

RESULT 5
US-11-155-478A-49
; Sequence 49, Application US/11155478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE L'AVL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; PRIOR FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 759
; TYPE: DNA
; ORGANISM: human metapneumovirus
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)...(759)
; OTHER INFORMATION: human metapneumovirus, strain Quebec Isolate No
; OTHER INFORMATION: C-63778
US-11-155-478A-49

```

Query Match	1.2%	Score 41.4	DB 8	Length 759
Best Local Similarity	46.9%	Pred. No. 0.023		
Matches	129	Conservative	0	Mismatches 146; Indels 0; Gaps 0;
QY	411	TTGGGGGAGTGCCTCTTGGGGTTGCACATGCGCGACAATTAACAGCGCGCCGAGCTTGA	470	
DB	314	TAGGTGCATATGCTCTTGTTGTTGCCACAGACGACGATGCACAGCGCATTTGGGATNG	373	
QY	471	TACAAGCCMAACAAATATGCTGCCAACATCTCCGACTTAAAGAGCATTCGCCAACCA	530	
DB	374	CCAAACCATTAAGCGTTGAGAGTGAGTGAATGCAATCAAAAGTCTCTCAAAACAAACA	433	
QY	531	ATGAGGCTGTGCATGAGGTCACTGACGAGTTATCGCAACTGACGATGCTTGGGAAGA	590	
DB	434	ACGAGGCGAGTATCCACTAGGAAATGGAGTGCAGTCTTGCCACCACGATTAAGAGGC	493	
QY	591	TGCACGAGTTGTTAATATGACCAATTTATATAAAGCTCAGAGAAATTAAGTCATCAAAA	650	
DB	494	TGAAGAATTTGTGTGCAAAAACCTGACTAATGCAATTAACAAAGAAATGTGACATTG	553	
QY	651	TTGCACAGCAAGTTGGTGTAGAGCTCAACCTGTAC	685	
DB	554	CTGATCTGAAATGCGCTTCAAGCTTCAGTCAATTC	588	

```

RESULT 6
US-11-155-478A-51
; Sequence 51, Application US/11155478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-1480S
; CURRENT APPLICATION NUMBER: US/11/155, 478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994

```

```
;; PRIOR FILING DATE: 2003-12-19
;; NUMBER OF SEQ ID NOS: 174
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 51
;; LENGTH: 759
;; TYPE: DNA
;; ORGANISM: human metapneumovirus
;; FEATURE:
;; NAME/KEY: gene
;; LOCATION: (1)...(759)
;; OTHER INFORMATION: human metapneumovirus, strain Quebec Isolate No
;; OTHER INFORMATION: C-64200
US-11-155-478A-51
```

Query Match 1.2%; Score 41.4; DB 8; Length 759;

Best Local Similarity 46.9%; Pred. No. 0.023;

Matches 129; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

```
Qy 411 TTGGCGGTGCTCTTGGGGTTGCAACTGCCGCAAAATACGCGCCGCACTCTGA 470
Db 314 TAGGTGCAATAGCTCTTGTTGTCACACGACGACGAGTCACATTCGATAG 373
Qy 471 TACAGCCAAACAAATGCTGCCAATCTCCGACTTAAGAGAGATTGCCCAACA 530
Db 374 CCAAAACATTAAGGCTTGAGAGTGAATGCAATCAAAAGTGCTCTCAAAACA 433
Qy 531 ATGAGCTGTGATGAGTCACTGACGATTAATGCAATGAGTGGAGAG 590
Db 434 ACAGGCGAGTATCCACATGGAATGAGTGCAGTCTGACCGCAGTAAGAGC 493
Qy 591 TGCAGCAGTTTGTAAATGACCAATTTAATAAAGCTCAGGATTTAGATCATCAA 650
Db 494 TGAAGAAATTTGTAGCAAAAACCTGACTAGTGAATTAACAAACAAATGTGACATTG 553
Qy 651 TTGCACAGCAAGTTGTGTAGAGCTCAACTGTAC 685
Db 554 CTGATCTGAAGATGCTGTCTCAGCTTCAGTCAATTC 588
```

#### RESULT 7

```
US-11-155-478A-52
;; Sequence 52, Application US/11155478A
;; Publication No. US20060014140A1
;; GENERAL INFORMATION:
;; APPLICANT: Boivin, Guy
;; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
;; FILE REFERENCE: 6013-148US
;; CURRENT APPLICATION NUMBER: US/11/155, 478A
;; PRIOR FILING DATE: 2005-06-20
;; PRIOR APPLICATION NUMBER: CA 2,411,264
;; PRIOR FILING DATE: 2002-12-19
;; PRIOR APPLICATION NUMBER: CA 2,418,004
;; PRIOR FILING DATE: 2003-01-24
;; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
;; NUMBER OF SEQ ID NOS: 174
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 52
;; LENGTH: 759
;; TYPE: DNA
;; ORGANISM: human metapneumovirus
;; FEATURE:
;; NAME/KEY: gene
;; LOCATION: (1)...(759)
;; OTHER INFORMATION: human metapneumovirus, strain Quebec Isolate No
;; OTHER INFORMATION: C-64536
US-11-155-478A-52
```

Query Match 1.2%; Score 41.4; DB 8; Length 759;

Best Local Similarity 46.9%; Pred. No. 0.023;

Matches 129; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

```
Qy 411 TTGGCGGTGCTCTTGGGGTTGCAACTGCCGCAAAATACGCGCCGCACTCTGA 470
Db 314 TAGGTGCAATAGCTCTTGTTGTCACACGACGACGAGTCACATTCGATAG 373
Qy 471 TACAGCCAAACAAATGCTGCCAATCTCCGACTTAAGAGAGATTGCCCAACA 530
Db 374 CCAAAACATTAAGGCTTGAGAGTGAATGCAATCAAAAGTGCTCTCAAAACA 433
Qy 531 ATGAGCTGTGATGAGTCACTGACGATTAATGCAATGAGTGGAGAG 590
Db 434 ACAGGCGAGTATCCACATGGAATGAGTGCAGTCTGACCGCAGTAAGAGC 493
Qy 591 TGCAGCAGTTTGTAAATGACCAATTTAATAAAGCTCAGGATTTAGATCATCAA 650
Db 494 TGAAGAAATTTGTAGCAAAAACCTGACTAGTGAATTAACAAACAAATGTGACATTG 553
Qy 651 TTGCACAGCAAGTTGTGTAGAGCTCAACTGTAC 685
Db 554 CTGATCTGAAGATGCTGTCTCAGCTTCAGTCAATTC 588
```

#### RESULT 8

```
US-11-155-478A-53
;; Sequence 53, Application US/11155478A
;; Publication No. US20060014140A1
;; GENERAL INFORMATION:
;; APPLICANT: Boivin, Guy
;; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
;; FILE REFERENCE: 6013-148US
;; CURRENT APPLICATION NUMBER: US/11/155, 478A
;; PRIOR FILING DATE: 2005-06-20
;; PRIOR APPLICATION NUMBER: CA 2,411,264
;; PRIOR FILING DATE: 2002-12-19
;; PRIOR APPLICATION NUMBER: CA 2,418,004
;; PRIOR FILING DATE: 2003-01-24
;; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
;; NUMBER OF SEQ ID NOS: 174
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 53
;; LENGTH: 759
;; TYPE: DNA
;; ORGANISM: human metapneumovirus
;; FEATURE:
;; NAME/KEY: gene
;; LOCATION: (1)...(759)
;; OTHER INFORMATION: human metapneumovirus, strain Quebec Isolate No
;; OTHER INFORMATION: C-73769
US-11-155-478A-53
```

Query Match 1.2%; Score 41.4; DB 8; Length 759;

Best Local Similarity 46.9%; Pred. No. 0.023;

Matches 129; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

```
Qy 411 TTGGCGGTGCTCTTGGGGTTGCAACTGCCGCAAAATACGCGCCGCACTCTGA 470
Db 314 TAGGTGCAATAGCTCTTGTTGTCACACGACGACGAGTCACATTCGATAG 373
Qy 471 TACAGCCAAACAAATGCTGCCAATCTCCGACTTAAGAGAGATTGCCCAACA 530
Db 374 CCAAAACATTAAGGCTTGAGAGTGAATGCAATCAAAAGTGCTCTCAAAACA 433
Qy 531 ATGAGCTGTGATGAGTCACTGACGATTAATGCAATGAGTGGAGAG 590
Db 434 ACAGGCGAGTATCCACATGGAATGAGTGCAGTCTGACCGCAGTAAGAGC 493
Qy 591 TGCAGCAGTTTGTAAATGACCAATTTAATAAAGCTCAGGATTTAGATCATCAA 650
Db 494 TGAAGAAATTTGTAGCAAAAACCTGACTAGTGAATTAACAAACAAATGTGACATTG 553
```



OY 651 TTGCACAGCAAGTTGTGTAGAGCTCAACTGTAC 685  
Db 554 CTGATCTGAAGATGGCTGTGCTGAGCTTCACTCAATTC 588

## RESULT 9

US-11-155-478A-54  
; Sequence 54, Application US/11155478A  
; Publication No. US20060014140A1  
; GENERAL INFORMATION:

APPLICANT: Bolivian Guy  
APPLICANT: UNIVERSITE LAVAL  
TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING  
FILE REFERENCE: 6013-148US  
CURRENT APPLICATION NUMBER: US/11/155,478A  
CURRENT FILING DATE: 2005-06-20  
PRIOR APPLICATION NUMBER: CA 2,411,264  
PRIOR FILING DATE: 2002-12-19  
PRIOR APPLICATION NUMBER: CA 2,418,004  
PRIOR FILING DATE: 2003-01-24  
PRIOR APPLICATION NUMBER: PCT/CA2003/001994  
PRIOR FILING DATE: 2003-12-19  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 54  
LENGTH: 759  
TYPE: DNA  
ORGANISM: human metapneumovirus  
FEATURE:  
NAME/KEY: gene  
LOCATION: (1)...(759)  
OTHER INFORMATION: human metapneumovirus, strain Quebec Isolate No  
OTHER INFORMATION: C-74501  
US-11-155-478A-54

Query Match 1.2%; Score 41.4; DB 8; Length 759;  
Best Local Similarity 46.9%; Pred. No. 0.023;  
Matches 12; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

OY 411 TTGGCGGTGTGCTCTTGGGTTGCACTGCCGCAAAATACAGCGCGCCGAGCTTGA 470  
Db 314 TAGGTGCAATAGCTCTTGGTGTGTCACAGCAGCAGCAGTCACTTGGGAATG 373  
OY 471 TACAGCCAAACAAATGCTCCCAATCTCCCACTTAAAGAGAGATTGCCGAACCA 530  
Db 374 CCAAAACCATTAAGGCTTGAAGTGAAGTGAATGCATCAAAAGTCTCTCAAAACACCA 433  
OY 531 ATGAGGCTGTGCTAGAGGTCACGATTAATGCACTAGCAGTGCAGTTGGGAAGA 590  
Db 434 ACGAGGCAATTCACACTAGAAATGAGTCCAGTCTTAGCCACTGCACTAAGAGAGC 493  
OY 591 TGCAGAGTTTGTAAATGACCAATTTAATAAAGCTCAGGAATTAGATGATCAAAA 650  
Db 494 TGAAGAATTTGTGAGCAAAAACCTGACTAGTCAATTAACAAGAAATGTGACATTG 553  
OY 651 TTGCACAGCAAGTTGTGTAGAGCTCAACTGTAC 685  
Db 554 CTGATCTGAAGATGGCTGTGCTGAGCTTCACTCAATTC 588

## RESULT 10

US-11-155-478A-27  
; Sequence 27, Application US/11155478A  
; Publication No. US20060014140A1  
; GENERAL INFORMATION:

APPLICANT: Bolivian Guy  
APPLICANT: UNIVERSITE LAVAL  
TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING  
FILE REFERENCE: 6013-148US  
CURRENT APPLICATION NUMBER: US/11/155,478A  
CURRENT FILING DATE: 2005-06-20

;; PRIOR APPLICATION NUMBER: CA 2,411,264  
;; PRIOR FILING DATE: 2002-12-19  
;; PRIOR APPLICATION NUMBER: CA 2,418,004  
;; PRIOR FILING DATE: 2003-01-24  
;; PRIOR APPLICATION NUMBER: PCT/CA2003/001994  
;; PRIOR FILING DATE: 2003-12-19  
;; NUMBER OF SEQ ID NOS: 174  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 27  
;; LENGTH: 759  
;; TYPE: DNA  
;; ORGANISM: human metapneumovirus  
;; FEATURE:  
;; NAME/KEY: gene  
;; LOCATION: (1)...(759)  
;; OTHER INFORMATION: human metapneumovirus, strain Quebec Isolate No  
;; OTHER INFORMATION: C-67345  
US-11-155-478A-27

Query Match 1.2%; Score 41.2; DB 8; Length 759;  
Best Local Similarity 46.8%; Pred. No. 0.027;  
Matches 130; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

OY 408 TTATTGGCGGTGTGCTCTTGGGTTGCACTGCCGCAAAATACAGCGCGCCGAGCTC 467  
Db 311 TTCTGGAGCAATAGCACTCGTGTGCAAGCAGCAGTCACTGAGTGTGCA 370  
OY 468 TGATCAAGCCAAACAAATGCTGCCAATCTCCCACTTAAAGAGAGCATTTGCCGCA 527  
Db 371 TTGCCAAACCATTCGCGCTTGAAGTGAAGTGAATGCATTAAGATGCCCTCAAAACGA 430  
OY 528 CCAATGAGGCTGTGCTAGAGTCACTGACGATTAATGCACTAGCAGTGCAGTTGGA 587  
Db 431 CCAATGAAGCAATTCATCAATTTGGAATGAGATGAGTTCAGTGTGCAATCTGAGTGAAG 490  
OY 588 AGATGACAGCACTTTGTAAATGACCAATTTAATAAAGCTCAGGAATTAGATGATCA 647  
Db 491 AGCTGAAGACTTTGTGAGCAAAATTTAATCTGTGCAATCAACAAAGAGTGCACA 550  
OY 648 AAATTGCACAGCAAGTTGTGTAGAGCTCAACTGTAC 685  
Db 551 TTGATGACTTAAATAGCGCTTGAAGCTTCACTCAATTC 588

## RESULT 11

US-11-155-478A-28  
; Sequence 28, Application US/11155478A  
; Publication No. US20060014140A1  
; GENERAL INFORMATION:

APPLICANT: Bolivian Guy  
APPLICANT: UNIVERSITE LAVAL  
TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING  
FILE REFERENCE: 6013-148US  
CURRENT APPLICATION NUMBER: US/11/155,478A  
CURRENT FILING DATE: 2005-06-20  
PRIOR APPLICATION NUMBER: CA 2,411,264  
PRIOR FILING DATE: 2002-12-19  
PRIOR APPLICATION NUMBER: CA 2,418,004  
PRIOR FILING DATE: 2003-01-24  
PRIOR APPLICATION NUMBER: PCT/CA2003/001994  
PRIOR FILING DATE: 2003-12-19  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 28  
LENGTH: 759  
TYPE: DNA  
ORGANISM: human metapneumovirus  
FEATURE:  
NAME/KEY: gene  
LOCATION: (1)...(759)  
OTHER INFORMATION: human metapneumovirus, strain Can 97-83  
US-11-155-478A-28



```

; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; PRIOR FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173
; LENGTH: 13335
; TYPE: DNA
; ORGANISM: Viruses
; FEATURE:
; OTHER INFORMATION: CAN9783 genomic DNA
US-11-155-478A-173

```

```

Query Match      1.2%; Score 41.2; DB 8; Length 13335;
Best Local Similarity 46.8%; Pred. No. 0.19;
Matches 130; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

```

```

Qy 408 TTATTGGCGGTGCTTTGGGGTTGCACTGCCGCAAAATTAACAGCGCCGCACTC 467
Db 3377 TTCTAGGAGCAATGACCTCCGTTGCAACAGCAGCTGACAGCAGGTTTGC 3436

Qy 468 TGATCAAGCCAAACAAATCTGCCACATCCCGCTTAAGAGAGCAATTGCCGGA 527
Db 3437 TTGCCAAAACCATCCGCGTTAGAGTGAATGACAGCAATTAAGATCCCTCAAAA 3496

Qy 528 CCAATGAGGCTGTGCATAGGTCACTGACGATTATCGCACTAGCAGTGGAGGA 587
Db 3497 CCAATGAGGAGTATCTCATTTGGGGAATGAGATTCGAGTGTGGCACTGCA 3556

Qy 588 AGATGACAGCAGTTGTTAATGACCAATTTAATAAAGCTCAGGAATTAGATGATCA 647
Db 3557 AGCTGAAGACTTTGTGAGCAAGAAATTAACCTCGTCAATCAACAAAACAAAGTCCGACA 3616

Qy 648 AAATTGCACAGCAAGTGTGTAGAGCTCAACTGTAC 685
Db 3617 TTGATGACCTTAATAAATGCGCGTTAGCTTCACTCAATTC 3654

```

```

RESULT 15
US-11-155-478A-57
; Sequence 57, Application US/11/155,478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 759
; TYPE: DNA
; ORGANISM: human metapneumovirus
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)...(759)
; OTHER INFORMATION: human metapneumovirus, strain Quebec isolate No

```

```

; OTHER INFORMATION: hMPV-118
US-11-155-478A-57

```

```

Query Match      1.2%; Score 39.8; DB 8; Length 759;
Best Local Similarity 46.5%; Pred. No. 0.075;
Matches 128; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

```

```

Qy 411 TTGGCGGTGCTCTTTGGGGTTGCACTGCCGCAAAATTAACAGCGCCGCACTGGA 470
Db 314 TAGGTGCAATAGCTCTTGTGTGTCCACAGCAGCAGTCAAGCAGGCAATGGCATAG 373

Qy 471 TACAAGCCAAACAAATGCTGCCAATCTCCGACTTAAGAGAGCAATCCCAACCA 530
Db 374 CCAAAACCATTAAGGCTTGAAGTGAATGAATGAATCAATCAAGTCTCAAAA 433

Qy 531 ATGAGCTGTGCATGAGGTCACTGACGATTAATGCACTAGCAGTGGCAATGGAAGA 590
Db 434 ACGAGGCGATATCCACACTAGAAATGGAATGCGAGTCTTAGCCACCGCATTAAGAGAC 493

Qy 591 TGCAGCAGTTTGTTAATGACCAATTTAATAAAGCTCAGAAATTAGATGCATCAAAA 650
Db 494 TGAAGAATTTGTGAGCAAAAACCTGACCACTGCAATTAACAAGAAACAAATGTGACATTG 553

Qy 651 TTGCAACAGCAAGTTGTGTAGAGCTCAACTGTAC 685
Db 554 CTGATCTGAAGATGGCTGTGACCTTCACTCAATTC 588

```

```

Search completed: February 5, 2006, 07:13:40
Job time : 542 secs

```

Page Blank (uspro)

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 21:39:15 ; Search time 12642 Seconds  
(without alignments)  
12427.703 Million cell updates/sec

Title: US-10-800-256-1

Perfect score: 3358  
Sequence: 1 acgggtagaagatcttgat.....cctaactctatagaacc 3358

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_hcc3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_est7: \*  
9: gb\_ges1: \*  
10: gb\_ges2: \*  
11: gb\_ges3: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	500.8	14.9	766	7	CK280174 SSH227 SS
2	87.8	2.6	692	2	BG661033 N339 SSH-
3	46.2	1.4	862	9	AZ538746 ENTDM69TF
4	46.2	1.4	886	9	AZ541254 ENTFA11TF
5	43.6	1.3	406	1	AY032979 AY032979
6	43.2	1.3	386	1	AW329422 N200657E
7	43.2	1.3	494	1	AL380807 MCBBS4F09
8	43.2	1.3	670	2	BF641250 NF058C11I
9	42.6	1.3	825	10	C2940314 322053 TO
10	42.6	1.3	1022	11	CD081007 MA3-9999U
11	42.4	1.3	507	6	CD081007 MA3-9999U
12	42.4	1.3	816	11	AL620307 T7_end of
13	42.4	1.3	816	11	CK335184 H3150E07-
14	42.4	1.3	651	7	CK335184 H3150E07-
15	42.4	1.3	687	5	BY732720 BY732720
16	42.4	1.3	719	3	BM950384 UI-M-EHOP
17	42.4	1.3	751	10	CL797382 OR_CBA000
18	41.8	1.2	1085	10	AL101102 Drosophila
19	41.6	1.2	845	10	AL053138 Drosophila
20	41.6	1.2	873	10	C2940484 322268 TO
21	41.4	1.2	551	10	C2784281 OC_Ba014
22	41.4	1.2	680	10	C2835932 OC_Ba021

C 23	41.4	1.2	1101	10	CNS001T2	AL078714 Drosophila
C 24	41.2	1.2	422	5	BU496251	BU496251 PESTOACO
C 25	41.2	1.2	847	10	CNS00097	AL053305 Drosophila
C 26	41.2	1.2	878	10	DU094707	DU094707 109747 TO
C 27	41.1	1.2	893	9	BH150882	BH150882 ENTFT21TR
C 28	40.8	1.2	1079	5	BX375722	BX375722 BX375722
C 29	40.6	1.2	716	10	CE672698	CE672698 tigr-g86-
C 30	40.4	1.2	670	9	BH158224	BH158224 ENTSP70TF
C 31	40.4	1.2	714	9	AQ324694	AQ324694 mgx0019D
C 32	40.4	1.2	801	10	BX213898	BX213898 Danilo rer
C 33	40.4	1.2	894	10	C2950329	C2950329 260379 TO
C 34	40.4	1.2	904	10	C2929153	C2929153 246488 TO
C 35	40.4	1.2	997	10	C2949863	C2949863 263323 TO
C 36	40.2	1.2	779	9	AQ855008	AQ855008 Cpg2035B
C 37	40.2	1.2	825	10	DU057393	DU057393 96348 Tom
C 38	40.2	1.2	865	9	BH180441	BH180441 016 H_20-
C 39	40.2	1.2	865	11	CNS07MAN	AL617393 T3 end of
C 40	40.2	1.2	878	10	CNS0187R	AL108993 Drosophila
C 41	40.2	1.2	1101	10	CNS003FR	AL064653 Drosophila
C 42	40.2	1.2	1101	10	CG853182	CG853182 ND.L.12651
C 43	40.2	1.2	625	9	C2040511	C2040511 OM_Ba002
C 44	40.2	1.2	937	10	DU043874	DU043874 158239 TO
C 45	40.2	1.2	1032	10	CNS010NH	AL099191 Drosophila

#### ALIGNMENTS

RESULT 1  
LOCUS CK280174 766 bp mRNA linear EST 05-JAN-2004  
DEFINITION SSH227 SSH generated forward (3 days-2 days) subtracted cDNA  
library Phanerochaete chrysosporium cDNA, mRNA sequence.

ACCESSION CK280174  
KEYWORDS CK280174.1 GI:40556623

ORGANISM Phanerochaete chrysosporium (anamorph: Sporotrichum pulmosum)  
Phanerochaete chrysosporium  
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

REFERENCE 1 (bases 1 to 766)  
Aphyllophorales; Corticiaceae; Phanerochaete.

AUTHORS Jiang, M. and Zhang, Y.  
TITLE Screen for Temporal-specific Expression Genes of Phanerochaete  
chrysosporium Based on SSH and cDNA Microarrays

JOURNAL Unpublished (2003)  
COMMENT Contact: Yizheng Zhang

Sichuan Key Laboratory of Molecular Biology and Biotechnology  
College of Life Science, Sichuan University  
Chengdu, Sichuan, box610064 P.R. CHINA  
Tel: 86 028 85412738  
Email: yizhang@scu.edu.cn

SSH generated forward (3 days-2 days) subtracted cDNA library of  
Phanerochaete chrysosporium; average insert size: 600 bp;  
Information: Isolation of total RNA from the mycelia incubated in  
shallow stationary culture (Kirk media) at 39\_

Insert Length: 766 Std Error: 0.00  
POLY(A)=No.

FEATURES  
location/Qualifiers  
1..766  
/organism="Phanerochaete chrysosporium"  
/mol\_type="mRNA"  
/strain="BKM-F-1767"  
/db\_xref="taxon:5306"  
/clone\_lib="SSH generated forward (3 days-2 days)  
subtracted cDNA library"  
/note="Vector: pMD18T-vector; SSH generated cDNA library  
of Phanerochaete chrysosporium incubated in N-limited  
shallow stationary culture"

#### ORIGIN

Query Match 14.9%; Score 500.8; DB 7; Length 766;  
Best Local Similarity 84.1%; Pred. No. 9.1e-137;  
Matches 565; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

```

Qy 43 CAGATGGGCTCCAGACCTTCTACCAAGACCAGACCTATGATGCTGACTATCCGGT 102
Db 95 CACCATGGGCTCCAACTTTCTACAGAGATCCAGCACTCTGATGCTGATCACCAGAT 154
Qy 103 TGCCCTGGCACTGAGTTGCTATCTGTCCGGCAAACTCCATTGATGGCAGGCTTTGACG 162
Db 155 TATCTGATATTTGGCGTGTATCCGTCCAGCAAGCTCTTTACCGCAGGCTTTGACG 214
Qy 163 TGCAGAAATTTGGTTACAGAGACAAGCGCTCAACATATACACCTGATCCAGACAG 222
Db 215 TGCAGAAATTTAGTAAACAGAGATAGGCAATATATACCTGTCTCAGACAG 274
Qy 223 ATCAATCATAGTTAAGCTCTCTCCGAATCTGCCAAGANTAAAGAGCATGTCCGAAG 282
Db 275 GTCAATCATAGTCAAGTTGCTCCGAATATGCCAGGATTAAGAGGCGTGTGCGAAAG 334
Qy 283 CCCCTTGATGATACAAACAGACATTGACCACTTTGTCTACCCCTTTGCTGATCTAT 342
Db 335 CCCATTAGAGGCAATATACAGAACCTGACTATTTGCTACTCTCTTTGGCACTCAT 394
Qy 343 CCGTAGAGTACAAAGTGTGTGACTACATCTGAGAGGGGAGACAGGGGCGCTTATAG 402
Db 395 CCGAAGATCCAGGGGTGTGTGTCCAGCTCTGAGAGAAAGAGCAAAAACCTTTATAG 454
Qy 403 CGCCATTATTTGGCGGTGTGCTCTTGGGGTTGCAACTGCCACAAATTAAGCGGCCG 462
Db 455 TGTGTTATTTGGCGGTGTAGCTCTTTGGGGTTGCAAGCGGCAAGATTAACAGACGTGC 514
Qy 463 AGCTCTGATACAAAGCAAAATGCTGCCAATCTCTCGACTTTAAAGAGACTTGC 522
Db 515 GGCCTTATATACCAACCAACCGGAATGCCCAACATCTCTCGGGCTTAAAGAGACATTC 574
Qy 523 CGCAACCAATAGGCTGTGATGAGTCACTGACGAGATTAACGAACTAAGAGAGTGGAGT 582
Db 575 TGCACCAATAGAGTGTGATGAGTCAACGAGATTAACGAACTAATAGTGGAGT 634
Qy 583 TGGAGAGTGCAGAGTTTGTAAATGACCAATTTAAATMAACAGCTCAGAAATTAAGATG 642
Db 635 TGGAGAGTGCAGAGTTTGTCAATGACAGTTTAAATMAATCGGGCGAGAAATGGACTG 694
Qy 643 CATCAAAATTTGCACAGCAAGTTGGTGTAGAGCTCAACTGTAACCTTAACCAATTAAGTAC 702
Db 695 TATTAATAATCACACAAACAGTTGGTGTAGAACTCAACCTATACCTTAATGAATGACTAC 754
Qy 703 AGTATGGAGCC 714
Db 755 AGTATCGGGCC 766

```

```

RESULT 2
BG661033 692 bp mRNA linear EST 26-APR-2001
LOCUS N339 SSH-HCA-U library Homo sapiens cDNA, mRNA sequence.
DEFINITION BG661033
ACCESSION BG661033
VERSION BG661033.1 GI:13805211
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 692)
Zhang, Z. and Dubois, R.N.
Detection of differentially expressed genes in human colon cancer
cells treated with NS-398 using suppression subtractive
hybridization and differential screening
Unpublished (2000)

```

```

JOURNAL COMMENT
Contact: Zhonghua Zhang
Department of Medicine
Vanderbilt Medical Center
MCN C-2104, 1161 21st Ave. South, Nashville, TN 37212, USA
Tel: 615 343 1369

```

```

Fax: 615 343 6229
Email: zhonghua.zhang@mcmail.vanderbilt.edu
DNA sequencing by: Vanderbilt Medical Center DNA sequencing core
laboratory. This is a fragment of gene that up-regulated by NS-398
treatment.
PCR primers
FORWARD: 5'-CTAATAGACTCACTATAGGC-3'
BACKWARD: 5'-TCGAGCGCGCCCGGCGAGGT-3'
Seq primer: M13 forward primer
High quality sequence stop: 692.
Location/Qualifiers
1..692
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="Colon cancer cell"
/cell_line="HCA-7"
/clone_lib="SSH-HCA-U library"
/note="Vector: PCR2.1-TOPO. Poly A RNA was isolated from
NS-398 treated and control cells, and suppression
subtractive hybridization was performed in forward and
reverse directions. The adapter sequences used in the
hybridization were as follows:
5'-CTAATAGACTCACTATAGGCCTCGACGGCCGCCGCGCAGGT-3'
(adapter 1) and
5'-CTAATAGACTCACTATAGGCAGCGGTGTCGCGCCGAGGT-3' (adapter
2R)."

```

## ORIGIN

```

Query Match 2.6%; Score 87.8; DB 2; Length 692;
Best Local Similarity 48.7%; Pred. No. 7.7e-14;
Matches 273; Conservative 0; Mismatches 282; Indels 6; Gaps 1;

```

```

Qy 219 CAGATCAATCATATGATTAAGTCTCTCCGATCTGCCAAGATTAAGAGGATGTGCGA 278
Db 132 CAGATCATTTGTTGTATAGTTAATGCTTACATATGACTCGCGATTAGTGAATATA 191
Qy 279 AAGCCCTTGATGATACACAGACAGCACTTTGCTACCCCTTGTGACT 338
Db 192 TAACATCAATTCAGAGTATTAAGCAACAGTGAACAAATCTTACAGCCGATGAGAGA 251
Qy 339 CTATCCGTAGATACAAAGTCTGTGACTAATCTGAGAGGGGAGACAGGGGCGCTTA 398
Db 252 ATTTGAGCAAAATTAAGAACCAATGATTCCACT-----CGAGGAGACGCCGATTTG 305
Qy 399 TAGCGCCATTATTTGGCGGTGTGCTCTTGGGGTTGCACTGCGCAAAATTAACAGCG 458
Db 306 CAGGGGTGTGATTTGATTTAGTGTGATTAAGAGTACTGCGCACAGTCACTGCCG 365
Qy 459 CCGAGCTGTGATACAGCCAAACAAATGCTGCAACATCTCCGACTTAAAGAGACA 518
Db 366 CAGTAGACTATGATTAAGCAAAATGAATGAAATCTCGGCTATATCTCAAAATGCAA 425
Qy 519 TTGCGGCAACCATAGAGCTGTGATGAGTCACTGACGATTAATGCCAATGCACTGAG 578
Db 426 TCCAAAACAAATGCGGAGTTGCAACGTGTGTCAGGCGCACAAATCTAGGAAACGG 485
Qy 579 CAGTTGGAGAGATGACAGCTTTGTTAATGACCAATTAATTAACACAGCTCAGGAATTAG 638
Db 486 CAGTTCAAGAGTTCAAGATCATATTAACAGTGTGTAGTCCAGCAATTAACAGACCA 545
Qy 639 ACTGCATCAAAATTTGCACAGCAAGTTGGTGTAGAGCTCAACCTGTACCAACCGAATGA 698
Db 546 ACTGTAGGCCCAAGAGTGTATATAGTGTGCTCAATCTCAATCTTATTAACGAGTTGA 605
Qy 699 CTACAGATTTGGACCAAAATCATCTTCACTGCTTTAAACAAAGTACTATTCAGGCAC 758
Db 606 CAATATCTTCCAAATCAAAATTAACAAACCTGATGAGTCTTATTAATCAATTCAGCTT 665
Qy 759 TTTACATCTAGCTGTGGA 779
Db 666 TAAAGATTTCTAGGGAGTA 686

```





AY032979/c  
LOCUS AY032979 406 bp mRNA linear EST 03-MAY-2002  
DEFINITION AY032979 upregulated by angiotensin II in mesangial cells Homo sapiens cDNA clone Angm-52f, mRNA sequence.  
ACCESSION AY032979  
VERSION AY032979.1 GI:20429781  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 406)  
Zhou, A., Zhang, H. and Wang, H.  
Cloning and identification of a novel gene up-regulated in human mesangial cells stimulated by angiotensin II  
Unpublished (2002)  
Contact: Zhou, A., Zhang, H. and Wang, H.  
Institute of Nephrology  
Peking University  
No. 8, Xishiku St., Beijing, 100034, P. R. China.  
Location/Qualifiers  
1..406  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="Angm-52f"  
/clone\_1b="upregulated by angiotensin II in mesangial cells"  
FEATURES  
source  
ORIGIN  
Query Match 1.3%; Score 43.6; DB 1; Length 406;  
Best Local Similarity 47.2%; Pred. No. 0.91;  
Matches 133; Conservative 0; Mismatches 149; Indels 0; Gaps 0;  
401 GCGGCATTAATGGCGGTGCTCTTGGGGTTCGAATCGCCGACAAATPACAGCGCC 460  
282 GGGGCGGTCATCGGTGAGTTGTCATTAGGGGTGGCGATTCAGCGCAGATTACAGCAGGC 223  
461 GCAGCTCTGATACAGCCAAACAAATGCTGCCAATCTCCGACATTAAAGAGAGATT 520  
222 GTTGCTTTCACAACTCATTCAGAAATGCAATGCTATTTTGACAGCTCAAGATTCTATC 163  
521 GCCGCAACATGAGCTGTGTCATGAGTCACTGACGATTAATGCAATGACAGTGGCA 580  
162 AGCAGCTTAACAAGAAATACAAAGATTACAAACACTATGTCTACACTGTCTGTG 103  
581 GTTGGGAAGATGACAGCTTTGTTAATGACCAATTAAATAAACAGCTCAGAAATTAGAC 640  
102 TTAATGCTCTCCAGGACAGAAATTAATCAGTTGGCCGACGCTATTAATTTCTTAGA 43  
641 TGCATCAAAATTCACAGCAAGTTGCTAGAGCTCAAGCTG 682  
42 TGCAGGTGGTGTCTAATACCTAGTCTAAATTAACAG 1  
RESULT 6  
AM329422 386 bp mRNA linear EST 01-MAY-2000  
LOCUS AM329422  
DEFINITION N200657e rootphos(-) Medicago truncatula cDNA clone MHRP-19H9, mRNA sequence.  
ACCESSION AM329422  
VERSION AM329422.1 GI:6800017  
KEYWORDS EST.  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.  
1 (bases 1 to 386)  
Harrison, M. J., Liu, J., Harris, A. R., Scott, A. D., Gonzalez, R. A., Gonzalez, M. B. and Ellis, L.

TITLE ESTs from phosphate starved roots  
JOURNAL Unpublished (1999)  
COMMENT Contact: Harrison M.J.  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73401  
Tel: 580-223-5810  
Fax: 580-221-7380  
Email: mjharrison@noble.org  
Date: 1/23/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at 'http://chryslr.tamu.edu/medicago'.  
Seq primer: T3.  
Location/Qualifiers  
1..386  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/cullivar="Jemalong, line A17"  
/db\_xref="taxon:3880"  
/clone="MHRP-19H9"  
/issue\_type="roots"  
/dev\_stage="phosphate starved"  
/clone\_1b="rootphos(-)"  
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, they were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from the roots. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-zap phage using Ex-assist helper phage and propagated in SOLR cells."  
ORIGIN  
Query Match 1.3%; Score 43.2; DB 1; Length 386;  
Best Local Similarity 50.0%; Pred. No. 1.2;  
Matches 108; Conservative 0; Mismatches 108; Indels 0; Gaps 0;  
1394 ATCAAGATTCCTCAAGTAATATPACAGGCAATCTGATATCTCACTGAGCTTGGGAAT 1453  
81 ATAGCATTAACCCCTACCAATTAATGCTAAAGTAATCTCACAGTGGCTTTAGT 140  
1454 GTCACAACTCGATCAGTAATGCTTTGAATPAGTAAGAGAAACAAGAAACTAGAC 1513  
141 GTAAACATCTGCTCAAGAACATGAATGTTGTTCCGAAGAGACAGAAAGAGAG 200  
1514 AAGTCATGTCAAATGACTACACATGCTCTCATTAATGCTTTTGAATATC 1573  
201 AGATCAAGTTGTAATATCTTCTTAACGGAAGCTTTGTAAGTTGTGTAATATC 260  
1574 ATATCTTGTGTTTGGTATCTTAGCCTGATTTCTA 1609  
261 ATACGTTGAGTTAGTTGCTTTTGTGACCTTTA 296  
RESULT 7  
AL380807 494 bp mRNA linear EST 03-AUG-2000  
LOCUS AL380807  
DEFINITION MCBBS4F09R1 MBB Medicago truncatula cDNA clone MCBBS4F09 T7, mRNA sequence.  
ACCESSION AL380807  
VERSION AL380807.1 GI:9680559  
KEYWORDS EST.  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.  
1 (bases 1 to 494)

## AUTHORS

**TITLE**

JOURNAL  
COMMENT

unpublished (2000)  
contact: Genoscope

## FEATURES

**BOURCE**

Genoscope Centre National de Séquençage  
2 rue Gaston Creteilux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: [segreff@genoscope.cns.fr](mailto:segreff@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Contact : Pascal Gams and Etienne-Pascal Journé, Laboratoire de  
Biologie Moléculaire des Relations Plantes-Microorganismes,  
CNRS-INRA, BP 27, 31326 Castelnau-Tolosan Cedex, France (Email :  
[Mc-est@couliouze.inra.fr](mailto:Mc-est@couliouze.inra.fr) WebSite :  
<http://sequence.toulouse.inra.fr/Mruncatula.html> ).  
Location/Qualifiers

1. .494  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/cultivar="Jemalong"  
/db\_xref="taxon:3880"  
/clone="MdB34P09"  
/tissue\_type="symbiotic root nodules"  
/dev\_stage="harvested 4 days post inoculation with  
Sinorhizobium meliloti"  
/clone\_id="MdB3"  
/note="Vector: pBluescript pSK, Site\_1: EcoRI, Site\_2:  
XhoI; Plants were grown in an aeroponic chamber on  
nitrogen-rich medium for 21 days. Three days before  
inoculation with Sinorhizobium meliloti, the medium was  
replaced by N-free medium. Root nodules (+ short adjacent  
root segments) were harvested 4 days post inoculation.  
cDNA was prepared from polyA+ enriched RNA. The cDNA was  
directionally ligated into Uni-zap XR vector from  
Stratagene and packaged using Gigapack Gold packaging  
extracts. Plasmids containing cDNA inserts were  
mass-excised from phage stocks using Exseltis helper phage  
and propagated in SOUR cells. Clone ordering and  
sequencing was performed in the Centre National de  
sequençage (Genoscope, Evry, France)."

**ORIGIN**

Query Match	1.3%	Score 43.2;	DB 1;	Length 494;
Best Local Similarity	50.0%;	Pred. No. 1.3;		
Matches 108;	Conservative	0;	Mismatches 108;	Indels 0;
				Gaps 0;

Qy	1394	ATACAAAGTTCTCAAGTAATAATAACAGGCATCTTGATATCTCACTGAGCTTGGCAAT	1453
Db	190	ATAGCATTAACCTTCGCAATTTTGGTCTTAATTAATCTCACAGTCGCTTTAGGT	249
Qy	1454	GTCAACACTGCATCATGTAATGCTTTGAAATAGTTAGAGAAAGCAACAGAAACTAGAC	1513
Db	250	GTAACACATCGTGGTCAAGACACATGAATTGGTTCTGAGAGAGACAGAGAAAGAGAG	309
Qy	1514	AAAGTCATGTCMAAATGACTGACATCTGCTCTCATTACTTAATGTTTGACTATC	1573
Db	310	AGATCAAGTTGTAAATATCTTCTTAAACGAGAACCTTTGTAAATTTGTGTGTAATTC	369
Qy	1574	ATATCTCTGTTTTGTATACTTAACCGCAATCTCA	1609
Db	370	ATACGGTTGAGTTAGTTGCTTTTTTGGACTTTA	405

RESULT 8	
BP641250/c	
LOCUS	BF641250 670 bp mRNA
DEFINITION	NF058C11IN.F1085 Insect herbivory Medicago truncatula cDNA clone
ACCESSION	NF058C11IN.5', mRNA sequence.
VERSION	BF641250
KEYWORDS	BF641250.1 GI:11905408
SOURCE	EST.
ORGANISM	Medicago truncatula (barrel medic)
	Medicago truncatula

## REFERENCE

**TITLE**

1 (bases 1 to 670)  
 Klotz, H.K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,  
 Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.  
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago.  
 rosids, eucoside I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae.

JOURNAL  
COMMENT

Medicago truncatula insect-nerdivory library  
Unpublished (2000)  
Contact: Korth K

## FEATURES

Dept. of Plant Pathology  
University of Arkansas  
217 Plant Science Building, Fayetteville, AR 72701, USA  
Tel: 501 575 5191  
Fax: 501 575 7601  
Email: khorch@comp.uark.edu  
Insert length: 670 Std Error: 0.00  
plate: 058 row: C column: 11  
Seq primer: TCACACGGAACACGCTTCAC.  
Location/Qualifiers  
1..670

```

/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF058C11IN"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/clone_1lb="Insect herbivory"
/note="Vector: lambda zap; library was produced from full
expanded M. truncatula leaves of plants fed upon by
Spodoptera exigua (beet armyworm)" for 24 hours. Systemic
(unamaged leaves from injured plants) and wounded leaves
were harvested and pooled."

```

## ORIGIN

Query Match	1.3%	Score 43.2;	DB 2;	Length 670;
Best Local Similarity	50.0%;	Pred. No. 1.4;		
Matches 108;	Conservative	0;	Mismatches 108;	Indels 0;
			Gaps	0

QY  
139 ATTCAGATGATTCAGATGAATAATAACAGGCATCTTGATATCTCACTGAGCTGGGAAT 145

Db  
241 ATAGCATTAACCTTGATGCATATTTGGTGTCTAAATATATATCTCACACGTGGCTTTAGGT 182

QY  
1454 GTCCACCACTGCATCAGTAATGCTTTGATTAATGTAAGGAAACCAACAGAAAATGAG 151

Db  
181 GTAAACATGTGTGTCAAGAACCAATGAATTTGGTTCTGAAAGAGACAGAGAAAGAG 122

QY  
1514 AAAGTCATGTCAACTGACTAGACATCTGCTCTCAATACCTATATATCGTTTGAATATC 157

Db  
121 AGATCAAGTTTGAATAATATCTCTTAAACGGAAGACTTTGAAGTTGTGTGTAAATC 62

QY  
1574 ATATCTCTGTTTTGGATTAATTAAGCCTGATCTCA 1609

Db  
61 ATACGGTTGAGTTAGTTTGGCTTTTGGACCTTGA 26

RESULT 9				
C2940314/c				
LOCUS	C2940314	825 bp	DNA	linear
DEFINITION	322053 Tomato ECORI BAC Library Lycopersicon esculentum genomic			
	clone SL EcorI0012A21 5, genomic survey sequence.			
ACCESSION	C2940314_			
VERSION	C2940314.1	GI:72273291		
KEYWORDS	GSS.			
SOURCE	Lycopersicon esculentum (Solanum lycopersicum)			
ORGANISM	Lycopersicon esculentum			
	Eukaryota; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
	asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.			
REFERENCE	1 (bases 1 to 825)			
AUTHORS	Mueller, L.A., Buels, R.M., Wang, Y., Tanksley, S.D., Giovannoni, J.J.,			
	van Eck, J. and Stack, S.			

TITLE BAC end sequencing from three *Solanum lycopersicon* libraries  
JOURNAL Unpublished (2005)  
COMMENT Other GSSs: 308295  
Contact: Lukas Mueller  
Tankley Lab, Dept. of Plant Breeding  
Cornell University  
251 Emerson Hall, Ithaca, NY 14853, USA  
Tel: 607-255-6557  
Fax: 607-255-6683  
Email: segn-feedback@segn.cornell.edu  
Plate: 12 row: A column: 21  
Seq primer: T7  
Class: BAC ends  
High quality sequence start: 23  
High quality sequence stop: 782.  
Location/Qualifiers  
1. 825  
/organism="Lycopersicon esculentum"  
/mol\_type="genomic DNA"  
/cultivar="Heinz 1706"  
/db\_xref="taxon:4081"  
/clone="SL\_ECOR10012A21"  
/lab\_host="E. coli"  
/clone\_lib="Tomato EcorI BAC Library"  
/note="Vector: unk; Site\_1: EcorI"

ORIGIN  
Query Match 1.3%; Score 42.6; DB 10; Length 825;  
Best Local Similarity 51.9%; Pred. No. 2.4;  
Matches 96; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 1357 TGGGGAATTCGATGTAATCTATCAGAAATATCTCAATCAAGATTCTCAAGTAATAT 1416  
DB 526 TCGTATATTCGATTAATCTAGCCATTAATTTATTTATTTAAAAAATTT 467  
QY 1417 AACAGGAACTTCATATCTCACTGAGCTTGGAAATGTCAACAATCGATCACTATGC 1476  
DB 466 GTGAGCCAAATTTTGGCATAAGACTAATCTTGCAATATATGGAATCTAGAAATATGT 407  
QY 1477 TTGAATTAAGTTAGAGAAAGCAAGAAAATGACAAAGTCAAACTGACTAG 1536  
DB 406 TAACAAATTTTGGCAGAGCCAACTTTCACCTGACAAATGTCATAGATATCATTAG 347  
QY 1537 CACAT 1541  
DB 346 CTAAT 342

RESULT 10  
CNS03RIF 1022 bp DNA linear GSS 01-SEP-2000  
LOCUS Tetradon nigroviridis genome survey sequence PUC-ori end of clone  
DEFINITION 049107 of library G from Tetradon nigroviridis, genomic survey  
sequence.  
ACCESSION AL257280  
VERSION AL257280.1 GI:7978292  
KEYWORDS GSS: genome survey sequence.  
SOURCE Tetradon nigroviridis  
ORGANISM Tetradon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.  
1  
REFERENCE  
AUTHORS Reest Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
TITLE Estimate of human gene number provided by genome-wide analysis  
JOURNAL using Tetradon nigroviridis DNA sequence  
PUBMED Nat. Genet. 25 (2), 235-238 (2000)  
10835645  
2  
REFERENCE  
AUTHORS Reest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coestaz,C.,

TITLE Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,  
Saurin,W., Bernot,A. and Weissenbach,J.  
COMMENT Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetradon nigroviridis  
JOURNAL Genome Res. 10 (7), 939-949 (2000)  
PUBMED 10899143  
REFERENCE 3 (bases 1 to 1022)  
AUTHORS  
JOURNAL  
TITLE  
COMMENT  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetradon nigroviridis  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/tetradon.  
Location/Qualifiers  
1. 1022  
/organism="Tetradon nigroviridis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:99883"  
/clone="049107"  
/clone\_lib="G"  
/note="Tetradon genome sequence ID : COB6049CF048P1  
end : PUC-ori"

ORIGIN  
Query Match 1.3%; Score 42.6; DB 11; Length 1022;  
Best Local Similarity 49.3%; Pred. No. 2.6;  
Matches 111; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 1360 GGAATTCGATGTAATCTATCAGAAATATCTCAATCAAGATTCTCAAGTAATATAC 1419  
DB 837 GGTATTAAGAAATTCGATCAACCAATATTTCTATATGCTAAATGGCAAGTAATGAAG 778  
QY 1420 AGCAATCTTGATATCTCAATCTGAGCTTGGAAATGTCAACAATCGATCAATGCTT 1479  
DB 777 GAAATTCGATTAATCTTCCAGAGTCAAGAGTTGCAATCACTATTTCTATGCTTT 718  
QY 1480 GAATTAAGTTAGAGAAAGCAAGAAAATGACAAAGTCAAACTGACTAGCAC 1539  
DB 717 AAACAAATTTGGGAGAACCCAAAGTATATGTCATCTGAAATATATGAAAGCTC 658  
QY 1540 ATCTGCTTCATTAATCTATATCGTTTGAATCAATATCTTGT 1584  
DB 657 TGAATGATTATTAACAAACATGTTTCATCTTTCAACAAATAT 613

RESULT 11  
CD081007 507 bp mRNA linear EST 14-SEP-2003  
LOCUS MA3-9999U-MA17-D07-U.G MA3-0001 Schistosoma mansoni cDNA clone  
DEFINITION MA3-9999U-MA17-D07.G, mRNA sequence.  
ACCESSION CD081007  
VERSION CD081007.1 GI:34632000  
KEYWORDS EST.  
SOURCE Schistosoma mansoni  
ORGANISM Schistosoma mansoni  
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
Strigeidae; Schistosomatidae; Schistosomatidae; Schistosoma.  
1 (bases 1 to 507)  
REFERENCE  
AUTHORS Verjovski-Almeida,S., Demarco,R., Martins,E.A.L., Guimaraes,P.E.M.,  
Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y., Jr.,  
Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,  
Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,  
Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,  
Nascimento,A.L.T.O., Oliveira,F.P., Reis,E.M., Ribeiro,M.A.,  
Sa,R.G., Stuckart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,  
Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,  
Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.  
TITLE Transcription analysis of the acetonate human parasite Schistosoma  
mansoni  
JOURNAL Nat. Genet. 35 (2), 148-157 (2003)

PUBMED  
12973350  
COMMENT Contact: Dr. Sergio Verjovski-Almeida  
Departamento de Bioquímica  
Instituto de Química - Universidade de São Paulo  
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 São Paulo - SP,  
Brasil  
Tel: +55-11-3091-2173  
Fax: +55-11-3091-2186  
Email: verjowski@usp.br  
This sequence was derived from the PAPBP Schistosoma mansoni EST  
Genome Project. All sequences in the project were assembled and  
annotated. This entry and all the assembled sequences can be seen  
in the following URL <http://bioinfo.iq.usp.br/schisto/>  
Plate: M33-99990-M317 row: 7 column: D.  
FEATURES  
source  
1. 507  
/organism="Schistosoma mansoni"  
/mol\_type="mRNA"  
/db\_xref="taxon:6183"  
/clone="M33-99990-M317-D07.G"  
/sex="mixed pool"  
/dev\_stage="adult"  
/lab\_host="Mus musculus"  
/clone\_lib="M33-0001"  
ORIGIN  
Query Match 1.3%; Score 42.4; DB 6; Length 507;  
Best Local Similarity 49.4%; Pred. No. 2.3;  
Matches 88; Conservative 0; Mismatches 90; Indels 0; Gaps 0;  
Gy 1481 AATAGTTAGAGGAGCAAGCAAGAACTAGACAAAGTCAATGTCAACTGACTAGACACA 1540  
Db 130 AACAGTTCCGCAATATCAACAGACACAGACACCGTTATTAAGGCTTACAGCTAA 189  
Gy 1541 TCGCTCTCATCTACTATATGTTTGGACTATCATCTCTGTTTGGTATACCTTAGC 1600  
Db 190 ACCTGTCTCATCTAGCTTATCTCTGAATATTATTCAGACATTATCTCTCACTTGA 249  
Gy 1601 CTGATTTAGAGCTACTATATGTATAGCAAGCAAGGCGCAACAAACCTTATAT 1658  
Db 250 TCCAACTTCTATGTTTACGTTTACCAAGGAGATNNNNNNNNNNNNNAGCAATTAAT 307

Class: BAC ends  
High quality sequence stop: 816.  
FEATURES  
source  
Location/Qualifiers  
1. 816  
/organism="Schistosoma mansoni"  
/mol\_type="genomic DNA"  
/strain="Puerto-Rican"  
/db\_xref="taxon:6183"  
/clone="023G14"  
/sex="mixed"  
/dev\_stage="cercariae"  
/lab\_host="Blomphalaria glabrata"  
/clone\_lib="SmbAC1"  
/note="Vector: pBelOBAC 11; Site 1: Hind III; Partially  
Hind III digested and size-selected S. mansoni cercarial  
DNA was ligated into Hind III digested pBelOBAC 11 vector  
and used to transform E. coli DH10B. The complete library  
contains 23808 clones from 4 independent  
sizing-ligation-transformations. Average insert size  
ranges from 70-127 kb and genome coverage is 7.9-fold."  
ORIGIN  
Query Match 1.3%; Score 42.4; DB 9; Length 816;  
Best Local Similarity 35.8%; Pred. No. 2.7;  
Matches 81; Conservative 41; Mismatches 104; Indels 0; Gaps 0;  
Gy 1375 TTATCAAGAAATATCTCATACAGATCTCAAGTATATATACAGCAATCTTGATAT 1434  
Db 536 TTAGAGAAAAAAT 477  
Gy 1435 CTCAACTAGCTGGGATGTCACAACTCGATCATGATGCTTGAATATAGTAGGA 1494  
Db 476 AT 417  
Gy 1495 AAGCAAGCAAACTATACAAAGTCAATGTCAACTAGACATCTGCTCATATAC 1554  
Db 416 AAAAAAAYAAAGATATMAAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAA 357  
Gy 1555 CTATATGTTTGGACTATCATATCTCTGTTTGGTATACCTTAGC 1600  
Db 356 YGYBYKTKYKTYGTTGTTGKTGKTGTGGBGCKMGYAGC 311

RESULT 13  
CNS070UL/c 816 bp DNA linear GSS 30-NOV-2001  
LOCUS  
DEFINITION T7 end of clone 023BD07 of library SmbAC1 from strain Puerto-Rican  
ACCESSION AL620307  
VERSION AL620307.1 GI:16034449  
KEYWORDS GSS.  
SOURCE Schistosoma mansoni  
ORGANISM Schistosoma mansoni  
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
Strigeidae; Schistosomatidae; Schistosomatidae; Schistosoma.  
REFERENCE  
1 (bases 1 to 816)  
Le Paslier M.C., Pierce R.J., Merlin F., Hirai H., Wu W.,  
Williams D.U., Johnston D., Loverde P.T. and Le Paslier D.  
Construction and characterization of a Schistosoma mansoni  
bacterial artificial chromosome library  
Genomics 65 (2), 87-94 (2000)  
JOURNAL PUBMED 10783255  
PUBMED  
REFERENCE  
2 (bases 1 to 816)  
Genoscope.  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Direct Submission  
Submitted (05-OCT-2001) Genoscope - Centre National de Séquençage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
Partially Hind III digested and size-selected S. mansoni cercarial  
DNA was ligated into Hind III digested pBelOBAC 11 vector and used  
to transform E. coli DH10B. The complete library contains 23808  
clones from 4 independent sizing-ligation-transformations. Average  
insert size ranges from 70-127 kb and genome coverage is 7.9-fold.

```

FEATURES
Source
    location/Qualifiers
        1..816
            /organism="Schistosoma mansoni"
            /mol_type="genomic DNA"
            /strain="Puerto-Rican"
            /db_xref="taxon:6183"
            /clone="023BD07"
            /clone_1ib="SmBAC1"
            /note="Tend : T7"

ORIGIN

Query Match      1.3%, Score 42.4; DB 11; Length 816;
Best Local Similarity 35.8%; Pred. No. 2.7;
Matches 81; Conservative 41; Mismatches 104; Indels 0; Gaps 0;

QY      1375 TTATCAGAGAAATTCTTCATATACAAGATTCTCAAGTAATAATTAACAGGCAATCTTGATAT 1434
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       536 TTACAGAAAAAANNTATATATATATATTAATATAMAAAATMATAMAAAAATATATATATAT 477

QY      1435 CTCACAGAGCTGGGAATGCACAACATCGATCAGTAATCCCTTTGAATAAGTTAGAGA 1494
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       476 ATATATATATAAAAATTAAMWATATATTAATTTGTMTATATAAAGMMAAAAAAAAAAAAAAN 417

QY      1495 AAGCAACAGAAAATCTAGCAACATGCTAAATGTCAAACCTGACTAGCACATCGCTCATTAAC 1554
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       416 AAAAAAAAAAYADAATATAMAAAAAAAAAAAAAAAAAAAAAAYANHABVHBYVVYGYYSY 357

QY      1555 CTATATCGTTTTGACTATCATATATCTCTGTTTTTGGTAACTTAGC 1600
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db       356 YGYBYVKYTKYTGTGTTGKTGKGTGTGBCBCKMGWGAGC 311

RESULT 14
LOCUS      CKJ35184/c
DEFINITION H3150E07-5 N1A Mouse 15K cDNA Clone Set Mus musculus CDNA clone
VERSION     CKJ35184
KEYWORDS    CKJ35184.1 GI:40290797
SOURCE      EST.
ORGANISM    Mus musculus (house mouse)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 651)
AUTHORS     Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X.,
            Grabovac,M.J., Pantano,S., Sano,Y., plao,Y., Nagarsja,R., Dol,H.,
            Wood,W.H. III, Becker,K.G. and Ko,M.S.H.
TITLE       Genome-wide expression profiling of mid-gestation placenta and
            embryo using a 15,000 mouse developmental CDNA microarray
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
COMMENT     10922068
            Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@igsun.gfc.nia.nih.gov
            Plate: H3150 row: E column: 07
            Seq primer: M13 Reverse
            High quality sequence stop: 651
            POLYA=No.

FEATURES
Source
    location/Qualifiers
        1..651
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="C57BL/6J"
            /db_xref="nabst:H3150E07-5"
            /db_xref="taxon:10090"
            /clone="H3150E07"
            /sex="Clones arrayed from a variety of cDNA libraries"
            /dev_stage="Clones arrayed from a variety of cDNA
            libraries"

```

/lab nosc="Dh10B"  
 /clone lib="NIA Mouse 15K CDNA Clone Set"  
 /note=vector: pSPORT1, Site 1: SalI; site 2: NotI; This  
 clone is among a retrieved set of 15,247 clones from 11  
 embryo cDNA libraries (including preimplantation stage  
 embryos from unfertilized egg to blastocyst, embryonic  
 part of E7.5 embryos, extraembryonic part of E7.5  
 embryos, and E12.5 female mesonephros/gonad) and one  
 newborn ovary cDNA library. Average insert size 1.5 kb.  
 All source libraries are cloned unidirectionally with  
 Oligo(dT)-Not primers. References include: (1)  
 Genome-wide expression profiling of mid-gestation  
 placenta and embryo using a 15,000 mouse developmental  
 cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97:  
 9127-9132; (2) Large-scale cDNA analysis reveals phased  
 gene expression patterns during preimplantation mouse  
 development, 2000, Development, 127: 1737-1749; (3)  
 Genome-wide mapping of unselected transcripts from  
 extraembryonic tissue of 7.5-day mouse embryos reveals  
 enrichment in the t-complex and under-representation on  
 the X chromosome, 1998, Hum Mol Genet 7: 1967-1978. "



**TITLE**  
**JOURNAL**  
**PUBMED**  
**COMMENT**

well, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carinici, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aikawa, K., Arikawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 12466851  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/

Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watabiki, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

**FEATURES**  
**source**

Location/Qualifiers  
 1..687  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="F430213110"  
 /tissue\_type="spleen"  
 /dev\_stage="6 days neonate"  
 /clone\_lib="RIKEN full-length enriched, 6 days neonate spleen"

**ORIGIN**

Query Match 1.3% Score 42; DB 5; Length 687;  
 Best Local Similarity 53.7% Pred. No. 3.3; Indels 0; Gaps 0;  
 Matches 87; Conservative 0; Mismatches 75;  
 511 AGAGAGCATTCGCCGACCAATGAGCTGTGCATGAGTCAAGATTAATGCAACT 570  
 360 AAAGCCATGTCGAACCCACACGATGTAAGATCACTGCTGCTCCTGAACCG 301  
 571 AGCACTGCAGTTGGAGATGACAGCTTTGTATATGACCAATTAATAAAGCTCA 630  
 300 TCCATATGACTTGAGAAATTCGAAGTTCTTCTTGCAAGAAATTAATTTCTCCT 241  
 631 GGAATTAGCTGCATCAAAATGACAGCAAGTGGTGTAGA 672

Db 240 GGAAGTTTACACACTGGAAGTGAACGCCAGTGGTAAAGA 199  
 Search completed: February 5, 2006, 06:20:47  
 Job time : 12647 secs

100-156000-100